

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 20, 2002, 10:35:59 ; Search time 228.86 Seconds
(without alignments)
13.589 Million cell updates/sec

Title: US-09-544-664-55
Perfect score: 148
Sequence: 1 KNLMAQRKRGRLRMHSDPEFGSKGLK 28

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802:*

- 1: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1980.DAT:*
- 2: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1981.DAT:*
- 3: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1982.DAT:*
- 4: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1983.DAT:*
- 5: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1984.DAT:*
- 6: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1985.DAT:*
- 7: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1986.DAT:*
- 8: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1987.DAT:*
- 9: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1988.DAT:*
- 10: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1989.DAT:*
- 11: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1990.DAT:*
- 12: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1991.DAT:*
- 13: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1992.DAT:*
- 14: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1993.DAT:*
- 15: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1994.DAT:*
- 16: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1995.DAT:*
- 17: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1996.DAT:*
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- 19: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1998.DAT:*
- 20: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1999.DAT:*
- 21: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA2000.DAT:*
- 22: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	148	100.0	28	21	AA1980
2	143	96.6	27	21	AA1981
3	138	93.2	26	21	AA1982
4	138	93.2	26	21	AA1983
5	138	93.2	26	21	AA1984
6	138	93.2	26	21	AA1985
7	138	93.2	26	21	AA1986
8	138	93.2	26	21	AA1987
9	138	93.2	26	21	AA1988
10	138	93.2	26	21	AA1989
11	138	93.2	26	21	AA1990

12	138	93.2	204	19	AA1991
13	138	93.2	204	22	AA1992
14	138	93.2	204	22	AA1993
15	138	93.2	204	22	AA1994
16	138	93.2	204	22	AA1995
17	138	93.2	204	22	AA1996
18	138	93.2	204	22	AA1997
19	138	93.2	204	22	AA1998
20	138	93.2	204	22	AA1999
21	138	93.2	204	22	AA2000
22	138	93.2	204	22	AA2001
23	138	93.2	204	22	AA2002
24	138	93.2	204	22	AA2003
25	138	93.2	204	22	AA2004
26	138	93.2	204	22	AA2005
27	138	93.2	204	22	AA2006
28	138	93.2	204	22	AA2007
29	138	93.2	204	22	AA2008
30	138	93.2	204	22	AA2009
31	138	93.2	204	22	AA2010
32	138	93.2	204	22	AA2011
33	138	93.2	204	22	AA2012
34	138	93.2	204	22	AA2013
35	138	93.2	204	22	AA2014
36	138	93.2	204	22	AA2015
37	138	93.2	204	22	AA2016
38	138	93.2	204	22	AA2017
39	138	93.2	204	22	AA2018
40	138	93.2	204	22	AA2019
41	138	93.2	204	22	AA2020
42	138	93.2	204	22	AA2021
43	138	93.2	204	22	AA2022
44	138	93.2	204	22	AA2023
45	138	93.2	204	22	AA2024

ALIGNMENTS

RESULT 1

AA1980

AA1981

AA1982

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AA2715

PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for
 PT treating neurodegenerative disorders, stroke, or cancer

Claim 18; Page 19; 74pp; English.

CC The invention relates to a peptide conjugate having the formula:
 CC (R-X)n-peptide where n = 1-10; x = C=O, when the R-X group is attached
 CC to the N-terminus of the peptide, or a side chain of the peptide where
 CC the functional group of the side chain is NH2 or OH; or x = O or NH.
 CC When the R-X group is attached to the C-terminus of the peptide, or a
 CC side chain of the peptide, where the side chain functional group is COOH
 CC or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkenyl optionally
 CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain
 CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples
 CC of the peptide portion of the conjugate. The peptides represent analogues
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of
 CC the Bcl-2 domain of the cell death agonist Bad. The peptide conjugate is
 CC useful for modulating apoptosis in the cells of a subject, or for
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockade of
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2
 CC function. In particular, the peptide conjugate is useful for treating a
 CC subject afflicted with a cancer characterized by cancer cells that
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric,
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
 CC conjugate is also useful for treating disorders characterized by
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.

Sequence 28 AA:

Query Match 100.0%; Score 148; DB 21; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1e-15; Mismatches 0;
 Matches 28; Conservative 0; Indels 0; Gaps 0;

OY 1 KNLMAAQRGRLRMSDEFGSFKGLK 28
 ||||||||||||||||||||||||
 Db 1 knlwaagrygrelrmsdelegsfkglk 28

RESULT 2
 AAB37056
 ID AAB37056 standard; peptide: 27 AA.

AC AAB37056;

DT 28-FEB-2001 (first entry)

DE Bcl2 polypeptide BH3 domain peptide #56.

KW Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;
 KW cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;
 KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;
 KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;
 KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
 KW stroke; myocardial infarction.

OS Homo sapiens.

PN W0200059526-A1.

PD 12-OCT-2000.

PP 06-APR-2000; 2000WO-US09352.

PR 07-APR-1999; 99US-0128202.

PA (UYJE-) UNIV JEFFERSON THOMAS.

XX Huang Z, Wang J, Zhang Z, Shan S, Lu Z;

XX WPI; 2000-679325/66.

DR New peptide conjugates for modulating apoptosis or for inhibiting B
 XX cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for
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Claim 18; Page 19; 74pp; English.

CC The invention relates to a peptide conjugate having the formula:
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 CC to the N-terminus of the peptide, or a side chain of the peptide where
 CC the functional group of the side chain is NH2 or OH; or x = O or NH,
 CC when the R-X group is attached to the C-terminus of the peptide, or a
 CC side chain of the peptide, where the side chain functional group is COOH
 CC or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkenyl optionally
 CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally
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 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockade of
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 CC function. In particular, the peptide conjugate is useful for treating a
 CC subject afflicted with a cancer characterized by cancer cells that
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 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
 CC conjugate is also useful for treating disorders characterized by
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.

Sequence 27 AA:

Query Match 96.6%; Score 143; DB 21; Length 27;
 Best Local Similarity 100.0%; Pred. No. 5.7e-15;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KNLMAAQRGRLRMSDEFGSFKGL 27
 ||||||||||||||||||||||||
 Db 1 knlwaagrygrelrmsdelegsfkgl 27

RESULT 3
 AAB37001
 ID AAB37001 standard; peptide: 26 AA.

AC AAB37001;

DT 28-FEB-2001 (first entry)

DE Bcl2 polypeptide BH3 domain peptide #1.

KW Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;
 KW cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;
 KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;
 KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;
 KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
 KW stroke; myocardial infarction.

OS Homo sapiens.

PN W0200059526-A1.

PD 12-OCT-2000.

PP 06-APR-2000; 2000WO-US09352.

PR 07-APR-1999; 99US-0128202.

XX (UYJE-) UNIV JEFFERSON THOMAS.
 PA Huang Z, Wang J, Zhang Z, Shan S, Lu Z;
 PI WPI: 2000-679325/66.
 DR
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 PT New peptide conjugates for modulating apoptosis or for inhibiting B
 PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for
 PT treating neurodegenerative disorders, stroke, or cancer
 PS
 PS Claim 18; Page 17; 74pp; English.
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 CC when the R-X group is attached to the C-terminus of the peptide, or a
 CC side chain of the peptide, where the side chain functional group is COOH
 CC or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one
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 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
 CC conjugate is also useful for treating disorders characterized by
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
 CC
 CC Sequence 26 AA:
 SQ
 Query Match 93.2%; Score 138; DB 21; Length 26;
 Best Local Similarity 100.0%; Pred. No. 3.2e-14;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 NIMAAQRYGRELRRMSDEFGSFKGL 27
 ||||||||||||||||||||
 DB 1 nlwaagrygrelrrmsdefgsfkgl 26
 RESULT 4
 AAB37002 standard; peptide; 26 AA.
 ID AAB37002:
 AC AAB37002:
 XX
 DT 28-FEB-2001 (first entry)
 XX
 DE Bcl2 polypeptide B3 domain peptide #2.
 XX
 KW Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;
 KW cardiant; Bcl-2 superfamily; B3 domain; cell death agonist; Bad;
 KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;
 KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;
 KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
 KW stroke; myocardial infarction.
 XX
 OS Homo sapiens.
 XX
 PN WO200059526-A1.
 XX
 PD 12-OCT-2000.

XX 06-APR-2000: 2000MO-US09352.
 PF
 PR 07-APR-1999: 99US-0128202.
 XX
 XX (UYJE-) UNIV JEFFERSON THOMAS.
 PA Huang Z, Wang J, Zhang Z, Shan S, Lu Z;
 PI WPI: 2000-679325/66.
 DR
 XX
 PT New peptide conjugates for modulating apoptosis or for inhibiting B
 PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for
 PT treating neurodegenerative disorders, stroke, or cancer
 PS
 PS Claim 18; Page 17; 74pp; English.
 XX
 CC The invention relates to a peptide conjugate having the formula:
 CC (R-X)n-peptide where n = 1-10; X = C=O, when the R-X group is attached
 CC to the N-terminus of the peptide, or a side chain of the peptide where
 CC the functional group of the side chain is NH2 or OH; or X = O or NH,
 CC when the R-X group is attached to the C-terminus of the peptide, or a
 CC side chain of the peptide, where the side chain functional group is COOH
 CC or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one
 CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain
 CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples
 CC of the peptide portion of the conjugate. The peptides represent analogues
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of
 CC the B3 domain of the cell death agonist Bad. The peptide conjugate is
 CC useful for modulating apoptosis in the cells of a subject, or for
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2
 CC function. In particular, the peptide conjugate is useful for treating a
 CC subject afflicted with a cancer characterized by cancer cells that
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric,
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
 CC conjugate is also useful for treating disorders characterized by
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
 CC
 CC Sequence 26 AA:
 SQ
 Query Match 93.2%; Score 138; DB 21; Length 26;
 Best Local Similarity 100.0%; Pred. No. 3.2e-14;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 NIMAAQRYGRELRRMSDEFGSFKGL 27
 ||||||||||||||||||||
 DB 1 nlwaagrygrelrrmsdefgsfkgl 26
 RESULT 5
 AAB37003 standard; peptide; 27 AA.
 ID AAB37003:
 AC AAB37003:
 XX
 DT 28-FEB-2001 (first entry)
 XX
 DE Bcl2 polypeptide B3 domain peptide #3.
 XX
 KW Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;
 KW cardiant; Bcl-2 superfamily; B3 domain; cell death agonist; Bad;
 KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;
 KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;
 KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
 KW stroke; myocardial infarction.
 XX
 OS Homo sapiens.

XX WO200059526-A1.
 XX 12-OCT-2000.
 XX 06-APR-2000; 2000WO-US09352.
 XX 07-APR-1999; 99US-0128202.
 XX (UYJE-) UNIV JEFFERSON THOMAS.
 XX Huang Z, Wang J, Zhang Z, Shan S, Lu Z;
 XX WPI: 2000-679325/66.
 XX
 XX New peptide conjugates for modulating apoptosis or for inhibiting B
 XX cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for
 XX treating neurodegenerative disorders, stroke, or cancer -
 XX
 XX Claim 18: Page 17: 74pp: English.

XX The invention relates to a peptide conjugate having the formula:
 CC (R-X)_n-peptide where n = 1-10; X = C-O, when the R-X group is attached
 CC to the N-terminus of the peptide, or a side chain of the peptide where
 CC the functional group of the side chain is NH₂ or OH; or X = O or NH,
 CC when the R-X group is attached to the C-terminus of the peptide, or a
 CC side chain of the peptide, where the side chain functional group is COOH
 CC or CONH₂; and R = 2-18C alkyl or alkoxy, 2-14C alkenyl containing one
 CC or two double bonds; cyclobutyl, cyclopentyl, cyclohexyl optionally
 CC monosubstituted with a 1-3C straight or branched chain alkyl group,
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain
 CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples
 CC of the peptide portion of the conjugate. The peptides represent analogues
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of
 CC the BH3 domain of the cell death agonist Bad. The peptide conjugate is
 CC useful for modulating apoptosis in the cells of a subject, or for
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2
 CC function. In particular, the peptide conjugate is useful for creating a
 CC subject afflicted with a cancer characterized by cancer cells that
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric, or
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
 CC conjugate is also useful for treating disorders characterized by
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
 XX
 XX Sequence 27 AA:

Query Match 93.2%; Score 138; DB 21; Length 27;
 Best Local Similarity 100.0%; Pred. No. 3, 4e-14;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NMAAORYGRELRRMSDEPGSFKGL 27
 DB 1 nlwaagrygrellrmsdefgsfkyl 26

RESULT 6
 AAB70370
 ID AAB70370 standard; Protein: 162 AA.
 AC AAB70370;
 DT 02-MAY-2001 (first entry)
 XX Shorter murine BAD mutant amino acid sequence SEQ ID NO:3.
 XX
 XX Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;
 XX immunostimulant; neuroprotective; neurotropic; antischismatic; vlnetary;
 XX cytostatic; antiviral; antiarthritic; antiinflammatory; wound healing;
 XX immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;
 KW

KW immunodeficiency disease; neurodegenerative disease; viral infection;
 KW ischaemic cell death; reperfusion cell death; arthritis; infertility;
 KW lymphoproliferative condition; inflammation; autoimmune disease.
 XX
 XX Mus musculus.
 XX Synthetic.
 XX WO200110888-A1.
 XX 15-FEB-2001.
 XX 30-MAY-2000; 2000WO-US11864.
 XX 28-MAY-1999; 99US-0136783.
 XX (APOP-) APOPTOSIS TECHNOLOGY INC.
 XX Zhou X;
 XX WPI: 2001-138734/14.
 XX
 XX New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,
 XX useful for screening for candidate compounds which induce or inhibit
 XX apoptosis, comprises amino acid substitutions at Ser118, Ser155 or
 XX Ser113 -
 XX
 XX Claim 7: Page 148-149; 157pp: English.

XX The present invention describes an isolated or synthetic polypeptide
 CC (I) comprising a less than full length amino acid sequence of a mutant
 CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its
 CC fragment, which contains amino acid substitutions at Ser118 of a human
 CC BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine
 CC BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective,
 CC neurotropic, antischismatic, vulnerable, cytostatic, antiviral,
 CC antarthritic, antiinflammatory and immunosuppressive activities, and
 CC can be used as an apoptosis inducer or inhibitor. BAD polypeptides and
 CC polynucleotides can be used for screening candidate compounds and drugs
 CC for activity that promote cell survival or apoptosis. Other uses include
 CC inducing or inhibiting apoptosis in a cell. Candidate compounds
 CC identified and (mutant) BAD polypeptides are useful in treating
 CC immunodeficiency diseases, neurodegenerative diseases, ischaemic cell
 CC death, reperfusion cell death, wound healing, cancer, viral infections,
 CC lymphoproliferative conditions, arthritis, infertility, inflammation and
 CC autoimmune diseases. The present sequence represents a specifically
 CC claimed shorter murine BAD mutant amino acid sequence from the present
 CC invention.
 XX
 XX Sequence 162 AA:

Query Match 93.2%; Score 138; DB 22; Length 162;
 Best Local Similarity 100.0%; Pred. No. 2, 4e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NMAAORYGRELRRMSDEPGSFKGL 27
 DB 98 nlwaagrygrellrmsdefgsfkyl 123

RESULT 7
 AAR95168
 ID AAR95168 standard; Protein: 204 AA.
 AC AAR95168;
 DT 06-JAN-1997 (first entry)
 XX bcl-x(L)/bcl-2 associated death promoter protein.
 XX
 XX Epitope: murine; bcl-x(L)/bcl-2 associated death promoter; Bad; stroke;
 XX polypeptide; bcl-x; cell death; regulate; BH1; BH2; apoptotic cell death;
 KW cytokine deprivation; IL-3 dependent cell line; immunodeficiency; AIDS;

XX serine substituted mutant; apoptosis; cancer; viral infection.
XX Mus sp.
OS Synthetic.
XX MO9817682-A1.
XX
XX 30-APR-1998.
XX
XX 17-OCT-1997; 97MO-US19175.
XX
XX 18-OCT-1996; 960S-0733505.
XX
XX (UNIW) UNIV WASHINGTON.
XX
XX Korsmeyer SJ;
XX WPI: 1998-261422/23.
XX N-PSDB: AAV27834.
XX
XX New mutant BAD polypeptide with phosphorylatable serine replaced -
PT useful for, e.g. treating reduced apoptosis such as in cancer or
PT viral infection
XX
XX Claim 7; Page 59; 95pp; English.
XX
XX The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
CC death regulator) proteins, having an amino acid other than Ser at
CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
CC present sequence represents a mutant BAD protein. Also described are: (1)
CC fragments of mutant BAD protein able to decrease cell viability; (2)
CC fusion proteins of mutant BAD with a heterologous polypeptide that
CC increases intracellular delivery. Mutant BAD proteins are used to treat
CC or prevent diseases associated with reduced apoptosis, e.g. cancer,
CC viral infection, lymphoproliferation, arthritis, infertility,
CC inflammation and autoimmune disease. Polynucleotide sequences encoding
CC mutant BAD proteins can be used similarly by gene therapy or to produce
CC transgenic animals for use as disease models or in drug screening. BAD
CC proteins phosphorylated at specified Ser are used to screen for enhancers
CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful
CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,
CC aging or ischemic cell death. The apoptotic status of cells is
CC determined by measuring relative amounts of phosphorylated and non-
CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
CC greater death-promoting activity than wild-type BAD which can become
CC phosphorylated on the specified Ser, forming a product that does not
CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family
CC proteins in the cytosol, thus promoting cell survival. The mutants with
CC Ser substituted cannot bind 14-3-3.
XX
XX Sequence 204 AA:
SQ

Query Match 93.2%; Score 138; DB 19; Length 204;
Best Local Similarity 100.0%; Pred. No. 3.2e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NLNAAORYGRELRLMSDEFGSKFL 27
Db 140 nlwaagrygrelrlmsdeffgskfl 165

RESULT 10
AAW61317
ID AAW61317 standard; Protein: 204 AA.
XX
XX AAW61317;
AC
XX
XX 07-OCT-1998 (first entry)
XX
XX Mutant BCL-XL/BCL-2 associated cell death regulator #2.
XX
XX Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;

XX serine substituted mutant; apoptosis; cancer; viral infection.
XX Mus sp.
OS Synthetic.
XX MO9817682-A1.
XX
XX 30-APR-1998.
XX
XX 17-OCT-1997; 97MO-US19175.
XX
XX 18-OCT-1996; 960S-0733505.
XX
XX (UNIW) UNIV WASHINGTON.
XX
XX Korsmeyer SJ;
XX WPI: 1998-261422/23.
XX N-PSDB: AAV27835.
XX
XX New mutant BAD polypeptide with phosphorylatable serine replaced -
PT useful for, e.g. treating reduced apoptosis such as in cancer or
PT viral infection
XX
XX Claim 7; Page 60; 95pp; English.
XX
XX The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
CC death regulator) proteins, having an amino acid other than Ser at
CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
CC present sequence represents a mutant BAD protein. Also described are: (1)
CC fragments of mutant BAD protein able to decrease cell viability; (2)
CC fusion proteins of mutant BAD with a heterologous polypeptide that
CC increases intracellular delivery. Mutant BAD proteins are used to treat
CC or prevent diseases associated with reduced apoptosis, e.g. cancer,
CC viral infection, lymphoproliferation, arthritis, infertility,
CC inflammation and autoimmune disease. Polynucleotide sequences encoding
CC mutant BAD proteins can be used similarly by gene therapy or to produce
CC transgenic animals for use as disease models or in drug screening. BAD
CC proteins phosphorylated at specified Ser are used to screen for enhancers
CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful
CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,
CC aging or ischemic cell death. The apoptotic status of cells is
CC determined by measuring relative amounts of phosphorylated and non-
CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
CC greater death-promoting activity than wild-type BAD which can become
CC phosphorylated on the specified Ser, forming a product that does not
CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family
CC proteins in the cytosol, thus promoting cell survival. The mutants with
CC Ser substituted cannot bind 14-3-3.
XX
XX Sequence 204 AA:
SQ

Query Match 93.2%; Score 138; DB 19; Length 204;
Best Local Similarity 100.0%; Pred. No. 3.2e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NLNAAORYGRELRLMSDEFGSKFL 27
Db 140 nlwaagrygrelrlmsdeffgskfl 165

RESULT 11
AAW61318
ID AAW61318 standard; Protein: 204 AA.
XX
XX AAW61318;
AC
XX
XX 07-OCT-1998 (first entry)
XX
XX Mutant BCL-XL/BCL-2 associated cell death regulator #3.
XX
XX Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;

KM serine substituted mutant; apoptosis; cancer; viral infection.
 XX Mus sp.
 OS Synthetic.
 XX MO9817682-A1.
 PN 30-APR-1998.
 XX 17-OCT-1997; 97WO-US19175.
 XX 18-OCT-1996; 96US-0733505.
 PR (UNITV) UNIV WASHINGTON.
 XX Kormeyer SJ;
 PI WPI: 1998-261422/23.
 DR N-PSDB; NAAV27836.
 XX New mutant BAD polypeptide with phosphorylatable serine replaced
 PT useful for, e.g. treating reduced apoptosis such as in cancer or
 PT viral infection
 PS Claim 7; Page 60-61; 95pp; English.
 XX The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
 CC death regulator) proteins, having an amino acid other than Ser at
 CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
 CC present sequence represents a mutant BAD protein. Also described are: (1)
 CC fragments of mutant BAD protein able to decrease cell viability; (2)
 CC fusion proteins of mutant BAD with a heterologous polypeptide that
 CC increases intracellular delivery. Mutant BAD proteins are used to treat
 CC or prevent diseases associated with reduced apoptosis, e.g. cancer,
 CC viral infection, lymphoproliferation, arthritis, infertility,
 CC inflammation and autoimmune disease. Polynucleotide sequences encoding
 CC mutant BAD proteins can be used similarly by gene therapy or to produce
 CC transgenic animals for use as disease models or in drug screening. BAD
 CC proteins phosphorylated at specified Ser are used to screen for enhancers
 CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful
 CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,
 CC aging or ischemic cell death. The apoptotic status of cells is
 CC determined by measuring relative amounts of phosphorylated and non-
 CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
 CC greater death-promoting activity than wild-type BAD proteins and non-
 CC phosphorylated on the specified Ser, forming a product that does not
 CC heterodimerize with BCL-2 or BCL-XL but instead binds to 14-3-3 family
 CC proteins in the cytosol, thus promoting cell survival. The mutants with
 CC Ser substituted cannot bind 14-3-3.
 XX Sequence 204 AA:
 SO
 Query Match 93.2%; Score 138; DB 19; Length 204;
 Best Local Similarity 100.0%; Pred. No. 3.2e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 NLMAAQRVGRRLRRMSDEFGSFKGL 27
 Db 140 nlwaagrygrlrrmsdefgsfkgl 165
 RESULT 12
 ID AAM58832 standard; protein; 204 AA.
 XX AAM58832:
 AC AAM58832:
 XX 23-JUL-1998 (first entry)
 XX Murine BAD protein.
 DE Murine BAD protein.
 XX BAD protein; Bcl-XL/Bcl-2 associated cell death regulator; 14-3-3;

KM serine phosphorylation; post-translational modification; apoptosis;
 KM signal transduction regulator; phosphoserine phosphatase; senescence;
 KM immunodeficiency disease; neurodegenerative disease; infertility;
 KM cancer; viral infection; lymphoproliferative condition; arthritis;
 KM inflammation; autoimmune diseases.
 XX Mus sp.
 OS MO9809643-A1.
 PN 12-MAR-1998.
 XX 09-SEP-1997; 97WO-US15871.
 XX 09-SEP-1996; 96US-0707868.
 PR (UNITV) UNIV WASHINGTON.
 XX Kormeyer SJ;
 PI WPI: 1998-207049/18.
 DR Serine-phosphorylated Bcl-XL/Bcl-2 Associated cell death regulator
 XX polypeptide - useful for modulation of apoptosis associated with,
 PT e.g. cancer and immunodeficiency diseases
 PT Claim 3; Fig 8; 61pp; English.
 XX This sequence represents a novel serine-phosphorylated protein, BAD
 CC (Bcl-XL/Bcl-2 associated cell death regulator). The serine residue is
 CC phosphorylated in a post-translational modification and allows binding
 CC to the 14-3-3 protein which is a signal transduction regulator.
 CC Modulators of serine-phosphatase are useful for preventing/treating
 CC of a phosphoserine phosphatase. BAD, which act through inhibition/activation
 CC increased/decreased apoptosis in a cell. The increased apoptosis may
 CC result from immunodeficiency diseases, senescence, neurodegenerative
 CC disease, ischemic cell death, reperfusion cell death, infertility and
 CC wound-healing. Decreased apoptosis may result from cancer, viral
 CC infection, lymphoproliferative conditions, arthritis, infertility,
 CC inflammation and autoimmune diseases. Measuring the amount of
 CC phosphorylated and compared to unphosphorylated BAD polypeptide and/or total
 CC BAD in a cell is useful for determining the apoptotic state of a cell.
 XX Sequence 204 AA:
 SO
 Query Match 93.2%; Score 138; DB 19; Length 204;
 Best Local Similarity 100.0%; Pred. No. 3.2e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 NLMAAQRVGRRLRRMSDEFGSFKGL 27
 Db 140 nlwaagrygrlrrmsdefgsfkgl 165
 RESULT 13
 ID AAB70369 standard; protein; 204 AA.
 XX AAB70369:
 AC AAB70369:
 XX 02-MAY-2001 (first entry)
 XX Longer murine BAD mutant amino acid sequence seq ID NO:2.
 XX Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;
 KM immunostimulant; neuroprotective; neurotropic; antischismatic; vulnary;
 KM cytosolic; antiviral; antiarthritic; antiinflammatory; wound healing;
 KM immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;
 KM immunodeficiency disease; neurodegenerative disease; viral infection;
 KM ischemic cell death; reperfusion cell death; arthritis; infertility;
 KM lymphoproliferative condition; inflammation; autoimmune disease.
 XX

OS	Mus musculus.
XX	Synthetic.
PN	MO200110868-A1.
XX	
PD	15-FEB-2001.
XX	
PE	30-MAY-2000; 200OWO-US1864.
PR	28-MAY-1999; 99US-0136783.
PA	(APOP-) APOPTOSIS TECHNOLOGY INC.
PI	Zhou X;
DR	WPI: 2001-138734/14.
XX	
FT	New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,
P7	useful for screening for candidate compounds which induce or inhibit
P7	apoptosis, comprises amino acid substitutions at Ser118, Ser155 or
P7	Ser113 .
XX	
PS	Claim 4; Page 148; 157pp; English.
XX	
CC	The present invention describes an isolated or synthetic polypeptide
CC	(1) comprising a less than full length amino acid sequence of a mutant
CC	Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its
CC	fragment, which contains amino acid substitutions at Ser118 of a human
CC	BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine
CC	BAD (shorter murine BAD). (1) has immunostimulant, neuroprotective,
CC	neotropic, antischismic, vulnerary, cytoskeletal, antiviral,
CC	antiallergic, antiinflammatory and immunosuppressive activities, and
CC	can be used as an apoptosis inducer or inhibitor. BAD polypeptides and
CC	polynucleotides can be used for screening candidate compounds and drugs
CC	for activity that promote cell survival or apoptosis. Other uses include
CC	inducing or inhibiting apoptosis in a cell. Candidate compounds
CC	identified and (mutant) BAD polypeptides are useful in treating
CC	immunodeficiency diseases, neurodegenerative diseases, ischaemic cell
CC	death, reperfusion cell death, wound healing, cancer, viral infections,
CC	lymphoproliferative conditions, arthritis, infertility, inflammation and
CC	autoimmune diseases. The present sequence represents a specifically
CC	claimed longer murine BAD mutant amino acid sequence from the present
CC	invention.
XX	
SQ	Sequence 204 AA:
XX	
Query Match	93.2%; Score 138; DB 22; Length 204;
Best Local Similarity	100.0%; Pred. No. 3, 2e-13;
Matches 26; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	2 NLNAAQRYGRELFRMSDEFEGSKGL 27
	(((((((((((((((((((((((((((((
	140 nlwaaqrygyrelfrmsdefegskgl 165
RESULT 14	
AAU00220	standard; Protein: 567 AA.
XX	
AAU00220:	
XX	
DT	31-MAY-2001 (first entry)
XX	
DE	Bad-DTRR apoptosis-modifying fusion protein.
XX	
KW	Mouse; Bad-DTRR: apoptosis; cancer; spinal muscular atrophy;
KW	diphtheria toxin receptor binding domain; DTR: neoplasm; tumour;
KW	hyper-proliferation; Alzheimer's disease; neurodegenerative disorder;
KW	transient ischaemic neuronal injury; stroke; spinal cord injury;
KW	Huntington's disease.
XX	
OS	Chimeric - Mus sp.

[illegible]

XX BRC6 gene; cell death; cell cycle; Bcl2; human.
 KW Homo sapiens.
 OS
 XX US5663316-A.
 XX
 PN 02-SEP-1997.
 XX
 PD 18-JUN-1996; 96US-0665617.
 XX
 PF 18-JUN-1996; 96US-0665617.
 XX
 PR 18-JUN-1996; 96US-0665617.
 XX
 PA (CLON-) CLONTECH LAB INC.
 XX
 PI Xudong Y;
 XX
 DR WPI: 1997-447980/41.
 XX
 DR N-PSDB; AAT91561.
 XX
 PT Isolated BRC6 gene - encodes a protein that regulates cell death
 PT through interaction with Bcl-2
 XX
 PS Claim 1; Column 11-12; 7pp; English.
 XX
 CC The present sequence represents a protein of 166 amino acids. The
 CC sequence is disclosed as being a protein called BRC6 which regulates
 CC cell death through interaction with Bcl-2. The DNA may be used for the
 CC production of the recombinant protein, which can be used in unspecified
 CC therapeutic or diagnostic procedures, as a molecular weight marker, and
 CC to raise antibodies that can be used in unspecified diagnostic or
 CC therapeutic applications and to reduce or eliminate the biological
 CC activity of the BRC6 protein in vivo.
 XX
 SQ Sequence 166 AA;

Query Match 77.0%; Score 114; DB 18; Length 166;
 Best Local Similarity 91.7%; Pred. No. 1.2e-09;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 2 NLWAAORYGRELRLMSDEFGSFK 25
 Db 101 nlwaagrygreilrmsdeltvstik 124

Search completed: September 20, 2002, 10:35:59
 Job time: 427 sec

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OM protein - protein search, using sw model

Run on: September 20, 2002, 10:37:21 : Search time 75.64 Seconds
(without alignments)
9.042 Million cell updates/sec

Title: US-09-544-664-55

Perfect score: 148

Sequence: 1 KNLMAGRGRELRMSDEFFSGFKLK 28

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents, AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	138	93.2	204	1 US-08-333-565-2	Sequence 2, Appl
2	138	93.2	204	2 US-08-661-479-2	Sequence 2, Appl
3	138	93.2	204	2 US-08-733-505A-1	Sequence 1, Appl
4	138	93.2	204	2 US-08-733-505A-12	Sequence 13, Appl
5	138	93.2	204	2 US-08-733-505A-13	Sequence 13, Appl
6	138	93.2	204	2 US-08-733-505A-14	Sequence 3, Appl
7	135	91.2	204	2 US-08-717-123-3	Sequence 2, Appl
8	114	77.0	168	1 US-08-665-617-2	Sequence 2, Appl
9	114	77.0	168	2 US-08-717-123-2	Sequence 2, Appl
10	114	77.0	168	3 US-08-985-335-1	Sequence 1, Appl
11	114	77.0	168	3 US-08-985-335-7	Sequence 1, Appl
12	114	77.0	168	3 US-09-410-372-1	Sequence 7, Appl
13	114	77.0	168	4 US-09-410-372-7	Sequence 7, Appl
14	113	76.4	23	1 US-08-333-565-10	Sequence 10, Appl
15	113	76.4	23	2 US-08-661-479-10	Sequence 10, Appl
16	102	68.9	59	2 US-08-733-505A-55	Sequence 55, Appl
17	102	68.9	59	2 US-08-733-505A-56	Sequence 56, Appl
18	102	68.9	59	2 US-08-733-505A-57	Sequence 57, Appl
19	102	68.9	59	2 US-08-733-505A-58	Sequence 58, Appl
20	86	58.1	16	1 US-08-333-565-26	Sequence 26, Appl
21	86	58.1	16	1 US-08-661-479-26	Sequence 26, Appl
22	61	41.2	11	2 US-08-733-505A-34	Sequence 69, Appl
23	61	41.2	11	2 US-08-706-741B-69	Sequence 69, Appl
24	61	41.2	11	2 US-08-924-695A-69	Sequence 40, Appl
25	51	34.5	66	3 US-08-867-087B-40	Sequence 3, Appl
26	46	31.1	946	4 US-09-324-542-94	Sequence 94, Appl
27	46	31.1	946	4 US-09-324-542-94	Sequence 94, Appl

28	44	29.7	263	4	US-09-651-656-27	Sequence 27, Appl
29	43	29.1	81	1	US-08-497-312-19	Sequence 19, Appl
30	43	29.1	213	3	US-08-718-738-18	Sequence 18, Appl
31	43	29.1	213	4	US-09-221-844-18	Sequence 18, Appl
32	43	29.1	380	1	US-08-153-848-40	Sequence 40, Appl
33	43	29.1	380	3	US-09-299-843A-40	Sequence 40, Appl
34	43	29.1	380	4	US-09-088-337B-40	Sequence 40, Appl
35	42	28.4	380	5	PCT-US93-11153-40	Sequence 7, Appl
36	42	28.4	322	4	US-09-359-161-7	Sequence 7, Appl
37	42	28.4	348	2	US-08-997-080-170	Sequence 170, App
38	42	28.4	348	2	US-08-997-362-170	Sequence 170, App
39	42	28.4	348	4	US-09-095-855-170	Sequence 170, App
40	42	28.4	348	4	US-09-324-542-170	Sequence 94, Appl
41	42	28.4	393	2	US-08-997-080-94	Sequence 94, Appl
42	42	28.4	393	3	US-08-997-362-94	Sequence 94, Appl
43	42	28.4	393	4	US-08-873-970-94	Sequence 94, Appl
44	42	28.4	393	3	US-09-095-855-94	Sequence 94, Appl
45	42	28.4	393	4	US-09-324-542-94	Sequence 94, Appl

ALIGNMENTS

RESULT 1
US-08-333-565-2
Sequence 2, Application US/0833565
Patent No. 5622852
GENERAL INFORMATION:
APPLICANT: KORMEYER, Stanley J.
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,565
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..204
OTHER INFORMATION: /note="Deduced amino acid sequence
OTHER INFORMATION: of mouse BAD."

Query Match 93.2% Score 138: DB 1: Length 204;
Best Local Similarity 100.0% Pred. No. 1e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 N1MAAQRVGRRLRMSDEFGSKGL 27
DB 140 N1MAAQRVGRRLRMSDEFGSKGL 165

RESULT 2
US-08-661-479-2
Sequence 2, Application US/08661479
Patent No. 5834209
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl-X/Bcl-2 ASSOCIATED CELL DEATH
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,479
FILING DATE: 11-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/333,565
FILING DATE: 31-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..204
OTHER INFORMATION: /note= "Deduced amino acid sequence
OTHER INFORMATION: of mouse BAD."
US-08-661-479-2

Query Match 93.2% Score 138: DB 2: Length 204:
Best Local Similarity 100.0% Pred. No. 1e-13: 0:
Matches 26: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
QY 2 N1MAAQRVGRRLRMSDEFGSKGL 27
DB 140 N1MAAQRVGRRLRMSDEFGSKGL 165
RESULT 3
US-08-733-505A-1
Sequence 1, Application US/08733505A
Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR

NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-733-505A-1

Query Match 93.2% Score 138: DB 2: Length 204:
Best Local Similarity 100.0% Pred. No. 1e-13:
Matches 26: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
QY 2 N1MAAQRVGRRLRMSDEFGSKGL 27
DB 140 N1MAAQRVGRRLRMSDEFGSKGL 165

RESULT 4
US-08-733-505A-12
Sequence 12, Application US/08733505A
Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:

TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-733-505A-12

Query Match 93.2%; Score 138; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 1e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NLMAAQRGRELRLMSDEFGSGKGL 27
DB 140 NLMAAQRGRELRLMSDEFGSGKGL 165

RESULT 5
US-08-733-505A-13
Sequence 13, Application US/08733505A
Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-733-505A-13

Query Match 93.2%; Score 138; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 1e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NLMAAQRGRELRLMSDEFGSGKGL 27
DB 140 NLMAAQRGRELRLMSDEFGSGKGL 165

RESULT 6

US-08-733-505A-14
Sequence 14, Application US/08733505A
Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-733-505A-14

Query Match 93.2%; Score 138; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 1e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NLMAAQRGRELRLMSDEFGSGKGL 27
DB 140 NLMAAQRGRELRLMSDEFGSGKGL 165

RESULT 7
US-08-717-123-3
Sequence 3, Application US/08717123
Patent No. 5965703
GENERAL INFORMATION:
APPLICANT: HORNE, WILLIAM A.
TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,335
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SYNORAB01
CLONE: 358673
US-08-985-335-1

Query Match 77.0%; Score 114; DB 3; Length 168;
Best Local Similarity 91.7%; Pred. No. 3.8e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 NMAAORYGRELRRMSDEFGSK 25
Db 103 NMAAORYGRELRRMSDEFGSK 126

RESULT 11
US-08-985-335-7
Sequence 7, Application US/08985335
Patent No. 6080847
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,335
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 1683637
US-08-985-335-7

Query Match 77.0%; Score 114; DB 3; Length 168;
Best Local Similarity 91.7%; Pred. No. 3.8e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 NMAAORYGRELRRMSDEFGSK 25
Db 103 NMAAORYGRELRRMSDEFGSK 126

RESULT 12
US-09-410-372-1
Sequence 1, Application US/09410372
Patent No. 6281334
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/410,372
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985,335
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SYNORAB01

CLONE: 358673
US-09-410-372-1

Query Match 77.0%; Score 114; DB 4; Length 168;
Best Local Similarity 91.7%; Pred. No. 3.8e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 NLMAAQRGRLRMSDEFGSFK 25
DB 103 NLMAAQRGRLRMSDEFGSFK 126

RESULT 13
US-09-410-372-7

Sequence 7, Application US/09410372
Patent No. 6281334
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Lai, Preci
APPLICANT: Shah, Puri
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/410,372
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985,335
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1683637
US-09-410-372-7

Query Match 77.0%; Score 114; DB 4; Length 168;
Best Local Similarity 91.7%; Pred. No. 3.8e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 NLMAAQRGRLRMSDEFGSFK 25
DB 103 NLMAAQRGRLRMSDEFGSFK 126

RESULT 14

US-08-333-565-10
Sequence 10, Application US/08333565
Patent No. 5622852

GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US

ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,565
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-333-565-10

Query Match 76.4%; Score 113; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 6.1e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 NLMAAQRGRLRMSDEFG 22
DB 3 NLMAAQRGRLRMSDEFG 23

RESULT 15
US-08-661-479-10

Sequence 10, Application US/08661479
Patent No. 5834209
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US

ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,479

RESULT 15

Fri Sep 20 11:03:16 2002

us-09-544-664-55.ra1

Page 7

1 FILING DATE: 11-JUN-1995
 2 CLASSIFICATION: 435
 3 PRIOR APPLICATION DATA:
 4 APPLICATION NUMBER: US 08/333,565
 5 FILING DATE: 31-OCT-1994
 6 ATTORNEY/AGENT INFORMATION:
 7 NAME: Smith, William M
 8 REGISTRATION NUMBER: 30,223
 9 REFERENCE/DOCKET NUMBER: 15726A-000700
 10 TELECOMMUNICATION INFORMATION:
 11 TELEPHONE: (415) 326-2400
 12 TELEFAX: (415) 326-2422
 13 INFORMATION FOR SEQ ID NO: 10:
 14 SEQUENCE CHARACTERISTICS:
 15 LENGTH: 23 amino acids
 16 TYPE: amino acid
 17 STRANDEDNESS: single
 18 TOPOLOGY: linear
 19 MOLECULE TYPE: peptide
 20 US-08-661-479-10

Query	March	75.4%	Score	113	DB	2	Length	23	
Best Local	Similarity	100.0%	Pred.	No.	6,1e-11				
Matches	21	Conservative	0	Mismatches	0	Indels	0	Gaps	0
QY	2	NLMAAQRGRELRRMSDEFE	G	22					
Db	3	NLMAAQRGRELRRMSDEFE	G	23					

Search completed: September 20, 2002, 10:37:21
Job time: 409 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 20, 2002, 10:39:12 : Search time 95.59 Seconds
(without alignments)

28.146 Million cell updates/sec

Title: US-09-544-664-55

Perfect score: 148

Sequence: 1 KNLMAQRGRRLRMSDFEGSFKGLK 28

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : PTR_71:*

1: ptr1:*
2: ptr2:*
3: ptr3:*
4: ptr4:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	138	93.2	204	2 A55671	bad protein - mous
2	54	36.5	946	2 JC5575	inter-alpha-trypsi
3	53	35.8	223	2 D70760	hypothetical prote
4	53	35.8	946	2 S54354	inter-alpha-inhibi
5	52	35.1	370	2 S38185	2-dehydro-3-deoxy
6	51	34.5	232	2 A42095	floral homeotic pr
7	50	33.8	374	2 C84338	spermidine/putresc
8	50	33.8	374	2 A96753	probable threonine
9	50	33.8	1378	2 A81193	DNA-directed RNA p
10	49.5	33.4	127	2 A11210	glycerol-3-phospha
11	49	33.1	453	2 E83517	conserved hypoteta
12	48.5	32.8	134	2 S40376	ig kappa chain - h
13	48.5	32.8	314	2 T02975	annexin P35 - maiz
14	48	32.4	206	2 C36365	transforming prote
15	48	32.4	220	2 F72289	oxidoreductase, so
16	48	32.4	526	2 T08545	threonine synthase
17	48	32.4	1164	2 T24806	hypothetical prote
18	47.5	32.1	334	2 A39172	Antho-Rhamide neur
19	47.5	32.1	1140	2 T09486	hypothetical prote
20	47	31.8	287	2 S43852	neuropeptide pol-R
21	47	31.8	957	2 G82308	oxaloacetate decar
22	47	31.8	967	2 F82668	oxaloacetate decar
23	47	31.8	5138	2 T02961	hypothetical prote
24	46.5	31.4	314	2 T02961	annexin P33 - maiz
25	46.5	31.4	435	2 A44308	Antho-Rhamide prec
26	46	31.1	165	2 S59899	chlorococciurin chai
27	46	31.1	399	2 T35440	probable polyamine
28	46	31.1	946	2 IYHU2	inter-alpha-trypsi
29	45.5	30.7	261	2 G69510	conserved hypotet

30	45.5	30.7	327	2 D97636	probable secreted
31	45.5	30.7	327	2 AF2859	conserved hypotet
32	45.5	30.7	562	2 C71473	hypothetical prote
33	45.5	30.7	905	2 G83314	NADH dehydrogenase
34	45.5	30.7	1014	2 T36031	exonuclease ABC C
35	45	30.4	273	2 S06736	photosystem II oxy
36	45	30.4	273	2 AG2287	manganese-stabiliz
37	45	30.4	295	2 F83201	conserved hypotet
38	45	30.4	346	2 B95406	conserved hypotet
39	45	30.4	486	2 T31294	hypothetical prote
40	45	30.4	591	2 B44465	sodium ion pump ox
41	45	30.4	591	2 AB0509	oxaloacetate decar
42	45	30.4	591	2 AE0909	oxaloacetate decar
43	45	30.4	596	2 A28088	probable membrane
44	45	30.4	715	2 S52675	env polyprotein -
45	45	30.4	864	1 VCLJG4	

ALIGNMENTS

RESULT 1
A55671
bad protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 05-Nov-1999
C:Accession: A55671
R:Yang, E.; Zha, J.; Jockel, J.; Boise, L.H.; Thompson, C.B.; Kormeyer, S.J.
Cell 80, 285-291, 1995
A>Title: Bad, a heterodimeric partner for Bcl-x-L and Bcl-2, displaces Bax and promot
A:Reference number: A55671; MUID:95136361
A:Accession: A55671
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-204 <YAN>
A:Cross-references: CB:L37296; NID:g639778; PIDN:AAA64465.1; PID:g639779
C:Keywords: heterodimer

Query Match 93.2%; Score 138; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 1,2e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NNLMAQRGRRLRMSDFEGSFKGL 27
DB 140 NNLMAQRGRRLRMSDFEGSFKGL 165

RESULT 2
JC5575
inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster
C:Species: Mesocricetus auratus (golden hamster)
C:Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 20-Jun-2000
R:Nakatsani, T.; Suzuki, Y.; Yamamoto, T.; Sinochara, H.
J. Biochem. 122, 71-82, 1997
A>Title: Molecular cloning and sequencing of cDNAs encoding three heavy-chain precurs
sin inhibitor heavy chain family.
A:Reference number: JC5574; MUID:97420688
A:Accession: JC5575
A:Molecule type: mRNA
A:Residues: 1-946 <NAK>
A:Cross-references: DDBJ:D89286; NID:g1694689; PIDN:BAAI3939.1; PID:g1694690
A:Experimental source: Liver
A:Accession: PC4485
A:Molecule type: protein
A:Residues: 55-64;140-146;151-156;424-447;500-528;577-605 <NA2>
C:Comment: In the plasma three inter-alpha-trypsin inhibitor heavy chains 1, 2 and 3
that the complexes play important role for pancreatic cancer.
C:Superfamily: inter-alpha-trypsin inhibitor complex component II
F:261-264,717-916/Disulfide bonds: #status predicted

Query Match 36.5%; Score 54; DB 2; Length 946;
 Best Local Similarity 34.6%; Pred. No. 11;
 Matches 9; Conservative 5; Mismatches 12; Indels 0; Gaps 0;
 Oy 2 NLMMAORYGRELRRMSDFEGSGFKL 27
 Db 212 NWVIELOGMRFLLHVPDTEFGHFGV 237

RESULT 3
 D70760
 hypothetical protein Rv2014 - Mycobacterium tuberculosis (strain H37RV)
 C:Species: Mycobacterium tuberculosis
 C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
 C:Accession: D70760
 R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garlier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holtroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393: 537-544, 1998
 A:Authors: Squares, R.; Sultston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A>Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A70500; MUID:98295987
 A:Accession: D70760
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-223 <COL>
 A:Cross-references: GB:274025; GB:AL123456; NID:g3261586; PIDN:CAA98415.1; PID:e1299911;
 A:Experimental source: strain H37RV
 C:Genetics:
 A:Gene: Rv2014

Query Match 35.8%; Score 53; DB 2; Length 223;
 Best Local Similarity 58.8%; Pred. No. 3.6;
 Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
 Oy 2 NLMMAORYGRELRRMSD 18
 Db 165 NLMMAORYNRAIRAGHD 181

RESULT 4
 S54354
 Inter-alpha-inhibitor H2 chain - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 20-Aug-1999
 C:Accession: S54354
 R:Chan, P.; Risler, J.L.; Raguenez, G.; Saller, J.P.
 Biochem. J. 308, 505-512, 1995
 A>Title: The three heavy-chain precursors for the inter-alpha-inhibitor family in mouse
 A:Reference number: S54353; MUID:95194326
 A:Accession: S54354
 A>Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-946 <CHA>
 A:Cross-references: EMBL:X70382; NID:g695633; PIDN:CAA49842.1; PID:g695634
 C:Superfamily: Inter-alpha-tryptsin inhibitor complex component II

Query Match 35.8%; Score 53; DB 2; Length 946;
 Best Local Similarity 34.6%; Pred. No. 16;
 Matches 9; Conservative 5; Mismatches 12; Indels 0; Gaps 0;
 Oy 2 NLMMAORYGRELRRMSDFEGSGFKL 27
 Db 212 NWVIELOGMRFLLHVPDTEFGHFGV 237

RESULT 5
 S38185
 2-dehydro-3-deoxyphosphohexonate aldolase (EC 4.1.2.15) ARO4 - yeast (Saccharomyces cerevisiae)
 M:Alternate names: 3-deoxy-D-erythron-heptulosonate-7-phosphate synthase; DAP synthase;
 C:Species: Saccharomyces cerevisiae

C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
 C:Accession: S38185; S46126; S46130; JN0322; B48651
 R:Dolignon, F.; Bileau, N.; Aigle, M.; Crouzet, M.
 Yeast 9, 1131-1137, 1993
 A>Title: The complete sequence of a 6794 bp segment located on the right arm of chrom
 A:Reference number: S38185; MUID:94078675
 A:Accession: S38185
 A>Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-370 <DOI>
 A:Cross-references: GB:L20296; NID:g311101; PIDN:AAA65607.1; PID:g311102
 R:Aljilovic, G.; Pohl, F.M.; Pohl, T.M.
 submitted to the Protein Sequence Database, August 1994
 A:Reference number: S45906
 A:Accession: S46126
 A:Molecule type: DNA
 A:Residues: 1-370 <ALJ>
 A:Cross-references: EMBL:236118; NID:g536664; PIDN:CAA85212.1; PID:g536665; MIPS:YBR2
 R:Aigle, M.; Bacle, M.C.; Barthe, C.; Bileau, N.; Crouzet, M.; Dolignon, F.
 submitted to the Protein Sequence Database, August 1994
 A:Reference number: S45940
 A:Accession: S46130
 A:Molecule type: DNA
 A:Residues: 1-370 <ARG>
 A:Cross-references: EMBL:236118; NID:g536664; PIDN:CAA85212.1; PID:g536665; MIPS:YBR2
 R:Kuenzler, M.; Paravicini, G.; Egli, C.M.; Imiger, S.; Braus, G.H.
 Gene 113, 67-74, 1992
 A>Title: Cloning, primary structure and regulation of the ARO4 gene, encoding the tyr
 A:Reference number: JN0322; MUID:92225349
 A:Accession: JN0322
 A:Molecule type: DNA
 A:Residues: 1-204, 208-370 <KUE>
 A:Cross-references: EMBL:X61107
 R:Kuenzler, M.; Balmeil, T.; Egli, C.M.; Paravicini, G.; Braus, G.H.
 J. Bacteriol. 175, 5548-5558, 1993
 A>Title: Cloning, primary structure, and regulation of the HIS7 gene encoding a bifun
 A:Reference number: A48651; MUID:93374850
 A:Accession: B48651
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 352-370 <KU2>
 A:Cross-references: GB:X61107
 C:Comment: This enzyme catalyzes the condensation of phosphoenolpyruvate and D-erythr
 C:Genetics:
 A:Gene: SGD:ARO4
 A:Cross-references: SGD:S0000453; MIPS:YBR249c
 A:Map position: 2R
 C:Function:
 A:Description: aldehyde-lyase; carbon-carbon lyase
 A:Pathway: aromatic amino acid biosynthesis; shikimate pathway
 A>Note: first step in shikimate pathway
 C:Superfamily: phospho-2-dehydro-3-deoxyheptonate aldolase
 C:Keywords: aldehyde-lyase; aromatic amino acid biosynthesis; carbon-carbon lyase; cy

Query Match 35.1%; Score 52; DB 2; Length 370;
 Best Local Similarity 47.6%; Pred. No. 8.4;
 Matches 10; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
 Oy 2 NLMMAORYGRELRRMSDFEG 22
 Db 80 DLEMAOEVALRKLSDLELKG 100

RESULT 6
 A42095
 floral homeotic protein APETALA3 (AP3) - Arabidopsis thaliana
 M:Alternate names: homeotic protein APETALA3; MADS-box regulatory protein AP3
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
 C:Accession: A42095; S52633; T47593
 R:Jack, T.; Brockman, L.L.; Meyerowitz, E.M.
 Cell 68, 683-697, 1992

glycerol-3-phosphate cytidyltransferase (gct), cdp-glycerol pyrophosphorylase (telcho)
C:Species: *Listeria monocytogenes*
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: A11210
R:Glaeser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fehl, H.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kref, J.; Kuhn, M.; Kunst, F.; Kurapat, G.; Madueno, E.; Maitournam, A.; Me
Ok, C.; Schueter, T.; Sines, N.; Tietter, A.; Vazquez-Boland, J.A.; Voss, H.; Weiland,
A:Title: Comparative genomics of *Listeria* species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: A11210
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-127 <GLA>
A:Cross-references: GB:NC_003210; PIDN:CAC9167.1; PID:g16410491; GSPDB:GN00177
C:Experimental source: strain EGD-e
C:Genetics:
A:Gene: tagD

Query Match 33.4% Score 49.5; DB 2; Length 127;
Best Local Similarity 36.4% Pred. No. 6.6;
Matches 12; Conservative 6; Mismatches 10; Indels 5; Gaps 1;
QY 1 KULMAOR-----YGRRLMSDFEGSFKLK 28,
DB 71 ENNWEOKRDIKRYGIDVWGDWGEPRFLK 103

RESULT 11
E83517
conserved hypothetical protein PA1031 (Imported) - *Pseudomonas aeruginosa* (strain PA01)
C:Species: *Pseudomonas aeruginosa*
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: E83517
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho
A:Reference number: AB2950; MUID:20437337
A:Accession: E83517
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-453 <STO>
A:Cross-references: GB:AE004535; GB:AE004091; MID:g9446936; PIDN:AAG04420.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA1031

Query Match 33.1% Score 49; DB 2; Length 453;
Best Local Similarity 55.6% Pred. No. 28;
Matches 10; Conservative 4; Mismatches 2; Indels 2; Gaps 1;
QY 4 MAAORTGR--ELRRMSDE 19
DB 65 WASERGREDEURLASE 82

RESULT 12
S40376
Ig kappa chain - human
C:Species: *Homo sapiens* (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40376
R:Klein, R.; Jernichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chl genes and their hypermutation.
A:Reference number: S40312; MUID:9408091
A:Accession: S40376

A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-134 <KLE>
A:Cross-references: EMBL:X72486; MID:g441440; PIDN:CAA51154.1; PID:g441441
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:34-113/Domain: immunoglobulin homology <IMM>

Query Match 32.8% Score 48.5; DB 2; Length 134;
Best Local Similarity 38.2% Pred. No. 9.7;
Matches 13; Conservative 1; Mismatches 9; Indels 11; Gaps 1;
QY 4 MAAORYGRELRM-----SDEFGSFKG 26
DB 58 WFRQGRGRSPRLIVNYSKRDGSDRFGSGSG 91

RESULT 13
T02975
annexin p35 - maize
C:Species: *Zea mays* (maize)
C>Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
C:Accession: T02975
R:Battley, N.H.; James, N.C.; Greenland, A.J.
Plant Physiol. 112, 1391-1396, 1996
A:Title: CDNA isolation and gene expression of maize annexins p33 and p35.
A:Reference number: Z14796; MUID:97092863
A:Accession: T02975
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-314 <BAT>
A:Cross-references: EMBL:X98245; MID:g1370602; PIDN:CAA66901.1; PID:g1370603
A:Experimental source: cultivar clipper; root tip
C:Superfamily: annexin I; annexin repeat homology
F:14-85/Domain: annexin repeat homology <AXR>

Query Match 32.8% Score 48.5; DB 2; Length 314;
Best Local Similarity 47.6% Pred. No. 23;
Matches 10; Conservative 4; Mismatches 6; Indels 1; Gaps 1;
QY 6 AQRXGRE-LRRMSDFEGSFK 25
DB 54 AEAYGKELRLALGDELHGKE 74

RESULT 14
C36365
transforming protein homolog MRAS3 - *Rhizomucor racemosus*
C:Species: *Rhizomucor racemosus*
C>Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 19-Jan-2001
C:Accession: C36365
R:Casale, W.L.; McConnell, D.G.; Wang, S.Y.; Lee, Y.J.; Linz, J.E.
Mol. Cell. Biol. 10, 6654-6663, 1990
A:Title: Expression of a gene family in the dimorphic fungus *Mucor racemosus* which ex
A:Reference number: A36365; MUID:91061774
A:Accession: C36365
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-206 <CAS>
A:Cross-references: GB:M55177
C:Superfamily: ras transforming protein; translation elongation factor Tu homology
C:Keywords: GTP binding; nucleotide binding; P-loop
F:11-126/Domain: translation elongation factor Tu homology <FTU>
F:17-24/Region: nucleotide-binding motif A (P-loop)
F:123-126/Region: GTP-binding NKXD motif
F:153-155/Region: GTP-binding SAK/L motif
F:23,24,42,123,124,126,153/Binding site: Mg-GTP (Lys, Ser, Thr, Asn, Lys, Asp, Ser) #
Query Match 32.4% Score 48; DB 2; Length 206;
Best Local Similarity 62.5% Pred. No. 18;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 20, 2002, 11:04:34 ; Search time 44.99 Seconds
(without alignments)
24.098 Million cell updates/sec

Title: US-09-544-664-55
Perfect score: 148
Sequence: 1 KNLMAORYGRELRLMSDEFGSFKGLK 28

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt.40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	138	93.2	204	1	BAD_MOUSE
2	138	93.2	205	1	BAD_MOUSE
3	114	77.0	168	1	BAD_HUMAN
4	54	36.5	946	1	ITR2_MESAU
5	53	35.8	946	1	ITR2_MESAU
6	52	35.1	370	1	AROG_YEAST
7	51	34.5	232	1	AP3_ARATH
8	50	33.8	1378	1	RPOB_CAMTE
9	49	33.1	453	1	RMUC_PSEAE
10	48	32.4	205	1	RAS3_RHIRA
11	48	32.4	220	1	6PGL_THEMA
12	48	32.4	519	1	THRC_SOLTY
13	48	32.4	526	1	THRC_ARATH
14	47.5	32.1	334	1	FMRA_CALPA
15	47	31.8	198	1	BIM_HUMAN
16	47	31.8	287	1	PRFA_POLPE
17	46.5	31.4	429	1	FMK2_ANTEL
18	46.5	31.4	435	1	FMK1_ANTEL
19	46	31.1	946	1	ITR2_HUMAN
20	45.5	30.7	1014	1	UVRA_STROO
21	45	30.4	273	1	PSBO_AMASP
22	45	30.4	328	1	SNR4_KLUIA
23	45	30.4	580	1	DCOA_SALTY
24	45	30.4	585	1	DCOA_KLEPN
25	45	30.4	653	1	HTZA_HUMAN
26	45	30.4	865	1	ENV_STVAT
27	45	30.1	1557	1	LMU1_CAEEL
28	44.5	30.1	907	1	NDOG_ECOLI
29	44.5	29.7	196	1	BIM_MOUSE
30	44	29.7	196	1	BIM_MOUSE
31	44	29.7	196	1	BIM_MOUSE
32	44	29.7	262	1	ENDB_ECOLI
33	44	29.7	629	1	SYM_THEMA

34	44	29.7	768	1	ENV_STVAT	P27577 simian immu
35	44	29.7	877	1	ENV_STVAT	P27577 simian immu
36	44	29.7	978	1	RA50_AQUAE	O67124 aquifex aeo
37	44	29.7	1790	1	USOL_YEAST	P25386 saccharomyc
38	44	29.7	1966	1	MYSB_CAEEL	P02586 caenorhabdl
39	43.5	29.4	217	1	UREF_SYNY3	P73327 synecocyst
40	43.5	29.4	1200	1	DPGL_XENLA	O91684 xenopus lae
41	43	29.1	377	1	APJ_MOUSE	O9w008 mus musculu
42	43	29.1	380	1	APJ_HUMAN	P35424 homo sapien
43	43	29.1	380	1	APJ_MOUSE	O97666 macaca muli
44	43	29.1	453	1	DRAP_MOUSE	P47759 mus musculu
45	43	29.1	463	1	Y050_NPVAC	P41434 autographa

ALIGNMENTS

RESULT 1
BAD_MOUSE STANDARD: PRT: 204 AA.
ID BAD_MOUSE
AC Q61337;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Bcl2-antagonist of cell death (BAD) (Bcl-2 binding component 6) (Bcl-XL/Bcl-2 associated death promoter).
DE BAD OR BRC6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, and Thymus;
RX MEDLINE=95136361; PubMed=7834748;
RA Yang E., Zha J., Jockel J., Boise L.H., Thompson C.B., Korsmeyer S.J.;
RT "Bad, a heterodimeric partner for Bcl-XL and Bcl-2, displaces Bax and promotes cell death.";
RT Cell 80:285-291(1995).
RN [2]
RP PHOSPHORYLATION, AND MUTAGENESIS OF SER-112 AND SER-136.
RX MEDLINE=98022383; PubMed=9381178;
RA Del Peso L., Gonzalez-Garcia M., Page C., Herrera R., Nunez G.;
RT "Interleukin-3-induced phosphorylation of BAD through the protein kinase Akt.";
RT Science 278:687-689(1997).
RN [3]
RP MUTAGENESIS OF SERINE RESIDUES.
RX MEDLINE=20403302; PubMed=10949026;
RA Datta S.R., Katsov A., Hu L., Petros A., Fesik S.W., Yaffe M.B., Greenberg M.E.;
RT "14-3-3 proteins and survival kinases cooperate to inactivate BAD by BH3 domain phosphorylation.";
RT Mol. Cell 6:41-51(2000).
RL -I- FUNCTION: Promotes cell death. Successfully competes for the binding to Bcl-X(L), Bcl-2 and Bcl-w, thereby affecting the level of heterodimerization of these proteins with BAX. Can reverse the death repressor activity of Bcl-X(L), but not that of Bcl-2.
CC Appears to act as a link between growth factor receptor signaling and the apoptotic pathways.
CC -I- SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-X(L), Bcl-2 and Bcl-w. Also binds protein Sl00A0 (By similarity).
CC The Ser-112/Ser-136 phosphorylated form binds 14-3-3 proteins.
CC -I- SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon phosphorylation, localizes to the cytoplasm.
CC -I- DOMAIN: Interacts with Bcl-2 domain is required by BAX, BID, BAK, BAD AND BAX for their pro-apoptotic activity and for their interaction with anti-apoptotic members of the Bcl-2 family.
CC -I- PTM: Phosphorylated on Ser-112 in response to survival stimuli. Subsequent phosphorylation on Ser-136 promotes heterodimerization with 14-3-3 proteins. This interaction then facilitates the phosphorylation at Ser-155, a site within the BH3 domain, leading to the release of Bcl-X(L) and the promotion of cell survival.

Ser-136 is the major site of AKT/PKB phosphorylation, Ser-155 the major site of protein kinase A (CAPK) phosphorylation.

-1- SIMILARITY: CONTAINS A BCL-3 HOMOLOG DOMAIN 3 (BH3).

-1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

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DR EMBL: L37296; AAA64465.1; -.

DR MGD: MGI:1096330; Bad.

DR InterPro: IPR000712; Bcl_2.

DR ProSite: PS01259; BH3; FALSE_NEG.

DR Apoptosis; Phosphorylation.

KW DOMAIN 147 161 BH3.

FT MOD_RES 112 112 PHOSPHORYLATION (BY CAPK AND PKB).

FT MOD_RES 136 136 PHOSPHORYLATION (BY CAPK AND PKB).

FT MOD_RES 155 155 PHOSPHORYLATION (BY CAPK AND PKB).

FT MUTAGEN 112 112 S->A: NO PHOSPHORYLATION.

FT MUTAGEN 136 136 S->A: NO PHOSPHORYLATION.

FT MUTAGEN 155 155 S->A: NO PHOSPHORYLATION; INTERACTS WITH BCL-X(L).

FT SEQUENCE 204 AA: 22080 MW: 6C2BA910205053F7 CRC64;

Query Match 93.2%; Score 138; DB 1; Length 204;
Best Local Similarity 100.0%; Pred. No. 1.7e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 N1MAA0RGRELRRMSDEPSSFKGL 27
|||||

DB 140 N1MAA0RGRELRRMSDEPSSFKGL 165

RESULT 2
ID BAD_RAT STANDARD; PRT; 205 AA.
AC 035147; 070256; 09JHX1;
DT 16-OCT-2001 (Rel. 40; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 01-MAR-2002 (Rel. 41; Last annotation update)
DE Bcl2-antagonist of cell death (BAD) (Bcl-2 binding component 6) (Bcl-xL/Bcl-2 associated death promoter).
GN BAD.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF SER-113 AND SER-137.
RC TISSUE-Ovary;
RX MEDLINE-98034386; PubMed-9369453;
RA Hsu S.-Y., Kalpita A., Zhu L., Hsueh A.J.W.;
RT "Interference of BAD (Bcl-xL/Bcl-2-associated death promoter)-induced apoptosis in mammalian cells by 14-3-3 isoforms and p11.";
RL Mol. Endocrinol. 11:1858-1867(1997).
RM [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Brain;
RX MEDLINE-98194755; PubMed-9535132;
RA D'Agata V., Magro G., Travali S., Cavallaro S.;
RT "Cloning and expression of the programmed cell death regulator BAD in the rat brain.";
RL Neurosci. Lett. 243:137-140(1998).
RM [3]
RN SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RC TISSUE-Brain;
RX MEDLINE-21109372; PubMed-11161472;
RA Hamner S., Arumae U., Yu L.-Y., Sun Y.-F., Saarna M., Lindholm D.;

Functional characterization of two splice variants of rat BAD and RT their interaction with Bcl-w in sympathetic neurons.;
RL Mol. cell. Neurosci. 17:97-106(2001).

CC -1- FUNCTION: Promotes cell death. Successfully competes for the binding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level of heterodimerization of these proteins with BAX. Can reverse the death repressor activity of Bcl-x(L), but not that of Bcl-2 (by similarity). Appears to act as a link between growth factor receptor signaling and the apoptotic pathways.

CC -1- SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-x(L), Bcl-2 and Bcl-w. Also binds protein S100A10. The Ser-113/Ser-137 phosphorylated form binds 14-3-3 proteins.

CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon phosphorylation, located to the cytoplasm (by similarity).

CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; alpha (shown here) and beta; are produced by alternative splicing. They differ only in their C-terminal regions.

CC -1- TISSUE SPECIFICITY: Expressed in all tissues tested, including brain, liver, spleen and heart. In the brain, restricted to epithelial cells of the choroid plexus. Isoform alpha is the more abundant form.

CC -1- DOMAIN: Interact BH3 domain is required by BIK, BID, BAK, BAD AND BAX for their pro-apoptotic activity and for their interaction with anti-apoptotic members of the Bcl-2 family.

CC -1- PTM: Phosphorylated on Ser-113 in response to survival stimuli. Subsequent phosphorylation on Ser-137 promotes heterodimerization with 14-3-3 proteins. This interaction then facilitates the phosphorylation at Ser-156, a site within the BH3 domain, leading to the release of Bcl-x(L) and the promotion of cell survival.

CC Ser-137 is the major site of AKT/PKB phosphorylation, Ser-156 the major site of protein kinase A (CAPK) phosphorylation (by similarity).

CC -1- SIMILARITY: CONTAINS A BCL-3 HOMOLOG DOMAIN 3 (BH3).

CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

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DR EMBL: AF003523; AAC53374.1; -.

DR EMBL: AF031227; AAC15100.1; -.

DR EMBL: AF276910; AAF91427.1; -.

DR EMBL: AF279911; AAF91428.1; -.

DR InterPro: IPR000712; Bcl_2.

DR ProSite: PS01259; BH3; FALSE_NEG.

KW Apoptosis; Phosphorylation; Alternative splicing.

FT MOD_RES 113 162 BH3.

FT MOD_RES 137 137 PHOSPHORYLATION (BY CAPK AND PKB) (BY SIMILARITY).

FT MOD_RES 137 137 PHOSPHORYLATION (BY CAPK AND PKB) (BY SIMILARITY).

FT MOD_RES 156 156 PHOSPHORYLATION (BY CAPK AND PKB) (BY SIMILARITY).

FT VANSPLIC 166 205 LPPKSGATQKROSASWTRITIGSMDRNKGGSGTSPQ
-> EELTVSEELPVVALMEGSPMLWSFSPHTLPPTP
EVAMFRLRYWTALRLC (IN ISOFORM BETA).

FT MUTAGEN 113 113 S->A: NO EFFECT ON HETERO DIMERIZATION WITH 14-3-3 PROTEINS.

FT MUTAGEN 137 137 S->A: NO HETERO DIMERIZATION WITH 14-3-3 PROTEINS. NO EFFECT ON HETERO DIMERIZATION WITH BCL2 NOR WITH PROTEIN P11.

FT CONFLICT 29 34 SDAGGR -> ERGRGR (IN REF. 1).

FT SEQUENCE 205 AA: 22228 MW: 7AFA71D9E9CF4A81 CRC64;

Query Match 93.2%; Score 138; DB 1; Length 205;
Best Local Similarity 100.0%; Pred. No. 1.7e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NLMNAORYGRELRRMSDEFEGRFKGL 27
 DB 141 NLMNAORYGRELRRMSDEFEGRFKGL 166

RESULT 3
 BAD_HUMAN ID BAD_HUMAN STANDARD: PRT: 168 AA.

AC 092934; 014803; (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 41, Last annotation update)
 DE Bcl-2 antagonist of cell death (BAD) (Bcl-2 binding component
 6) (Bcl-XL/Bcl-2 associated death promoter).
 GN BAD OR BCL6 OR BCL2L8.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OC NCB1_TaxID=9606;
 RN 11
 RP SEQUENCE FROM N.A.
 RA Yin D.X., Li Z., Huang B., Chen S., Zhou H.;
 RT "A human protein that interacts with Bcl-2 and have homology to mouse
 BAD.";
 RT Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
 RL 12
 RP SEQUENCE FROM N.A., AND PHOSPHORYLATION BY RAF-1.
 RX MEDLINE=97083574; PubMed=8929532;
 RA Wang H.-G., Rapp U.R., Reed J.C.;
 RT "Bcl-2 targets the protein kinase Raf-1 to mitochondria.";
 RL Cell 87:629-638(1995).
 RN 13
 RP SEQUENCE FROM N.A.
 RA Takayama S., Reed J.C.;
 RL Submitted (OCT-1997) to the EMBL/Genbank/DBJ databases.
 RN 14
 RP SEQUENCE FROM N.A., AND DIMERIZATION.
 RC TISSUE=Bone marrow;
 RX MEDLINE=98049554; PubMed=9388232;
 RA Oltjale S., Diaz J.-L., Horne W., Chang J., Wang Y., Wilson G.,
 RT Chang S., Weeks S., Fritz L.C., Oltersdorf T.;
 RL "Dimerization properties of human BAD.";
 RL J. Biol. Chem. 272:30866-30872(1997).
 RN 15
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Strausberg R.;
 RL Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.
 RN 16
 RP STRUCTURE BY NMR OF 103-127.
 RX MEDLINE=21073561; PubMed=11206074;
 RA Petros A.M., Neftshelm D.G., Wang Y., Olejniczak E.T., Meadows R.P.,
 RA Mack J., Swift K., Matayoshi E.D., Zhang H., Thompson C.B.,
 RA Pesik S.W.;
 RT "Rationale for Bcl-XL/Bad peptide complex formation from structure,
 RT mutagenesis, and biophysical studies.";
 RL Protein Sci. 9:2528-2534(2000).
 CC -1- FUNCTION: Promotes cell death. Successfully competes for the
 binding to Bcl-X(L), Bcl-2 and Bcl-w, thereby affecting the level
 of heterodimerization of these proteins with BAX. Can reverse the
 death repressor activity of Bcl-X(L), but not that of Bcl-2 (By
 similarity). Appears to act as a link between growth factor
 receptor signaling and the apoptotic pathways.
 CC -1- SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-
 X(L), Bcl-2 and Bcl-w. Also binds protein S100A10 (By similarity).
 CC The Ser-75/Ser-99 phosphorylated form binds 14-3-3 proteins (By
 similarity).
 CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon
 phosphorylation, locates to the cytoplasm.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
 CC -1- DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND
 BAX for their pro-apoptotic activity and for their interaction
 with anti-apoptotic members of the Bcl-2 family.

CC -1- PTM: Phosphorylated on Ser-75 in response to survival stimuli.
 CC Subsequent phosphorylation on Ser-99 promotes heterodimerization
 CC with 14-3-3 proteins. This interaction then facilitates the
 CC phosphorylation at Ser-118, a site within the BH3 domain, leading
 CC to the release of Bcl-X(L) and the promotion of cell survival.
 CC Ser-99 is the major site of AKT/PKB phosphorylation, Ser-118 the
 CC major site of protein kinase A (CAK) phosphorylation (by
 CC similarity).
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 3 (BH3).
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
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 CC -----
 DR EMBL: U66879; AAB36516.1; -
 DR EMBL: AF021792; AAB72092.1; -
 DR EMBL: AF031523; AAB88124.1; -
 DR EMBL: BC001901; AAB01901.1; -
 DR PDB: 1G5F; 07-FEB-01.
 DR MIM: 603167; -
 DR InterPro: IPR000712; BCL-2.
 DR PROSITE: PS01259; BH3; FALSE_NEG.
 KW Apoptosis; Phosphorylation; 3D-structure.
 FT DOMAIN 110 124
 FT MOD_RES 75 75 BH3.
 FT MOD_RES 99 99 PHOSPHORYLATION (BY CAK AND PKB) (BY
 FT SIMILARITY).
 FT MOD_RES 118 118 PHOSPHORYLATION (BY CAK AND PKB) (BY
 FT SIMILARITY).
 FT CONFLICT 64 91 AGAVEIRSRHSYVPAGTDDDEGMEEPS -> RMGCGDPES
 FT POLLPGRDGRRRDGGGAO (IN REF. 1).
 SQ SEQUENCE 168 AA; 18392 MW; 69FDBD27DDEE3241 CRC64.

QY 2 NLMNAORYGRELRRMSDEFEGRFKGL 25
 DB 103 NLMNAORYGRELRRMSDEFEGRFKGL 126

RESULT 4
 ITH2_MESAU ID ITH2_MESAU STANDARD: PRT: 946 AA.

AC P97279;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITI heavy
 DE chain H2) (HC2).
 GN ITH2.
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 OC NCB1_TaxID=10036;
 RN 11
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=97420688; PubMed=9276673;
 RA Nakatani T., Suzuki T., Yamamoto T., Sinohara H.;
 RT "Molecular cloning and sequencing of cDNAs encoding three heavy-chain
 RT precursors of the inter-alpha-trypsin inhibitor in Syrian hamster:
 RT implications for the evolution of the inter-alpha-trypsin inhibitor
 RT heavy chain family.";

Query Match 77.0%; Score 114; DB 1; Length 168;
 Best Local Similarity 91.7%; Pred. No. 5 3e-10;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

RL J. Blochem. 122:71-82(1997).
RN (2)
RP SEQUENCE OF 55-64; 140-146; 151-156; 424-447; 500-528 AND 577-605,
RC AND SUBUNITS.
RX TISSUE-Plasma;
RA MEDLINE-97018241; PubMed-8864857;
RT Yamamoto T., Yamamoto K., Shinohara H.;
RT Inter-alpha-trypsin inhibitor and its related proteins in Syrian
RT hamster urine and plasma.
RL J. Biochem. 120:145-152(1996).
CC -1- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A
CC BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,
CC INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE
CC LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE
CC ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
CC SIMILARITY).
CC -1- SUBUNIT: I-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM
CC ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,
CC BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2
CC AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND
CC BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.
CC -1- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN
CC 4-SULFATE BRIDGE TO THEIR C-TERMINAL ASPARTATE (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ITIH FAMILY.
CC -1- SIMILARITY: CONTAINS 1 VWFA DOMAIN.
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CC or send an email to license@sib-sib.ch).
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DR EMBL: D89286; BAA13939.1;
DR InterPro: IPR002035; VWFA.
DR Pfam: PF00092; VWFA.
DR SMART: SM00327; VWFA.1.
DR PROSITE: PS50234; VWFA.1.
DR Serine protease inhibitor; Repeat; Signal; Multigene family;
KW Glycoprotein.
FT SIGNAL 1 18 POTENTIAL.
FT PROPEP 19 54 BY SIMILARITY.
FT CHAIN 55 702 INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN
FT FT
FT PROPEP 703 946
FT DOMAIN 308 468 VWFA.
FT CARBOHYD 118 118 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 578 578 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT BINDING 702 702 CHONDROITIN 4-SULFATE, CROSS-LINK SITE
FT FT
FT CONFLICT 510 510 (BY SIMILARITY).
FT CONFLICT 595 595 V->Y (IN REF. 2).
FT CONFLICT 595 595 E->I (IN REF. 2).
SQ SEQUENCE 946 AA; 106580 MW; CA8BF565458E7B2E CRC64;

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Query Match 36.5%; Score 54; DB 1; Length 946;
Best Local Similarity 34.6%; Pred. No. 3.4;
Matches 9; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

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RESULT 5
ID ITIH2_MOUSE STANDARD: PRT; 946 AA.
AC 061703;
DT 15-JUL-1998 (Rel. 36, Created)

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DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITI heavy
DE chain H2).
GN ITIH2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId:10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6N; TISSUE-Liver;
RX MEDLINE-95194326; PubMed-7534067;
RA Chan P., Ristler J.-L., Baquenez G., Saller J.-P.;
RT "The three heavy-chain precursors for the inter-alpha-inhibitor
RT family in mouse: new members of the multicopper protein group
RT with differential transcription in liver and brain.
RL Biochem. J. 306:505-512(1995).
CC -1- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A
CC BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,
CC INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE
CC LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE
CC ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
CC SIMILARITY).
CC -1- SUBUNIT: I-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM
CC ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,
CC BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2
CC AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND
CC BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN BOTH LIVER AND BRAIN.
CC -1- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN
CC 4-SULFATE BRIDGE TO THEIR C-TERMINAL ASPARTATE (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ITIH FAMILY.
CC -1- SIMILARITY: CONTAINS 1 VWFA DOMAIN.
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DR EMBL: X70392; CAA49842.1;
DR MGD: MG1:96619; ITIH2.
DR InterPro: IPR002035; VWFA.
DR Pfam: PF00092; VWFA.
DR SMART: SM00327; VWFA.1.
DR PROSITE: PS50234; VWFA.1.
DR Serine protease inhibitor; Repeat; Signal; Multigene family;
KW Glycoprotein.
FT SIGNAL 1 18 POTENTIAL.
FT PROPEP 19 54 BY SIMILARITY.
FT CHAIN 55 702 INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN
FT FT
FT PROPEP 703 946
FT DOMAIN 308 468 VWFA.
FT CARBOHYD 118 118 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT BINDING 702 702 CHONDROITIN 4-SULFATE, CROSS-LINK SITE
FT FT
SQ SEQUENCE 946 AA; 105927 MW; 40DB6716433ED9DC CRC64;

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Query Match 35.8%; Score 53; DB 1; Length 946;
Best Local Similarity 34.6%; Pred. No. 4.8;
Matches 9; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

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ID ITIH2_MOUSE STANDARD: PRT; 946 AA.
AC 061703;
DT 15-JUL-1998 (Rel. 36, Created)

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RESULT 6
 ANOG_YEAST STANDARD: PRT: 370 AA.
 AC P32449;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Phospho-2-dehydro-3-deoxynephtonate aldolase, tyrosine-inhibited
 (EC 4.1.2.15) (Phospho-2-keto-3-deoxynephtonate aldolase) (DAHP
 synthetase) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase).
 GN ARO4 OR YBR249C OR YBR1701.
 OS *Saccharomyces cerevisiae* (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92225349; PubMed=1348717;
 RA Kuenzler M., Paravicini G., Egli C., Imiger S., Baus G.H.;
 RT "Cloning, primary structure and regulation of the ARO4 gene, encoding
 the tyrosine-inhibited 3-deoxy-D-arabino-heptulosonate-7-phosphate
 synthase from *Saccharomyces cerevisiae*.";
 RT Gene 113:67-74(1992).
 RN [2]
 RP REVISIONS TO 205-207.
 RA Kuenzler M.;
 RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=5288C;
 RX MEDLINE=94076675; PubMed=8255522;
 RA Daignon F., Bileau N., Aigle M., Crouzet M.;
 RT "The complete sequence of a 6794 bp segment located on the right arm
 of chromosome II of *Saccharomyces cerevisiae*. Finding of a putative
 yeast 9:1131-1137(1993)."
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=5288C;
 RA Altmann G., Pohl F.M., Pohl T.M.;
 RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: STEREOSPECIFIC CONDENSATION OF PHOSPHOENOLPYRUVATE (PEP)
 AND D-ERYTHROSE-4-PHOSPHATE (E4P) GIVING RISE TO 3-DEOXY-D-
 ARABINO-HEPTULOSONATE-7-PHOSPHATE (DAHP).
 CC -1- CATALYTIC ACTIVITY: 2-dehydro-3-deoxy-D-arabino-heptonate 7-
 phosphate + phosphate -> phosphoenolpyruvate + D-erythrose 4-
 phosphate + H(2)O.
 CC -1- ENZYME REGULATION: INHIBITED BY TYROSINE.
 CC -1- PATHWAY: FIRST STEP IN THE BIOSYNTHESIS OF CHORISMATE WITHIN
 THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE PATHWAY).
 CC -1- INDUCTION: BY AMINO ACID STARVATION.
 CC -1- SIMILARITY: BELONGS TO CLASS-1 DAHP SYNTHETASE FAMILY.
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 CC -----
 DR EMBL: X61107; CAA43419.1; -;
 DR EMBL: L20296; AAA65607.1; -;
 DR EMBL: Z61118; CAA85212.1; -;
 DR PIR: S38185; S38185.
 DR HSSP: P00866; I0R7.
 DR SGD: S0000453; ARO4.
 DR InterPro: IPR001785; DAHP_synth_1.
 DR Pfam: PF00793; DAHP_synth_1; 1.
 DR Prodom: P0005060; DAHP_synth_1; 1.
 KW Aromatic amino acid biosynthesis; Lyase; Multigene family.

SQL SEQUENCE 370 AA; 39749 MW; 594ED48F24175979 CRC64;
 Query Match 35.1%; Score 52; DB 1; Length 370;
 Best Local Similarity 47.6%; Pred. No. 2.4;
 Matches 10; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
 OY 2 NLMAQRGRELRRMSDEFEQ 22
 : 111 1 11111 1
 DB DLEAODEYALRLKLSDELK 100
 RESULT 7
 AP3_ARATH STANDARD: PRT: 232 AA.
 ID AP3_ARATH
 RC P35632; Q39003;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Floral homeotic protein APETALA3.
 GN AP3 OR AT3G54340 OR T12E18-30.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eustids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=petal;
 RX MEDLINE=92154682; PubMed=1346756;
 RA Jack T., Brockman L.L., Meyerowitz E.M.;
 RT "The homeotic gene APETALA3 of Arabidopsis thaliana encodes a MADS
 box and is expressed in petals and stamens.";
 RT Cell 68:683-697(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. LANDSBERG ERECTA;
 RX MEDLINE=95036018; PubMed=7948893;
 RA Okamoto H., Yano A., Shiraishi H., Okada K., Shimura Y.;
 RT "Genetic complementation of a floral homeotic mutation, *apetala3*,
 with an Arabidopsis thaliana gene homologous to DEFICIENS of
 Antirrhinum majus.";
 RT Antirrhinum majus.";
 RL Plant Mol. Biol. 26:465-472(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VARIOUS STRAINS;
 RX MEDLINE=99126449; PubMed=9927474;
 RA Purganan M.D., Sudduth J.I.;
 RT "Molecular population genetics of floral homeotic loci. Departures
 from the equilibrium-neutral model at the APETALA3 and PISTILLATA
 genes of Arabidopsis thaliana.";
 RL Genetics 151:839-848(1999).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RX MEDLINE=21016720; PubMed=11130713;
 RA Salanoubat M., Lemcke K., Rieger M., Ansoorge W., Unsel M.,
 FArlmann B., Valle G., Bloeker H., Perez-Alonso M., Obermayer B.,
 Delany M., Boutry M., Griwall L.A., Macho A., Casacuberta E.,
 De Simone V., Choisme N., Artiguenave F., Robert C., Brottier P.,
 Wincker P., Catullo L., Weissenbach J., Saurin W., Quetier F.,
 Wurmacher E., Drzonek H., Erle H., Jordan N., Bangert S.,
 Wiedemann R., Kranz H., Voss H., Holland R., Bandt P., Nykatura G.,
 Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simonati B.,
 Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordstik G.,
 Reichelt J., Scharfe M., Schöen O., Barges M., Terol J., Clement J.,
 Navarro P., Collado C., Perez-Perez A., Ottenwelder B., Masny D.,
 de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
 Montfort A., Argilou A., Flores M., Liguori R., Vitale D.,
 Manhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
 Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,

RA Rooney T., Rizzo M., Walts A., Uterback T., Fujii C.Y., Shea T.P.,
 RA Creaaty T.H., Haas B., Malt R., Wu D., Peterson J., Van Aken S.,
 RA Pal G., Miltcher J., Sellers P., Gall J.E., Feldblum T.V.,
 RA Preuss D., Lin X., Nieman W.C., Salzberg S.L., White O., Venter J.C.,
 RA Fraser C.M., Kaneo T., Nakamura Y., Salo S., Kato T., Asamizu E.,
 RA Sasamoto S., Kimura T., Idegawa K., Kawashima K., Kishida Y.,
 RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakayama S., Nakazaki N., Shino S., Takeuchi C., Wada T.,
 RA Nakarabe A., Yamada M., Yasuda M., Tabata S.,
 RT *Sequence and analysis of chromosome 3 of the plant Arabidopsis
 thaliana.*
 RT thaliana.*
 RL Mature 408:820-823(2000).
 CC -1- FUNCTION: TRANSCRIPTION FACTOR INVOLVED IN THE GENETIC CONTROL OF
 CC FLOWER DEVELOPMENT.
 CC -1- SUBUNIT: FORMS AN HETERODIMER WITH PISTILLATA.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN PETALS AND STAMENS.
 CC -1- MISCELLANEOUS: MUTATIONS IN AP3 CAUSE TRANSFORMATION OF PETALS
 CC INTO SEPAL AND STAMINA INTO CARPETS.
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
 CC FACTORS.
 CC -1- SIMILARITY: CONTAINS A PROBABLE DIMERIZATION DOMAIN FOUND IN
 CC SRP-TYPE TRANSCRIPTION FACTORS (K-BOX).
 CC -----
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 CC -----
 DR EMBL: M86357; AAA32740.1; -
 DR EMBL: D21125; BAA04665.1; -
 DR EMBL: AF115799; AAD51888.1; -
 DR EMBL: AF115800; AAD51889.1; -
 DR EMBL: AF115802; AAD51891.1; -
 DR EMBL: AF115804; AAD51893.1; -
 DR EMBL: AF115811; AAD51900.1; -
 DR EMBL: AF115814; AAD51903.1; -
 DR EMBL: AL132971; CAB81799.1; -
 DR PIR: A42095; A42095.
 DR HSSP: P11746; 1MNM.
 DR TRANSFAC: T01776; -
 DR InterPro: IPR002487; K-box.
 DR InterPro: IPR002100; MADS-box.
 DR Pfam: PF01486; K-box; 1.
 DR Pfam: PF00319; SRP-TE; 1.
 DR PRINTS: PR00404; MADSDOMAIN.
 DR SMART: SM00432; MADS; 1.
 DR PROSITE: PS00350; MADS_BOX_1; 1.
 DR PROSITE: PS50066; MADS_BOX_2; 1.
 DR Transcription regulation: DNA-binding; Activator; Nuclear protein;
 KW Developmental protein.
 FT DOMAIN 3 57 MADS.
 FT DOMAIN 3 165 K-BOX.
 FT CONFLICT 199 A -> R (IN REF. 2).
 SQ SEQUENCE 232 AA: 27341 MW: 669070319F9857C3 CRC64;

Query Match 34.5%; Score 51; DB 1; Length 232;
 Best Local Similarity 44.4%; Pred. No. 2;
 Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;
 QY 7 ORYG-----RELRRMSDEFGSFK 25
 DB 107 ORLGECLDELIDQELRLDEMENTFRK 133

RESULT 8
 ID PROB_CAMJE STANDARD: PRT; 1378 AA.
 AC 046124; 09P131;

DT 01-NOV-1997 (Rel. 35, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (Transcriptase
 DE beta chain) (RNA polymerase beta subunit).
 GN RPOB OR C00478.
 OS Campylobacter jejuni.
 OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
 OC Campylobacter.
 OX NCBI_Taxid:197;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN: NCTC 11168;
 RX MEDLINE:20150912; PubMed-10688204;
 RA Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
 RA Basham D., Chillingworth T., Davies R.M., Feltham T., Holtroyd S.,
 RA Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
 RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
 RA Whitehead S., Barrett B.G.,
 RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
 RT reveals hypervariable sequences.";
 RL Nature 403:665-668(2000).
 RL [2]
 RP SEQUENCE OF 338-1031 FROM N.A.
 RX MEDLINE:96084944; PubMed-7489896;
 RA Bustamante V.H., Puente J.L., Sanchez-Lopez F., Bobadilla M.,
 RA Calva E.;
 RT *Identification of Campylobacter jejuni and C. coli using the rpoB
 RT gene and a cryptic DNA fragment from C. jejuni.*;
 RL Gene 163:118(1995).
 CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
 CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
 CC SUBSTRATES.
 CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
 CC (RNA)(N).
 CC -1- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
 CC ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
 CC BETA CHAIN.
 CC -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
 CC -----
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 CC -----
 DR EMBL: AL139075; CAB75116.1; -
 DR EMBL: X77304; CA54509.1; -
 DR InterPro: IPR001572; RNA_POL_B.
 DR Pfam: PF00562; RNA_POL_B; 1.
 DR PROSITE: PS01166; RNA_POL_BETA; 1.
 DR Transcription: Transcription; DNA-directed RNA polymerase;
 KW Complete proteome.
 FT CONFLICT 338 347 NDLANGVDA -> MTWLMALMP (IN REF. 2).
 FT CONFLICT 558 558 A -> R (IN REF. 2).
 FT CONFLICT 671 671 C -> S (IN REF. 2).
 FT CONFLICT 691 691 A -> R (IN REF. 2).
 SQ SEQUENCE 1378 AA: 155915 MW: AB7467C305028B55 CRC64;

Query Match 33.8%; Score 50; DB 1; Length 1378;
 Best Local Similarity 40.6%; Pred. No. 20;
 Matches 13; Conservative 3; Mismatches 10; Indels 6; Gaps 2;
 QY 3 LMAORYG--RELRRM---SDEFGSFKGLK 28
 DB 1306 WALEAYGAHATREKLTIKSDVEGRFSAYK 1337

RESULT 9
 ID RPOB_PSEAE
 RMUC_PSEAE

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ID  RMUC_PSEAE  STANDARD;  PRT;  453 AA.
AC  091d03:
DT  01-MAR-2002 (Rel. 41, Created)
DT  01-MAR-2002 (Rel. 41, last sequence update)
DT  01-MAR-2002 (Rel. 41, last annotation update)
DE  DNA recombination protein rmuc homolog.
GN  RMUC OR PA1031.
OS  Pseudomonas aeruginosa.
OC  Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OX  Pseudomonas.
OY  NCBI_TaxID=287;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN-ATCC 15692 / PA01.
RX  MEDLINE-20437337; PubMed-10984043;
RA  Hickey C.K., Pham X.-O.T., Ervin A.L., Mizoguchi S.D., Warren P.,
RA  Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA  Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA  Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA  Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT  "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT  opportunistic pathogen."
RL  Nature 406:959-964(2000).
CC  -1- SIMILARITY: BELONGS TO THE RMUC FAMILY.
CC  -1- FUNCTION: Involved in DNA recombination (By similarity).
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC  use by non-profit institutions as long as its content is in no way
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CC  or send an email to license@sib-sib.ch).
CC  -----
DR  EMBL: AE004535; AAC04420.1;
DR  InterPro: IPR003798; DUF195;
DR  Pfam: PF02646; DUF195; 1.
KW  DNA recombination; Coiled coil; Complete proteome.
FT  DOMAIN
FT  16 201 COILED COIL (POTENTIAL).
SQ  SEQUENCE 453 AA; 51539 MW; 1E7EA57E82EC5E4B CRC64;

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Query Match      33.1%; Score 49; DB 1; Length 453;
Best Local Similarity 55.6%; Pred. No. 8.3;
Matches 10; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

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OY  4 WAAORYGR-ELRMSDE 19
DB  65 WASEHGRREELRLASE 82

RESULT 10
RAS3_RHIRA  STANDARD;  PRT;  205 AA.
ID  RAS3_RHIRA  STANDARD;  PRT;  205 AA.
AC  P22280:
DT  01-AUG-1991 (Rel. 19, Created)
DT  01-AUG-1991 (Rel. 19, last sequence update)
DT  30-MAY-2000 (Rel. 39, last annotation update)
DE  Ras-1-like protein 3.
GN  RAS3.
OS  Rhizomucor racemosus (Mucor circinelloides f. lusitanicus).
OC  Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;
OX  Mucor.
OY  NCBI_TaxID=4841;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN-ATCC 12168;
RX  MEDLINE-91061774; PubMed-171021;
RA  Casale W.L., McConnell D.G., Wang S.-Y., Lee Y.-J., Linz J.E.;
RA  "Expression of a gene family in the dimorphic fungus Mucor racemosus
RA  which exhibits striking similarity to human ras genes."
RT  Mol. Cell. Biol. 10:6654-6663(1990).

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CC  -1- ENZYME REGULATION: ALTERNATE BETWEEN AN INACTIVE FORM BOUND TO GDP
CC  AND AN ACTIVE FORM BOUND TO GTP. ACTIVATED BY A GUANINE
CC  NUCLEOTIDE-EXCHANGE FACTOR (GEF) AND INACTIVATED BY A GTPASE-
CC  ACTIVATING PROTEIN (GAP).
CC  -1- SUBCELLULAR LOCATION: PLASMA MEMBRANE.
CC  -1- DEVELOPMENTAL STAGE: IN SPORULATING MYCELIUM AND MUCH LESS IN
CC  GERMLING AND YEAST.
CC  -1- SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RAS FAMILY.
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  -----
DR  EMBL: M55177; AAA83379.1;
DR  PIR: C36365; C36365.
DR  HSP: P01112; 1PIL.
DR  InterPro: IPR003577; Ras.
DR  Pfam: PF00071; Ras_1.
DR  PRINTS: PR00449; RASTRNSFRNG.
DR  SMART: SM00173; Ras_1.
KW  GTP-binding; Prenylation; Lipoprotein.
FT  NP_BIND 16 23 GTP (BY SIMILARITY).
FT  NP_BIND 63 67 GTP (BY SIMILARITY).
FT  NP_BIND 122 125 GTP (BY SIMILARITY).
FT  DOMAIN 38 46 EFFECTOR REGION (PROBABLE).
FT  LIPID 202 202 FARNESYL (BY SIMILARITY).
SQ  SEQUENCE 205 AA; 23408 MW; DBF066466F090F50 CRC64;

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Query Match      32.4%; Score 48; DB 1; Length 205;
Best Local Similarity 62.5%; Pred. No. 4.9;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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OY  11 RELRMSDEFFGSRKG 26
DB  168 RELRMRKREDEGRSGK 183

RESULT 11
6PGL_THEMA  STANDARD;  PRT;  220 AA.
ID  6PGL_THEMA  STANDARD;  PRT;  220 AA.
AC  09X0N8:
DT  30-MAY-2000 (Rel. 39, Created)
DT  30-MAY-2000 (Rel. 39, last sequence update)
DT  16-OCT-2001 (Rel. 40, last annotation update)
DE  6-phosphogluconolactonase (EC 3.1.1.31) (6PGL).
GN  6GL OR DEVB OR TM1154.
OS  Thermotoga maritima.
OC  Bacteria; Thermotogales; Thermotoga.
OX  NCBI_TaxID=2336;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN-MSB8 / DSM 3109;
RX  MEDLINE-99287316; PubMed-10360571;
RA  Nelson K.E., Clayton R.A., Gill S.R., Gwin M.L., Dodson R.J.,
RA  Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA  McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA  Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA  Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA  Salzberg S.L., Smith R.O., Venter J.C., Fraser C.M.;
RT  "Evidence for lateral gene transfer between Archaea and Bacteria from
RT  genome sequence of Thermotoga maritima."
RL  Nature 399:323-329(1999).
CC  -1- FUNCTION: HYDROLYSIS OF 6-PHOSPHOGLUCONOLACTONE TO 6-
CC  PHOSPHOGLUCONATE.
CC  -1- CATALYTIC ACTIVITY: 6-phospho-D-glucono-1,5-lactone + H(2)O = 6-
CC  phospho-D-gluconate.
CC  -1- PATHWAY: SECOND STEP IN PENTOSE PHOSPHATE PATHWAY.

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CC -1- SIMILARITY: BELONGS TO THE GLUCOSAMINE/GALACTOSAMINE-6-PHOSPHATE
CC ISOMERASE FAMILY: 6-PHOSPHOGLUCONOLACTONASE SUPERFAMILY
CC -----
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CC -----
CC EMBL: AE001772; AAD36230.1; -
CC TIGR: TM154; -
CC InterPro: IPR000457; Glucosamine_1so.
CC Pfam: PF01182; Glucosamine_1so; 1.
CC Hydrolase: Complete proteome.
CC SEQUENCE 220 AA; 25325 MW; 9B0FD07EE01E60C3 CRC64;
SO

Query Match 32.4%; Score 48; DB 1; Length 220;
Best Local Similarity 34.8%; Pred. No. 5.3;
Matches 8; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

OY 5 AAGRYGRLRMSDEFSFKL 27
DB 111 ACEKEREIKSATDPAIDLQIM 133

RESULT 12
THRC_SQUTU STANDARD: PRT; 519 AA.
AC O9MT28;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Threonine synthase, chloroplast precursor (EC 4.2.99.2) (TS).
OS Solanum tuberosum (potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; eusterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RA Casazza P., Kaiser S., Willmitzer L., Hoefgen R., Hesse H.;
RT "Isolation and characterization of a cDNA encoding threonine synthase
RT from Solanum tuberosum";
RL Submitted (Aug-1998) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: O-phospho-L-homoserine + H(2)O = L-threonine +
CC phosphate.
CC -1- COFACTOR: Pyridoxal phosphate (By similarity).
CC -1- ENZYME REGULATION: Allosterically activated by S-adenosyl-
CC methionine (SAM) (By similarity).
CC -1- PATHWAY: Threonine biosynthesis; last step.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Chloroplast (By similarity).
CC -1- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
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CC -----
CC EMBL: AF082894; AAF74984.1; -
CC InterPro: IPR001926; B6-enzyme_beta.
CC Pfam: PF00291; PALP; 1.
CC PROSITE: PS00165; DEHYDRATASE_SER_THR; 1.
KW Threonine biosynthesis; lyase; Pyridoxal phosphate; Allosteric enzyme;
KW Chloroplast; Transit peptide.
FT TRANSIT 1 40 CHLOROPLAST (BY SIMILARITY).
FT CHAIN 41 519 THREONINE SYNTHASE.

FT BINDING 196 196 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SO SEQUENCE 519 AA; 57412 MW; 114C0979CD21464 CRC64;

Query Match 32.4%; Score 48; DB 1; Length 519;
Best Local Similarity 35.3%; Pred. No. 14;
Matches 12; Conservative 6; Mismatches 8; Indels 8; Gaps 1;

OY 2 NLMAAGRYGRLRMSD-----EFGCSFKL 27
DB 165 NLFWAERFGKQFLGMDLWVKRGISHTGSEFKL 198

RESULT 13
THRC_ARATH STANDARD: PRT; 526 AA.
AC O957B5; 039144;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Threonine synthase, chloroplast precursor (EC 4.2.99.2) (TS).
GN ATG62840 OR F27B13.80.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustersids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. Wassilewskija;
RX MEDLINE=99418329; PubMed=10490396;
RA Bartlem D., Tamaki Y., Naito S.;
RT "Genomic nucleotide sequence of the Arabidopsis threonine synthase
RT gene";
RL (In) Plant Gene Register PGR99-108.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=20083488; PubMed=10617198;
RA Mayer K.F.X., Scheller C., Wambutt R., Murphy G., Voelckert G.,
RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terry N.,
RA Harris B., Ansoorge W., Brandt P., Grivell L.A., Rieger M.,
RA Weichselgartner M., de Simone V., Obermaler B., Macho R., Mueller M.,
RA Kreis M., Dalseny M., Puigdomenech P., Watson M., Schmidheini T.,
RA Reichert B., Portetle D., Perez-Alonso M., Boutry M., Bancroft I.,
RA Vos P., Hohseil J., Zimmermann W., Medler H., Ridley P.,
RA Langham S.-A., McCullagh B., Blham L., Robben J.,
RA Van der Schuren J., Grymoprez B., Chuang Y.-J., Vandenussche F.,
RA Breken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
RA Weltzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
RA Holzner E., Brandt A., Peters S., van Staveren M., Dirse W.,
RA Moolman P., Klein lankhorst R., Rose M., Hauf J., Koeltter P.,
RA Benneiser S., Hempel S., Feldpausch M., Lambert S., Van den Daele H.,
RA De Keyser A., Buyschert C., Giesen J., Villarroel R., de Clercq R.,
RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Alton S.,
RA Clark L., Doggett J., Hall S., Kay M., Lemard N., Kclay K., Hayes R.,
RA Petek A., Rajandream N.A., Lyne M., Benes V., Kechnan S.,
RA Botkova D., Blocker H., Scharte M., Grimm M., Loehner T.-H.,
RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fairman B., Granderath K., Dauner D., Herzl A.,
RA Neumann S., Argirou A., Vitale D., Liqouri R., Pitravandi E.,
RA Massenet O., Quigley F., Clabaud G., Muendlin A., Felder R.,
RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Chedof R., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Barges M., Terol J., Torres A.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Heijman D., Schwarz S., Scholler P., Heber S., Francis P., Bleike C.,
RA Zacaria P., Bayan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Parnell L., Dehlin N., Guo J., Schutz K., Huang E., Spiegel L.,
RA Sektouk M., Murray J., Snel P., Cordes M., Abu-Threideh J.,
RA Stoneking T., Kallio J., Graves J., Harmon G., Edwards J.,
RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,

RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
 RA Kramar J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
 RA Nelson J., Splich J., Ryan E., Andrews S., Geisel C., Layman L.,
 RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,
 RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Jordan C.,
 RA Ma P., Zhong J., Preston R., Vill D., Shekher M., Matero A., Shah R.,
 RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
 RA Grant S., Shoddy N., Hasegawa A., Rodriguez M., Hoffman J., Till S.,
 RA Chen E., Marra M., Martienssen R., McCombie W.R.;
 RA "Sequence and analysis of chromosome 4 of the plant *Arabidopsis*
 RA *thaliana*.";
 RT Nature 402:769-777(1999).
 RL [3]
 RN SEQUENCE OF 2-526 FROM N.A., AND CHARACTERIZATION.
 RP STRAIN-CV. Columbia;
 RX PubMed-8706836;
 RA Curien G., Dumas R., Ravanet S., Douce R.;
 RT "Characterization of an *Arabidopsis thaliana* cDNA encoding an
 RT S-adenosylmethionine-sensitive threonine synthase. Threonine synthase
 RT from higher plants.";
 RL FEBS Lett. 390:85-90(1996).
 RN [4]
 RP CHARACTERIZATION.
 RX PubMed-9748328.
 RA Curien G., Job D., Douce R., Dumas R.;
 RT "Allosteric activation of *Arabidopsis thaliana* threonine synthase by
 RT S-adenosylmethionine.";
 RL Biochemistry 37:13212-13221(1998).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 41-526.
 RX PubMed-11344332;
 RA Thumazeau R., Curien G., Dumas R., Bion V.;
 RT "Crystal structure of threonine synthase from *Arabidopsis thaliana*.";
 RL Protein Sci. 10:638-648(2001).
 CC -1- CATALYTIC ACTIVITY: O-phospho-L-homoserine + H(2)O -> L-threonine +
 CC phosphate.
 CC -1- COFACTOR: Pyridoxal phosphate.
 CC -1- ENZYME REGULATION: Allosterically activated up to 20-fold by S-
 CC adenosyl-methionine (SAM).
 CC -1- PATHWAY: Threonine biosynthesis; last step.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Chloroplast.
 CC -1- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: AB027151; BAA77707.1; -;
 DR EMBL: AL050352; CAB43659.1; -;
 DR EMBL: AL161575; CAB79742.1; -;
 DR EMBL: LA1666; AAB04607.1; -;
 DR PDB: 1ESX; 02-AUG-01.
 DR InterPro: IPR001926; PALP.
 DR Pfam: PF00291; PALP.
 DR PROSITE: PS00165; DEHYDRATASE_SER_THR.1.
 KM Threonine biosynthesis; Lyase; Pyridoxal phosphate; Allosteric enzyme;
 KM Chloroplast; Transit peptide; 3D-structure.
 FT TRANSIT 1 40
 FT CHAIN 41 526 THREONINE SYNTHASE.
 FT BINDING 203 203 PYRIDOXAL PHOSPHATE.
 FT CONFLICT 2 2 A -> L (IN REF. 3).
 SQ SEQUENCE 526 AA; 57776 MW; B27787A57B882AD0 CRC64;

Query Match 32.4%; Score 48; DB 1; Length 526;
 Best Local Similarity 35.3%; Pred. No. 14;
 Matches 12; Conservative 6; Mismatches 8; Indels 8; Gaps 1;

QY 2 NLMAQRYGRELRLMSD-----EFEGSKGL 27
 ID 172 NLFWAERFGKFLGMDLWVKHCGISHTSFKDL 205
 Db
 RESULT 14
 FMRA_CALPA
 ID FMRA_CALPA STANDARD; PRT; 334 AA.
 AC 001133.
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Antho-RFamide neuropeptides precursor.
 OC Calliactis parasitica (sea anemone).
 OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actinoptera;
 OC Nymphaeae; Hormathididae; Calliactis.
 OX NCBI_TaxID=6114;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91172845; PubMed=1706527;
 RA Damer D., Schmutzler C., Diekhoff D., Grimmelikhuijzen C.J.P.;
 RT "Primary structure of the precursor for the sea anemone neuropeptide
 RT Antho-RFamide (<Glu-Gly-Arg-Phe-NH2>.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:2555-2559(1991).
 CC -1- FUNCTION: NOT KNOWN BUT IT COULD ACT AS A TRANSMITTER AT
 CC NEUROMUSCULAR SYNAPSES.
 CC -1- TISSUE SPECIFICITY: NEURONS ASSOCIATED WITH SMOOTH MUSCLE FIBERS.
 CC -----
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 CC -----
 DR EMBL: M59166; AAA27878.1; -;
 DR PIR: A39172; A39172.
 DR InterPro: IPR002544; FARP.
 DR Pfam: PF01581; FARP; 15.
 KM Neuropeptide; Amidation; Repeat; Signal.
 FT SIGNAL 1 26
 FT PEPTIDE 117 120
 FT PEPTIDE 126 129
 FT PEPTIDE 135 138
 FT PEPTIDE 143 146
 FT PEPTIDE 152 155
 FT PEPTIDE 161 164
 FT PEPTIDE 170 173
 FT PEPTIDE 179 182
 FT PEPTIDE 188 191
 FT PEPTIDE 197 200
 FT PEPTIDE 206 209
 FT PEPTIDE 215 218
 FT PEPTIDE 224 227
 FT PEPTIDE 234 237
 FT PEPTIDE 243 246
 FT PEPTIDE 253 256
 FT PEPTIDE 263 266
 FT PEPTIDE 272 275
 FT PEPTIDE 281 284
 FT PEPTIDE 120 129
 FT MOD_RES 129 138
 FT MOD_RES 138 146
 FT MOD_RES 146 155
 FT MOD_RES 155 164
 FT MOD_RES 164 173
 FT MOD_RES 173 182
 FT MOD_RES 182 191
 FT MOD_RES 191 200
 FT MOD_RES 200 209
 FT MOD_RES 209 218
 FT MOD_RES 218 218
 AMIDATION (G-121 PROVIDE AMIDE GROUP).
 AMIDATION (G-130 PROVIDE AMIDE GROUP).
 AMIDATION (G-139 PROVIDE AMIDE GROUP).
 AMIDATION (G-147 PROVIDE AMIDE GROUP).
 AMIDATION (G-156 PROVIDE AMIDE GROUP).
 AMIDATION (G-165 PROVIDE AMIDE GROUP).
 AMIDATION (G-174 PROVIDE AMIDE GROUP).
 AMIDATION (G-183 PROVIDE AMIDE GROUP).
 AMIDATION (G-192 PROVIDE AMIDE GROUP).
 AMIDATION (G-201 PROVIDE AMIDE GROUP).
 AMIDATION (G-210 PROVIDE AMIDE GROUP).
 AMIDATION (G-219 PROVIDE AMIDE GROUP).

FT MOD_RES 227 227 AMIDATION (G-228 PROVIDE AMIDE GROUP).
 FT MOD_RES 237 237 AMIDATION (G-228 PROVIDE AMIDE GROUP).
 FT MOD_RES 246 246 AMIDATION (G-247 PROVIDE AMIDE GROUP).
 FT MOD_RES 256 256 AMIDATION (G-257 PROVIDE AMIDE GROUP).
 FT MOD_RES 266 266 AMIDATION (G-267 PROVIDE AMIDE GROUP).
 FT MOD_RES 275 275 AMIDATION (G-276 PROVIDE AMIDE GROUP).
 FT MOD_RES 284 284 AMIDATION (G-285 PROVIDE AMIDE GROUP).
 SO SEQUENCE 334 AA: 39781 MW: 438E182C736EB583 CRC64;

Query Match 32.1%; Score 47.5; DB 1; Length 334;
 Best Local Similarity 44.0%; Pred. No. 9.9;
 Matches 11; Conservative 3; Mismatches 10; Indels 1; Gaps 1;

Oy 1 KNLMAAORYGREL-RMGDEFGSF 24
 Db 89 KRRYVPGRYGREGFGREFGGRF 113

RESULT 15

BIM_HUMAN STANDARD; PRT: 198 AA.
 ID BIM_HUMAN 043521; 043522;
 AC 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Bcl2-like protein 11 (Bcl2 interacting mediator of cell death).
 CN BCL2L1 OR BIM.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A., FUNCTION, AND ALTERNATIVE SPLICING.
 RC TISSUE=peripheral blood, and spleen;
 RX MEDLINE=98094360; PubMed=9430630;
 RA O'Connor L., Strasser A., O'Reilly L.A., Hausmann G., Adams J.M.,
 RA Cory S., Huang D.C.S.;
 RT "Bim: a novel member of the Bcl-2 family that promotes apoptosis.";
 RL EMBD J. 17:384-395(1998).
 CC -1- FUNCTION: INDUCES APOPTOSIS. ISOFORM BIML IS MORE POTENT THAN
 CC ISOFORM BIMEL.
 CC -1- SUBUNIT: FORMS HETERODIMERS WITH A NUMBER OF ANTIAPOPTOTIC BCL-2
 CC PROTEINS INCLUDING MCL-1, BCL-2, BCL-XL, BFL-1, AND BHRF-1. DOES
 CC NOT HETERODIMERIZE WITH PROAPOPTOTIC PROTEINS SUCH AS BAD, BOK,
 CC BAX OR BAK (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: ASSOCIATED WITH INTRACITOPLASMIC MEMBRANES
 CC (BY SIMILARITY).
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: BIMEL (SHOWN HERE) AND
 CC BIML; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- DOMAIN: THE BH3 DOMAIN IS REQUIRED FOR BCL-2 BINDING AND
 CC CYTOTOXICITY.
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOMOLOGY DOMAIN 3 (BH3).
 CC -----
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 CC -----
 CC EMBL: AF032457; AAC39593.1; -;
 CC EMBL: AF032458; AAC39594.1; -;
 CC MIM: 603827; -;
 DR InterPro: IPR000712; Bcl_2.
 DR PROSITE: PS01259; BH3; FALSE_NEG.
 KM Apoptosis; Alternative splicing; Membrane.
 FT DOMAIN 148 162 BH3.
 FT VARSPLIT 42 101 MISSING (IN ISOFORM BIML).
 SO SEQUENCE 198 AA: 22171 MW: D75735E469CA6997 CRC64;

Query Match 31.8%; Score 47; DB 1; Length 198;
 Best Local Similarity 45.5%; Pred. No. 6.6;
 Matches 10; Conservative 3; Mismatches 5; Indels 4; Gaps 1;

Oy 3 LMAAORYGREL-RMGDEFGSF 24
 Db 146 IWIAD-ELRRIGDEFNAY 163

Search completed: September 20, 2002, 11:04:35
 Job time: 1632 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 20, 2002, 11:03:47 ; Search time 172.19 Seconds
(without alignments)
28.131 Million cell updates/sec

Title: US-09-544-664-55
Perfect score: 148
Sequence: 1 KMLEAARYGRELIRMSDEFGSFKGLK 28

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_orfanelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_ricent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	91	61.5	146	13	Q919N2 brachydanio
2	53	35.8	223	16	Q10843 mycobacteri
3	52.5	35.5	505	8	Q47148 menziesia c
4	52.5	35.5	506	8	Q63960 rhododendro
5	52.5	35.5	506	8	Q62972 rhododendro
6	52.5	35.5	506	8	Q62973 rhododendro
7	52.5	35.5	506	8	Q62974 rhododendro
8	52.5	35.5	506	8	Q62975 rhododendro
9	52.5	35.5	506	8	Q62977 rhododendro
10	52.5	35.5	506	8	Q62978 rhododendro
11	52.5	35.5	506	8	Q62980 rhododendro
12	52.5	35.5	506	8	Q62981 rhododendro
13	52.5	35.5	506	8	Q62982 rhododendro
14	52.5	35.5	506	8	Q62983 rhododendro
15	52.5	35.5	506	8	Q62984 rhododendro
16	52.5	35.5	506	8	Q62988 rhododendro

17	52.5	35.5	506	8	Q62989 rhododendro
18	52.5	35.5	506	8	Q62990 rhododendro
19	52.5	35.5	506	8	Q62991 rhododendro
20	52.5	35.5	506	8	Q62992 ledum palus
21	52.5	35.5	506	8	Q62993 menziesia m
22	52.5	35.5	506	8	Q47149 rhododendro
23	52.5	35.5	506	8	Q47152 rhododendro
24	52.5	35.5	506	8	Q47155 rhododendro
25	52.5	35.5	506	8	Q47158 menziesia p
26	52.5	35.5	506	8	Q47170 rhododendro
27	52.5	35.5	506	8	Q47171 rhododendro
28	52.5	35.5	506	8	Q47173 rhododendro
29	52.5	35.5	506	8	Q47174 tsusithyil
30	52.5	35.5	506	8	Q47175 rhododendro
31	52.5	35.5	507	8	Q62985 rhododendro
32	52.5	35.5	507	8	Q62986 rhododendro
33	52.5	35.5	508	8	Q62979 rhododendro
34	51.5	34.8	506	8	Q47153 rhododendro
35	51.5	34.8	506	8	Q47160 rhododendro
36	51	34.5	231	10	Q9SE60 arabisdopsis
37	51	34.5	232	10	Q9SE703 arabisdopsis
38	51	34.5	232	10	Q9SE022 arabisdopsis
39	51	34.5	232	10	Q9SE021 arabisdopsis
40	51	34.5	232	10	Q9SE020 arabisdopsis
41	51	34.5	232	10	Q9SE019 arabisdopsis
42	51	34.5	232	10	Q9SE018 arabisdopsis
43	51	34.5	232	10	Q9SE017 arabisdopsis
44	51	34.5	232	10	Q9SE016 arabisdopsis
45	51	34.5	232	10	Q9SE015 arabisdopsis

ALIGNMENTS

RESULT 1
ID Q919N2 PRELIMINARY: PRT: 146 AA.
AC Q919N2
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE BAD.
GN BAD.
OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Danio.
OX NCBI_Taxid-7955;
RN [1]
RP SEQUENCE FROM N. A.
RX MEDLINE-20373792; PubMed-10917738;
RA Inohara N., Nunez G.,
RT Genes with homology to mammalian apoptosis regulators identified in
RT zebrafish.
RL Cell Death Differ. 7:509-510(2000).
DR EMBL: AF231017; AAF65962.2;
SQ SPROUNCE 146 AA; 16546 MW; 28A5650BB5107ECB CXC64;

Query Match 61.5%; Score 91; DB 13; Length 146;
Best local Similarity 61.5%; Pred. No. 1.3e-05;
Matches 16; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 3 LMAAORYGRELIRMSDEFGSFKGLK 28
DB 89 LMAAKRTGQGLRMSDEFGKMKRVK 114
RESULT 2
ID Q10843 PRELIMINARY: PRT: 223 AA.
AC Q10843
DT 01-NOV-1998 (TREMBLrel. 08, Created)

DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE HYPOPHICAL_24.1 KPA PROTEIN CY39.03C.
 GN RV2014 OR MYCY39.03C.
 OS MYCOBACTERIUM TUBERCULOSIS.
 OC Bacteria; Firmicutes; Actinobacteriia; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekaia F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Kiegh A., McLellan J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skellton S., Squares S., Squares R.,
 RA Stalton J.E., Taylor K., Whitehead S., Barrett B.G.,
 RT Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.
 RL Nature 393:537-544(1998).
 CC -1- SIMILARITY: TO M.PARATUBERCULOSIS IS900.
 DR EMBL: Z74025; CAA98415.1; -
 DR Tuberculist; RV2014: -
 DR InterPro: IPR003346; Transposase-20.
 DR Pfam: PF02371; Transposase-20; 1.
 KM Hypothetical protein; Complete proteome.
 SQ SEQUENCE 223 AA; 24132 MW; 7045675001FFEF37 CRC64;

Query Match 35.8%; Score 53; DB 16; Length 223;
 Best Local Similarity 58.8%; Pred. No. 7.6;
 Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
 Oy 2 NLNAAQRYGRLRMSD 18
 DB 165 NLNAAQRYGRLRMSD 181

RESULT 3
 ID 047148 PRELIMINARY; PRT; 505 AA.
 AC 047148;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE RIBOSOMAL MATURASE (FRAGMENT).
 GN MATK.
 OS Menziesia ciliolata.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Ericales; Ericaceae; Menziesia.
 OX NCBI_TaxID=9134;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kwon K.A.;
 RT "Phylogenetics of Rhododendroideae (Ericaceae).";
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U61331; AAC15245.2; -
 DR InterPro: IPR000442; Intron_maturase2.
 DR InterPro: IPR002866; MatK_N.
 DR Pfam: PF01348; Intron_maturase2; 1.
 DR Pfam: PF01824; MatK_N; 1.
 KW Chloroplast.
 FT NON_CODING
 SQ SEQUENCE 505 AA; 60233 MW; E5F927AD2E57DE5 CRC64;

Query Match 35.5%; Score 52.5; DB 8; Length 505;
 Best Local Similarity 37.5%; Pred. No. 23;

Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;
 Oy 1 KNLMAA-----QRYGRLRMSDEFGSK 25
 DB 390 KPYMAALSDSDIERGRIRNLSHYSGSLK 421

RESULT 4
 ID 063960 PRELIMINARY; PRT; 506 AA.
 AC 063960;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE RIBOSOMAL MATURASE.
 GN YCF14 OR MATK.
 OS Rhododendron tashiroi, and
 OS Rhododendron farreri.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Ericales; Ericaceae; Rhododendron.
 OX NCBI_TaxID=75382, 75380;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kusashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
 RA Yukawa T.;
 RL J. Jpn. Bot. 0:0-0(1998).
 DR EMBL: AB012749; BAA25870.1; -
 DR EMBL: AB012745; BAA25866.1; -
 DR InterPro: IPR000442; Intron_maturase2.
 DR InterPro: IPR002866; MatK_N.
 DR Pfam: PF01348; Intron_maturase2; 1.
 DR Pfam: PF01824; MatK_N; 1.
 KW Chloroplast.
 SQ SEQUENCE 506 AA; 60389 MW; DE0C07ARE608B787 CRC64;

Query Match 35.5%; Score 52.5; DB 8; Length 506;
 Best Local Similarity 37.5%; Pred. No. 23;
 Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;
 Oy 1 KNLMAA-----QRYGRLRMSDEFGSK 25
 DB 391 KPYMAALSDSDIERGRIRNLSHYSGSLK 422

RESULT 5
 ID 062972 PRELIMINARY; PRT; 506 AA.
 AC 062972;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE RIBOSOMAL MATURASE.
 GN MATK.
 OS Rhododendron ovatum.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Ericales; Ericaceae; Rhododendron.
 OX NCBI_TaxID=49169;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kusashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
 RA Yukawa T.;
 RT "Investigation of Sectional Relationships in the Genus
 Rhododendron(Ericaceae) based on matK Sequences.";
 RL J. Jpn. Bot. 0:0-0(1998).
 DR EMBL: AB012729; BAA25850.1; -
 DR InterPro: IPR000442; Intron_maturase2.
 DR InterPro: IPR002866; MatK_N.
 DR Pfam: PF01348; Intron_maturase2; 1.

DR Pfam: PF01824; Matk_N; 1.
 KW Chloroplast.
 SQ SEQUENCE 506 AA; 60493 MW; D230554B8C20FEF0 CRC64;

Query Match 35.5%; Score 52.5; DB 8; Length 506;
 Best Local Similarity 37.5%; Pred. No. 23;
 Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

QY 1 KNLMAA-----QRYGRLRMSDEFGSFK 25
 ID 062973 PRELIMINARY; PRT; 506 AA.
 AC 062973;
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE RIBOSOMAL MATURASE.
 GN MATK.
 OS Rhododendron stamineum.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Ericales; Ericaceae; Rhododendron.
 OX NCBI_TaxID=75575;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
 RA Yukawa T.;
 RT "Investigation of Sectional Relationships in the Genus
 RT Rhododendron(Ericaceae) based on matk Sequences.";
 RL J. Jpn. Bot. 0:0-0(1998).
 RL EMBL: AB012730; BAA25851.1;
 DR InterPro: IPR000442; Intron_maturase2.
 DR InterPro: IPR002866; Matk_N.
 DR Pfam: PF01348; Intron_maturase2; 1.
 DR Pfam: PF01824; Matk_N; 1.
 KW Chloroplast.
 SQ SEQUENCE 506 AA; 60611 MW; 53FA36E7CD99483C CRC64;

Query Match 35.5%; Score 52.5; DB 8; Length 506;
 Best Local Similarity 37.5%; Pred. No. 23;
 Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

QY 1 KNLMAA-----QRYGRLRMSDEFGSFK 25
 ID 062974 PRELIMINARY; PRT; 506 AA.
 AC 062974;
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE RIBOSOMAL MATURASE.
 GN MATK.
 OS Rhododendron albiflorum.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Ericales; Ericaceae; Rhododendron.
 OX NCBI_TaxID=49161;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
 RA Yukawa T.;

RESULT 7
 ID 062974 PRELIMINARY; PRT; 506 AA.
 AC 062974;
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE RIBOSOMAL MATURASE.
 GN MATK.
 OS Rhododendron albiflorum.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Ericales; Ericaceae; Rhododendron.
 OX NCBI_TaxID=49161;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
 RA Yukawa T.;

RT "Investigation of Sectional Relationships in the Genus
 RT Rhododendron(Ericaceae) based on matk Sequences.";
 RL J. Jpn. Bot. 0:0-0(1998).
 DR EMBL: AB012731; BAA25852.1;
 DR InterPro: IPR000442; Intron_maturase2.
 DR InterPro: IPR002866; Matk_N.
 DR Pfam: PF01348; Intron_maturase2; 1.
 DR Pfam: PF01824; Matk_N; 1.
 KW Chloroplast.
 SQ SEQUENCE 506 AA; 60491 MW; 3CCC930385B12DBC CRC64;

Query Match 35.5%; Score 52.5; DB 8; Length 506;
 Best Local Similarity 37.5%; Pred. No. 23;
 Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

QY 1 KNLMAA-----QRYGRLRMSDEFGSFK 25
 ID 062975 PRELIMINARY; PRT; 506 AA.
 AC 062975;
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE RIBOSOMAL MATURASE.
 GN MATK.
 OS Rhododendron ponticum.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Ericales; Ericaceae; Rhododendron.
 OX NCBI_TaxID=49628;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
 RA Yukawa T.;
 RT "Investigation of Sectional Relationships in the Genus
 RT Rhododendron(Ericaceae) based on matk Sequences.";
 RL J. Jpn. Bot. 0:0-0(1998).
 RL EMBL: AB012732; BAA25853.1;
 DR InterPro: IPR000442; Intron_maturase2.
 DR InterPro: IPR002866; Matk_N.
 DR Pfam: PF01348; Intron_maturase2; 1.
 DR Pfam: PF01824; Matk_N; 1.
 KW Chloroplast.
 SQ SEQUENCE 506 AA; 60449 MW; 21DEF700B071B588 CRC64;

Query Match 35.5%; Score 52.5; DB 8; Length 506;
 Best Local Similarity 37.5%; Pred. No. 23;
 Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

QY 1 KNLMAA-----QRYGRLRMSDEFGSFK 25
 ID 062977 PRELIMINARY; PRT; 506 AA.
 AC 062977;
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE RIBOSOMAL MATURASE.
 GN MATK.
 OS Rhododendron luteum.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

RESULT 9
 ID 062977 PRELIMINARY; PRT; 506 AA.
 AC 062977;
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE RIBOSOMAL MATURASE.
 GN MATK.
 OS Rhododendron luteum.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

RESULT 9
 ID 062977 PRELIMINARY; PRT; 506 AA.
 AC 062977;
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE RIBOSOMAL MATURASE.
 GN MATK.
 OS Rhododendron luteum.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Ericales; Ericaceae; Rhododendron.
 OX NCBI_TaxID=49467;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
 RA Yukawa T.;
 RT *Investigation of Sectional Relationships in the Genus
 RT Rhododendron(Ericaceae) based on matk Sequences.";
 RL J. Jpn. Bot. 0:0-0(1998)
 DR EMBL; AB012734; BAA25855.1; -
 DR InterPro: IPR000442; Intron_maturse2.
 DR InterPro: IPR002866; MatK_N.
 DR Pfam: PF01348; Intron_maturas2; 1.
 DR Pfam: PF01824; MatK_N; 1.
 DR Chloroplast.
 KW SEQUENCE 506 AA; 60350 MW; F2B1DAC4BF91A609 CRC64;

Query Match 35.5%; Score 52.5; DB 8; Length 506;
 Best Local Similarity 37.5%; Pred. No. 23;
 Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

OY 1 KNJMAA-----QRYGRELRRMSDEFGSFK 25
 DB 391 KPVMALSDSDIIFRGRIRYRLSHYSGSLK 422

RESULT 10
 ID 062978 PRELIMINARY; PRT; 506 AA.
 AC 062978;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE RIBOSOMAL MATURASE.
 GN MATK.
 OS Rhododendron canadense.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Ericales; Ericaceae; Rhododendron.
 OX NCBI_TaxID=49465;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
 RA Yukawa T.;
 RT *Investigation of Sectional Relationships in the Genus
 RT Rhododendron(Ericaceae) based on matk Sequences.";
 RL J. Jpn. Bot. 0:0-0(1998)
 DR EMBL; AB012735; BAA25856.1; -
 DR InterPro: IPR000442; Intron_maturse2.
 DR InterPro: IPR002866; MatK_N.
 DR Pfam: PF01348; Intron_maturas2; 1.
 DR Pfam: PF01824; MatK_N; 1.
 DR Chloroplast.
 KW SEQUENCE 506 AA; 60350 MW; 5E832589ED64EA25 CRC64;

Query Match 35.5%; Score 52.5; DB 8; Length 506;
 Best Local Similarity 37.5%; Pred. No. 23;
 Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

OY 1 KNJMAA-----QRYGRELRRMSDEFGSFK 25
 DB 391 KPVMALSDSDIIFRGRIRYRLSHYSGSLK 422

RESULT 11
 ID 062980 PRELIMINARY; PRT; 506 AA.
 AC 062980;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)

DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE RIBOSOMAL MATURASE.
 GN MATK.
 OS Rhododendron albrechtii.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Ericales; Ericaceae; Rhododendron.
 OX NCBI_TaxID=49463;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
 RA Yukawa T.;
 RT *Investigation of Sectional Relationships in the Genus
 RT Rhododendron(Ericaceae) based on matk Sequences.";
 RL J. Jpn. Bot. 0:0-0(1998)
 DR EMBL; AB012737; BAA25858.1; -
 DR InterPro: IPR000442; Intron_maturse2.
 DR InterPro: IPR002866; MatK_N.
 DR Pfam: PF01348; Intron_maturas2; 1.
 DR Pfam: PF01824; MatK_N; 1.
 DR Chloroplast.
 KW SEQUENCE 506 AA; 60301 MW; 9D5877E063E856CB CRC64;

Query Match 35.5%; Score 52.5; DB 8; Length 506;
 Best Local Similarity 37.5%; Pred. No. 23;
 Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

OY 1 KNJMAA-----QRYGRELRRMSDEFGSFK 25
 DB 391 KPVMALSDSDIIFRGRIRYRLSHYSGSLK 422

RESULT 12
 ID 062981 PRELIMINARY; PRT; 506 AA.
 AC 062981;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE RIBOSOMAL MATURASE.
 GN MATK.
 OS Rhododendron pentaphyllum.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Ericales; Ericaceae; Rhododendron.
 OX NCBI_TaxID=75576;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
 RA Yukawa T.;
 RT *Investigation of Sectional Relationships in the Genus
 RT Rhododendron(Ericaceae) based on matk Sequences.";
 RL J. Jpn. Bot. 0:0-0(1998)
 DR EMBL; AB012738; BAA25859.1; -
 DR InterPro: IPR000442; Intron_maturse2.
 DR InterPro: IPR002866; MatK_N.
 DR Pfam: PF01348; Intron_maturas2; 1.
 DR Pfam: PF01824; MatK_N; 1.
 DR Chloroplast.
 KW SEQUENCE 506 AA; 60449 MW; B138208746D99258 CRC64;

Query Match 35.5%; Score 52.5; DB 8; Length 506;
 Best Local Similarity 37.5%; Pred. No. 23;
 Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

OY 1 KNJMAA-----QRYGRELRRMSDEFGSFK 25
 DB 391 KPVMALSDSDIIFRGRIRYRLSHYSGSLK 422

RESULT 13
 ID 062982 PRELIMINARY; PRT; 506 AA.
 AC 062982;
 DT 01-AUG-1998 (TREMblrel. 07, Created)
 DT 01-AUG-1998 (TREMblrel. 07, Last sequence update)
 DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 OS RIBOSOMAL MATURASE.
 OC Rhododendron nipponicum.
 OG Chloroplast.
 OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
 OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots;
 OC Asteridae: Ericales: Ericaceae: Rhododendron.
 RN NCBL_TaxID=75577;
 [1]
 RP SEQUENCE FROM N.A.
 RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
 RA Yukawa T.;
 RT "Investigation of Sectional Relationships in the Genus
 RT Rhododendron (Ericaceae) based on matk Sequences."
 RL J. Jpn. Bot. 0:0-0(1998).
 DR EMBL: AB012739; BAA25860.1; -;
 DR InterPro: IPR000442; Intron_maturase2.
 DR InterPro: IPR002866; Matk_N.
 DR Pfam: PF01348; Intron_maturase2; 1.
 DR Pfam: PF01824; Matk_N; 1.
 KW Chloroplast.
 SQ SEQUENCE 506 AA; 60419 MW; 1F95132CCF4F6B40 CRC64;

Query Match 35.5%; Score 52.5; DB 8; Length 506;
 Best Local Similarity 37.5%; Pred. No. 23;
 Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

OY 1 KN1MAA-----QRYGRELRRMSDEFECSFK 25
 Db 391 KPVMALSDSDIIERGRIRYRLNLSHYSGSLK 422

RESULT 14
 ID 062983 PRELIMINARY; PRT; 506 AA.
 AC 062983;
 DT 01-AUG-1998 (TREMblrel. 07, Created)
 DT 01-AUG-1998 (TREMblrel. 07, Last sequence update)
 DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 OS RIBOSOMAL MATURASE.
 GN MATK
 OS Rhododendron primuliflorum.
 OG Chloroplast.
 OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;
 OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots;
 OC Asteridae: Ericales: Ericaceae: Rhododendron.
 RN NCBL_TaxID=75578;
 [1]
 RP SEQUENCE FROM N.A.
 RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
 RA Yukawa T.;
 RT "Investigation of Sectional Relationships in the Genus
 RT Rhododendron (Ericaceae) based on matk Sequences."
 RL J. Jpn. Bot. 0:0-0(1998).
 DR EMBL: AB012740; BAA25861.1; -;
 DR InterPro: IPR000442; Intron_maturase2.
 DR InterPro: IPR002866; Matk_N.
 DR Pfam: PF01348; Intron_maturase2; 1.
 DR Pfam: PF01824; Matk_N; 1.
 KW Chloroplast.
 SQ SEQUENCE 506 AA; 60393 MW; DAAB47A759CFEC46 CRC64;

Query Match 35.5%; Score 52.5; DB 8; Length 506;

Best Local Similarity 37.5%; Pred. No. 23;
 Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

OY 1 KN1MAA-----QRYGRELRRMSDEFECSFK 25
 Db 391 KPVMALSDSDIIERGRIRYRLNLSHYSGSLK 422

RESULT 15
 ID 062984 PRELIMINARY; PRT; 506 AA.
 AC 062984;
 DT 01-AUG-1998 (TREMblrel. 07, Created)
 DT 01-AUG-1998 (TREMblrel. 07, Last sequence update)
 DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 OS RIBOSOMAL MATURASE.
 GN MATK
 OS Rhododendron ferrugineum (Alpenrose).
 OG Chloroplast.
 OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;
 OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots;
 OC Asteridae: Ericales: Ericaceae: Rhododendron.
 RN NCBL_TaxID=49622;
 [1]
 RP SEQUENCE FROM N.A.
 RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
 RA Yukawa T.;
 RT "Investigation of Sectional Relationships in the Genus
 RT Rhododendron (Ericaceae) based on matk Sequences."
 RL J. Jpn. Bot. 0:0-0(1998).
 DR EMBL: AB012741; BAA25862.1; -;
 DR InterPro: IPR000442; Intron_maturase2.
 DR InterPro: IPR002866; Matk_N.
 DR Pfam: PF01348; Intron_maturase2; 1.
 DR Pfam: PF01824; Matk_N; 1.
 KW Chloroplast.
 SQ SEQUENCE 506 AA; 60534 MW; ADA44B25E92A36F8 CRC64;

Query Match 35.5%; Score 52.5; DB 8; Length 506;
 Best Local Similarity 37.5%; Pred. No. 23;
 Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

OY 1 KN1MAA-----QRYGRELRRMSDEFECSFK 25
 Db 391 KPVMALSDSDIIERGRIRYRLNLSHYSGSLK 422

Search completed: September 20, 2002, 11:03:47
 Job time: 1664 sec

GenCore version 4.5
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OM protein - protein search, using SW model

Run on: September 20, 2002, 10:35:59 : Search time 228.86 seconds
(without alignments)
13.104 Million cell updates/sec

Title: US-09-544-664-56

Sequence: 1 KNIMAMARKRELRMSDEFGSKGL

Scoring table: GAPOP 10.0, Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: A_Geneseq_032802.*

1: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	143	100.0	27	21	AA837056
2	143	100.0	26	21	AA837055
3	138	96.5	26	21	AA837001
4	138	96.5	26	21	AA837002
5	138	96.5	27	21	AA837003
6	138	96.5	16	22	AA870370
7	138	96.5	20	19	AA895168
8	138	96.5	20	19	AA861315
9	138	96.5	20	19	AA861316
10	138	96.5	20	19	AA861317
11	138	96.5	20	19	AA861318

12	138	96.5	204	19	AA858832
13	138	96.5	204	22	AA870369
14	138	96.5	567	22	AA800220
15	114	79.7	166	18	AA824476
16	114	79.7	168	19	AA855779
17	114	79.7	168	21	AA813512
18	114	79.7	168	22	AA870368
19	114	79.7	168	22	AA848287
20	114	79.7	168	22	AA867688
21	113	79.0	23	17	AA895166
22	102	71.3	59	19	AA861320
23	102	71.3	59	19	AA861321
24	102	71.3	59	19	AA861322
25	102	71.3	59	19	AA861323
26	93	65.0	26	22	AA896321
27	93	65.0	26	22	AA870371
28	84	58.7	16	17	AA895163
29	84	58.7	16	17	AA895164
30	84	58.7	16	21	AA870368
31	73	51.0	16	20	AA895421
32	72	50.3	18	22	AA870379
33	72	50.3	20	22	AA870380
34	72	50.3	20	22	AA870381
35	51	35.7	125	21	AA825219
36	51	35.7	171	21	AA825218
37	51	35.7	161	21	AA825217
38	51	35.7	186	21	AA825216
39	51	35.7	186	21	AA825215
40	51	35.7	232	21	AA825214
41	51	35.7	232	21	AA825213
42	51	35.7	236	21	AA825212
43	51	35.7	241	21	AA825211
44	51	35.7	241	21	AA825210
45	51	35.7	682	22	AA852836

ALIGNMENTS

RESULT 1

AA837056 standard; peptide: 27 AA.

AA837056;

28-FEB-2001 (first entry)

Bcl2 polypeptide B3 domain peptide #56.

Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;
cardiac; Bcl-2 superfamily; B3 domain; cell death agonist; Bad;
apoptosis; modulation; B cell lymphoma/leukemia 2; cancer; prostate;
colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;
melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
stroke; myocardial infarction.

Homo sapiens.

W0200059526-A1.

12-OCT-2000.

06-APR-2000; 2000WO-US09352.

07-APR-1999; 99US-0128202.

(YJJE-) UNIV JEFFERSON THOMAS.

Huang Z, Wang J, Zhang Z, Shan S, Lu Z;

WPI; 2000-679325/66.

New peptide conjugates for modulating apoptosis or for inhibiting B

PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for
 PT treating neurodegenerative disorders, stroke, or cancer
 XX
 PS Claim 18; Page 19; 74pp; English.
 XX
 CC The invention relates to a peptide conjugate having the formula:
 CC (R-X)_n-peptide where n = 1-10; X = C=O, when the R-X group is attached
 CC to the N-terminus of the peptide, or a side chain of the peptide where
 CC the functional group of the side chain is NH₂ or OH; or X = O or NH,
 CC when the R-X group is attached to the C-terminus of the peptide, or a
 CC side chain of the peptide, where the side chain functional group is COOH
 CC or CONH₂; and R = 2-18C alkyl or alkoxy, 2-14C alkenyl optionally
 CC containing one or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain
 CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples
 CC of the peptide portion of the conjugate. The peptides represent analogues
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of
 CC the Bcl-2 domain of the cell death agonist Bad. The peptide conjugate is
 CC useful for modulating apoptosis in the cells of a subject, or for
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of
 CC function. In particular, the peptide conjugate is useful for treating a
 CC subject afflicted with a cancer characterized by cancer cells that
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric,
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
 CC conjugate is also useful for treating disorders characterized by
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
 CC
 SO Sequence 27 AA:
 100.0%: Score 143; DB 21; Length 27;
 Query Match Best Local Similarity 100.0%: Pred. No. 5, 1e-15;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 KNTLMAORYGRELRLRMSPDEFGSPKGL 27
 1 kntlmaorygrelrlrmspdefgsfkgf 27
 DB 1 kntlmaorygrelrlrmspdefgsfkgf 27
 RESULT 2
 AAB37055 standard; peptide: 28 AA.
 XX
 AC AAB37055:
 XX
 DT 28-FEB-2001 (first entry)
 XX
 DE Bcl2 polypeptide Bcl2 domain peptide #55.
 XX
 KW Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;
 KW cardiant; Bcl-2 superfamily; Bcl2 domain; cell death agonist; Bad;
 KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;
 KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;
 KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
 KW stroke; myocardial infarction.
 XX
 OS Homo sapiens.
 XX
 PN WO200059526-A1.
 XX
 PD 12-OCT-2000.
 XX
 PF 06-APR-2000; 2000WO-US09352.
 XX
 PR 07-APR-1999; 99US-0128202.
 XX
 PA (UYJE-) UNIV JEFFERSON THOMAS.
 XX
 PI Huang Z, Wang J, Zhang Z, Shan S, Lu Z;

XX
 DR WPI; 2000-679325/66.
 XX
 PT New peptide conjugates for modulating apoptosis or for inhibiting B
 PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for
 PT treating neurodegenerative disorders, stroke, or cancer
 XX
 PS Claim 18; Page 19; 74pp; English.
 XX
 CC The invention relates to a peptide conjugate having the formula:
 CC (R-X)_n-peptide where n = 1-10; X = C=O, when the R-X group is attached
 CC to the N-terminus of the peptide, or a side chain of the peptide where
 CC the functional group of the side chain is NH₂ or OH; or X = O or NH,
 CC when the R-X group is attached to the C-terminus of the peptide, or a
 CC side chain of the peptide, where the side chain functional group is COOH
 CC or CONH₂; and R = 2-18C alkyl or alkoxy, 2-14C alkenyl optionally
 CC containing one or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain
 CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples
 CC of the peptide portion of the conjugate. The peptides represent analogues
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of
 CC the Bcl-2 domain of the cell death agonist Bad. The peptide conjugate is
 CC useful for modulating apoptosis in the cells of a subject, or for
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of
 CC function. In particular, the peptide conjugate is useful for treating a
 CC subject afflicted with a cancer characterized by cancer cells that
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric,
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
 CC conjugate is also useful for treating disorders characterized by
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
 CC
 SO Sequence 28 AA:
 100.0%: Score 143; DB 21; Length 28;
 Query Match Best Local Similarity 100.0%: Pred. No. 5, 3e-15;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 KNTLMAORYGRELRLRMSPDEFGSPKGL 27
 1 kntlmaorygrelrlrmspdefgsfkgf 27
 DB 1 kntlmaorygrelrlrmspdefgsfkgf 27
 RESULT 3
 AAB37001 standard; peptide: 26 AA.
 XX
 AC AAB37001:
 XX
 DT 28-FEB-2001 (first entry)
 XX
 DE Bcl2 polypeptide Bcl2 domain peptide #1.
 XX
 KW Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;
 KW cardiant; Bcl-2 superfamily; Bcl2 domain; cell death agonist; Bad;
 KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;
 KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;
 KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
 KW stroke; myocardial infarction.
 XX
 OS Homo sapiens.
 XX
 PN WO200059526-A1.
 XX
 PD 12-OCT-2000.
 XX
 PF 06-APR-2000; 2000WO-US09352.
 XX
 PR 07-APR-1999; 99US-0128202.
 XX

XX (UYJE-) UNIV JEFFERSON THOMAS.
 XX Huang Z, Wang J, Zhang Z, Shan S, Lu Z;
 XX WPI, 2000-679325/66.
 XX
 PT New peptide conjugates for modulating apoptosis or for inhibiting B
 PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for
 PT treating neurodegenerative disorders, stroke, or cancer
 XX
 PS Claim 18; Page 17; 74pp; English.
 XX
 CC The invention relates to a peptide conjugate having the formula:
 CC (R-X)_n-peptide where n = 1-10; X = C=O, when the R-X group is attached
 CC to the N-terminus of the peptide, or a side chain of the peptide where
 CC the functional group of the side chain is NH₂ or OH; or X = O or NH,
 CC when the R-X group is attached to the C-terminus of the peptide, or a
 CC side chain of the peptide, where the side chain functional group is COOH
 CC or CONH₂; and R = 2-18C alkyl or alkoxy, 2-14C alkenyl optionally
 CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain
 CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples
 CC of the peptide portion of the conjugate. The peptides represent analogues
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of
 CC the Bcl-2 domain of the cell death agonist Bad. The peptide conjugate is
 CC useful for modulating apoptosis in the cells of a subject, or for
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2
 CC function. In particular, the peptide conjugate is useful for treating a
 CC subject afflicted with a cancer characterized by cancer cells that
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric,
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
 CC conjugate is also useful for treating disorders characterized by
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
 XX
 SO Sequence 26 AA:
 Query Match 96.5%; Score 138; DB 21; Length 26;
 Best Local Similarity 100.0%; Pred. No. 2, 9e-14;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 NLMAAQRGRLRMSDEFSGFKGL 27
 Db 1 nlwaagrygreilrmsdefsgfkyl 26
 RESULT 4
 AAB37002
 ID AAB37002 standard; peptide: 26 AA.
 XX
 AC AAB37002;
 XX
 DT 28-FEB-2001 (first entry)
 XX
 DE Bcl2 polypeptide Bcl3 domain peptide #2.
 XX
 KW Cytostatic; neuroprotective; anti-HIV; virocidic; cerebroprotective;
 KW cardiast; Bcl-2 superfamily; Bcl3 domain; cell death agonist; Bad;
 KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;
 KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;
 KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
 KW stroke; myocardial infarction.
 XX
 OS Homo sapiens.
 XX
 PN WO200059526-A1.
 XX
 PD 12-OCT-2000.

A

XX 06-APR-2000; 2000WO-US09352.
 XX 07-APR-1999; 99US-0128202.
 XX
 XX (UYJE-) UNIV JEFFERSON THOMAS.
 XX Huang Z, Wang J, Zhang Z, Shan S, Lu Z;
 XX WPI, 2000-679325/66.
 XX
 PT New peptide conjugates for modulating apoptosis or for inhibiting B
 PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for
 PT treating neurodegenerative disorders, stroke, or cancer
 XX
 PS Claim 18; Page 17; 74pp; English.
 XX
 CC The invention relates to a peptide conjugate having the formula:
 CC (R-X)_n-peptide where n = 1-10; X = C=O, when the R-X group is attached
 CC to the N-terminus of the peptide, or a side chain of the peptide where
 CC the functional group of the side chain is NH₂ or OH; or X = O or NH,
 CC when the R-X group is attached to the C-terminus of the peptide, or a
 CC side chain of the peptide, where the side chain functional group is COOH
 CC or CONH₂; and R = 2-18C alkyl or alkoxy, 2-14C alkenyl optionally
 CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain
 CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples
 CC of the peptide portion of the conjugate. The peptides represent analogues
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of
 CC the Bcl-2 domain of the cell death agonist Bad. The peptide conjugate is
 CC useful for modulating apoptosis in the cells of a subject, or for
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2
 CC function. In particular, the peptide conjugate is useful for treating a
 CC subject afflicted with a cancer characterized by cancer cells that
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric,
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
 CC conjugate is also useful for treating disorders characterized by
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
 XX
 SO Sequence 26 AA:
 Query Match 96.5%; Score 138; DB 21; Length 26;
 Best Local Similarity 100.0%; Pred. No. 2, 9e-14;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 NLMAAQRGRLRMSDEFSGFKGL 27
 Db 1 nlwaagrygreilrmsdefsgfkyl 26
 RESULT 5
 AAB37003
 ID AAB37003 standard; peptide: 27 AA.
 XX
 AC AAB37003;
 XX
 DT 28-FEB-2001 (first entry)
 XX
 DE Bcl2 polypeptide Bcl3 domain peptide #3.
 XX
 KW Cytostatic; neuroprotective; anti-HIV; virocidic; cerebroprotective;
 KW cardiast; Bcl-2 superfamily; Bcl3 domain; cell death agonist; Bad;
 KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;
 KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;
 KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
 KW stroke; myocardial infarction.
 XX
 OS Homo sapiens.

A

XX WO200059526-A1.
 XX 12-OCT-2000.
 XX 06-APR-2000; 2000MO-US09352.
 XX 07-APR-1999; 99US-0128202.
 XX (UYJE-) UNIV JEFFERSON THOMAS.
 XX Huang Z, Wang J, Zhang Z, Shan S, Lu Z;
 XX WPI: 2000-679325/66.
 XX New peptide conjugates for modulating apoptosis or for inhibiting B
 XX cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for
 XX treating neurodegenerative disorders, stroke, or cancer -
 XX Claim 18; Page 17; 74pp; English.
 XX
 CC The invention relates to a peptide conjugate having the formula:
 CC (R-X)_n peptide where n = 1-10; X = C=O, when the R-X group is attached
 CC to the N-terminus of the peptide, or a side chain of the peptide where
 CC the functional group of the side chain is NH₂ or OH; or X = O or NH,
 CC when the R-X group is attached to the C-terminus of the peptide, or a
 CC side chain of the peptide, where the side chain functional group is COOH
 CC or CONH₂; and R = 2-18C alkyl or alkoxy, 2-14C alkenyl containing one
 CC or two double bonds, cycloalkyl, cyclopentyl, cyclohexyl optionally
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,
 CC phenyl optionally monosubstituted with a 1-3C straight or branched chain
 CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples
 CC of the peptide portion of the conjugate. The peptides represent analogues
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of
 CC the Bcl-2 domain of the cell death agonist Bad. The peptide conjugate is
 CC useful for modulating apoptosis in the cells of a subject, or for
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2
 CC function. In particular, the peptide conjugate is useful for treating a
 CC subject afflicted with a cancer characterized by cancer cells that
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric,
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
 CC conjugate is also useful for treating disorders characterized by
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
 XX
 SQ Sequence 27 AA:

Query Match 96.5%; Score 138; DB 21; Length 27;
 Best Local Similarity 100.0%; Pred. No. 3e-14;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 NLMNAQRYGRELRLMSDEFGSEFKGL 27
 1 nlmwaqrygrejrlmsdefegsfkgl 26

DB 1 nlmwaqrygrejrlmsdefegsfkgl 26

RESULT 6
 AAB70370
 ID AAB70370 standard; protein; 162 AA.
 XX AAB70370;
 XX 02-MAY-2001 (first entry)
 XX Shorter murine BAD mutant amino acid sequence SEQ ID NO:3.
 DE Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;
 XX immunostimulant; neuroprotective; neurotrophic; antischismatic; vlnuery;
 XX cytosolic; antiviral; antitumor; antiinflammatory; wound healing;
 KW immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;

KW immunodeficiency disease; neurodegenerative disease; viral infection;
 KW ischaemic cell death; reperfusion cell death; arthritis; infertility;
 KW lymphoproliferative condition; inflammation; autoimmune disease.
 XX Mus musculus.
 XX Synthetic.
 XX WO200110888-A1.
 XX 15-FEB-2001.
 XX 30-MAY-2000; 2000MO-US11864.
 XX 28-MAY-1999; 99US-0136783.
 XX (APOP-) APOPTOSIS TECHNOLOGY INC.
 XX Zhou X;
 XX WPI: 2001-138734/14.
 XX
 XX New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,
 XX useful for screening for candidate compounds which induce or inhibit
 XX apoptosis, comprises amino acid substitutions at Ser118, Ser155 or
 XX Ser113 -
 XX Claim 7; Page 148-149; 157pp; English.
 XX
 CC The present invention describes an isolated or synthetic polypeptide
 CC (1) comprising a less than full length amino acid sequence of a mutant
 CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its
 CC fragment, which contains amino acid substitutions at Ser118 of a human
 CC BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine
 CC BAD (shorter murine BAD). (1) has immunostimulant, neuroprotective,
 CC neurotrophic, antischismatic, vlnuery, cytosolic, antiviral,
 CC antitumor, antiinflammatory and immunosuppressive activities, and
 CC can be used as an apoptosis inducer or inhibitor. BAD polypeptides and
 CC polynucleotides can be used for screening candidate compounds and drugs
 CC for activity that promote cell survival or apoptosis. Other uses include
 CC inducing or inhibiting apoptosis in a cell. Candidate compounds
 CC identified and (mutant) BAD polypeptides are useful in treating
 CC immunodeficiency diseases, neurodegenerative diseases, ischaemic cell
 CC death, reperfusion cell death, wound healing, cancer, viral infections,
 CC lymphoproliferative conditions, arthritis, infertility, inflammation and
 CC autoimmune diseases. The present sequence represents a specifically
 CC claimed shorter murine BAD mutant amino acid sequence from the present
 CC invention.
 XX
 SQ Sequence 162 AA:

Query Match 96.5%; Score 138; DB 22; Length 162;
 Best Local Similarity 100.0%; Pred. No. 2.2e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 NLMNAQRYGRELRLMSDEFGSEFKGL 27
 98 nlmwaqrygrejrlmsdefegsfkgl 123

DB 98 nlmwaqrygrejrlmsdefegsfkgl 123

RESULT 7
 AAR95168
 ID AAR95168 standard; protein; 204 AA.
 XX AAR95168;
 XX 06-JAN-1997 (first entry)
 XX bcl-x(L)/Bcl-2 associated death promoter protein.
 DE bcl-x(L)/Bcl-2 associated death promoter; Bad; stroke;
 XX Epitope; murine; bcl-x(L)/Bcl-2 associated death promoter; Bad; stroke;
 XX polypeptide; bcl-x; cell death; regulator; BH1; BH2; apoptotic cell death;
 KW cytokine deprivation; IL-3 dependent cell line; immunodeficiency; AIDS;

neurodegenerative disease; senescence; ischaemia; neoplasia.

Mus musculus.

Key Location/Qualifiers

Key 147..149 /note="BHL conserved amino acids"

FT 191..192 /note="BH2 conserved amino acids"

FT 38..61 /note="PEST sequence"

FT 111..130 /note="PEST sequence"

FT /note="PEST sequence"

Domain

MO9613614-A1.

09-MAY-1996.

31-OCT-1995; 95WO-0514246.

31-OCT-1994; 94US-033565.

(UNIW) UNIV WASHINGTON.

Korsmeyer SJ;

WPI: 1996-251465/25.

N-PSDB: AAT929479.

polynucleotide encoding bcl-x(L)/bcl-2 associated death promoter -

useful to treat neoplasia and apoptosis and to identify agents

inhibiting its binding to bcl-2 or bcl-x(L) to form heteromultimers

Claim 3; Fig 1; 130pp: English.

This sequence represents the murine bcl-x(L)/bcl-2 associated death promoter (Bad) gene. Bad is a 22.1 kD protein which interacts with bcl-2 and bcl-x proteins and regulates cell death. It has homology to the bcl-2-related family clustered in the BHL and BH2 domain. Bad has been found to hybridize to bcl(L), and bcl-2 in yeast two-hybrid assays and in vitro in mammalian cells. Overexpressed Bad confers the death inhibitory activity of bcl-x(L), but is much less effective at countering the death inhibitory activity of bcl-2. Bad expression can accelerate apoptotic cell death induced by cytokine deprivation in an IL-3 dependent cell line expressing bcl-x(L), and its deletion counteracts the death repressor activity of bcl-x(L). Bad competes with Bak for binding to bcl-x(L). Bad may be used to identify agents which inhibit its binding to bcl-2 or bcl-x(L) to form heterodimers. Such agents may be used to treat neurodegenerative diseases, immunodeficiency diseases, e.g. AIDS, senescence or ischaemia.

Sequence 204 AA:

Query Match 96.5%; Score 138; DB 17; Length 204:

Best Local Similarity 100.0%; Pred. No. 2; Be-13;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0:

2 N L M A A O R K G E L R R M S D F R G S K G L (27)

140 nlwaagrygrrelrmsdfeqstkg1 165

RESULT 8

AA061315

AA061315 standard; Protein; 204 AA.

AA061315;

07-OCT-1998 (first entry)

Murine BCL-XL/BCL-2 associated cell death regulator.

lead

Subst

KW murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;
KM murine substituted mutant; apoptosis; cancer; viral infection.
OS Mus sp.
PN WO9817682-A1.
PD 30-APR-1998.
PE 17-OCT-1997; 97WO-US19175.
PR 18-OCT-1996; 96US-0733505.
PA (UNITED STATES OF AMERICA).
XX KORMEYER SJ;
P1 WPI; 1998-261422/23.
DR N-PDB; AAV27833.
XX New mutant BAD polypeptide with phosphorylatable serine replaced
PT useful for, e.g., treating reduced apoptosis such as in cancer or
PT viral infection
PS Claim 1; Fig 10; 95pp; English.

The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell death regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the murine BAD 204 aa sequence. The present sequence is the murine BAD protein. Also described are: (1) fragments of mutant BAD protein able to decrease cell viability; (2) fusion proteins of mutant BAD with a heterologous polypeptide that increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, inflammation and autoimmune disease. Polynucleotide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serine-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, aging or ischemic cell death. The apoptotic status of cells is determined by measuring relative amounts of phosphorylated and non-phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have greater death-promoting activity than wild-type BAD which can become phosphorylated on the specified Ser, forming a product that does not heterodimerise with Bcl-2 or bcl-XL but instead binds to 14-3-3 family proteins in the cytosol, thus promoting cell survival. The mutants with Ser substituted cannot bind 14-3-3.

Sequence 204 AA:

Query Match 96.5% Score 138; DB 19; Length 204;
Best Local Similarity 100.0%; Pred. NO. 2.8e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 NMAAQRGRLRNMSDFESSFGCL 27
||| ||||||||| ||||||||| |||
DB 140 nlwaqaqyrellrmdelegsiygl 165

RESULTS 9
AAW61316
ID AAW61316 standard; Protein; 204 AA.
XX
AC AAW61316;
XX
DT 07-OCT-1998 (first entry)
DE Mutant BCL-XL/BCL-2 associated cell death regulator #1.
KW Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;

```

KW serine substituted mutant; apoptosis; cancer; viral infection.
XX Mus sp.
OS Synthetic.
XX WO9817682-A1.
XX 30-APR-1998.
XX 17-OCT-1997; 97WO-US19175.
XX 18-OCT-1996; 96US-0733505.
XX (UNIV ) UNIV WASHINGTON.
XX Korsmeyer SJ;
XX WPI: 1998-261422/23.
XX N-PSDB; AAV27834.
XX New mutant BAD polypeptide with phosphorylatable serine replaced -
XX useful for, e.g. treating reduced apoptosis such as in cancer or
XX viral infection
XX Claim 7: Page 59; 95pp: English.
XX
XX The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
XX death regulator) proteins, having an amino acid other than Ser at
XX position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
XX present sequence represents a mutant BAD protein. Also described are: (1)
XX fragments of mutant BAD protein able to decrease cell viability; (2)
XX fusion proteins of mutant BAD with a heterologous polypeptide that
XX increases intracellular delivery. Mutant BAD proteins are used to treat
XX or prevent diseases associated with reduced apoptosis, e.g. cancer,
XX viral infection, lymphoproliferation, arthritis, infertility,
XX inflammation and autoimmune disease. Polynucleotide sequences encoding
XX mutant BAD proteins can be used similarly by gene therapy or to produce
XX transgenic animals for use as disease models or in drug screening. BAD
XX proteins phosphorylated at specified Ser are used to screen for enhancers
XX and inhibitors of serine-phosphatase. Inhibitors are potentially useful
XX in treatment of excessive apoptosis such as AIDS, neurodegeneration,
XX aging or ischemic cell death. The apoptotic status of cells is
XX determined by measuring relative amounts of phosphorylated and non-
XX phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
XX greater death-promoting activity than wild-type BAD which can become
XX phosphorylated on the specified Ser, forming a product that does not
XX heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family
XX proteins in the cytosol, thus promoting cell survival. The mutants with
XX Ser substituted cannot bind 14-3-3.
XX
XX Sequence 204 AA:
SQ
XX
XX Query Match 96.5%; Score 138; DB 19; Length 204;
XX Best Local Similarity 100.0%; Pred. No. 2,8e-13;
XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 NLMAGRYGRELRRMSDEFGSKG 27
XX ||||||||||||||||||||
Db 140 nlwaagrygrelrrmsdefgskgl 165
XX ||||||||||||||||||||

RESULT 10
AAW61317
ID AAW61317 standard; Protein: 204 AA.
XX
XX AAW61317:
AC
XX 07-OCT-1998 (first entry)
XX
XX Mutant BCL-XL/BCL-2 associated cell death regulator #2.
XX
XX Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;

```

```

KW serine substituted mutant; apoptosis; cancer; viral infection.
XX Mus sp.
OS Synthetic.
XX WO9817682-A1.
XX 30-APR-1998.
XX 17-OCT-1997; 97WO-US19175.
XX 18-OCT-1996; 96US-0733505.
XX (UNIV ) UNIV WASHINGTON.
XX Korsmeyer SJ;
XX WPI: 1998-261422/23.
XX N-PSDB; AAV27835.
XX New mutant BAD polypeptide with phosphorylatable serine replaced -
XX useful for, e.g. treating reduced apoptosis such as in cancer or
XX viral infection
XX Claim 7: Page 60; 95pp: English.
XX
XX The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
XX death regulator) proteins, having an amino acid other than Ser at
XX position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
XX present sequence represents a mutant BAD protein. Also described are: (1)
XX fragments of mutant BAD protein able to decrease cell viability; (2)
XX fusion proteins of mutant BAD with a heterologous polypeptide that
XX increases intracellular delivery. Mutant BAD proteins are used to treat
XX or prevent diseases associated with reduced apoptosis, e.g. cancer,
XX viral infection, lymphoproliferation, arthritis, infertility,
XX inflammation and autoimmune disease. Polynucleotide sequences encoding
XX mutant BAD proteins can be used similarly by gene therapy or to produce
XX transgenic animals for use as disease models or in drug screening. BAD
XX proteins phosphorylated at specified Ser are used to screen for enhancers
XX and inhibitors of serine-phosphatase. Inhibitors are potentially useful
XX in treatment of excessive apoptosis such as AIDS, neurodegeneration,
XX aging or ischemic cell death. The apoptotic status of cells is
XX determined by measuring relative amounts of phosphorylated and non-
XX phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
XX greater death-promoting activity than wild-type BAD which can become
XX phosphorylated on the specified Ser, forming a product that does not
XX heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family
XX proteins in the cytosol, thus promoting cell survival. The mutants with
XX Ser substituted cannot bind 14-3-3.
XX
XX Sequence 204 AA:
SQ
XX
XX Query Match 96.5%; Score 138; DB 19; Length 204;
XX Best Local Similarity 100.0%; Pred. No. 2,8e-13;
XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 NLMAGRYGRELRRMSDEFGSKG 27
XX ||||||||||||||||||||
Db 140 nlwaagrygrelrrmsdefgskgl 165
XX ||||||||||||||||||||

RESULT 11
AAW61318
ID AAW61318 standard; Protein: 204 AA.
XX
XX AAW61318:
AC
XX 07-OCT-1998 (first entry)
XX
XX Mutant BCL-XL/BCL-2 associated cell death regulator #3.
XX
XX Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;

```

KM serine substituted mutant; apoptosis; cancer; viral infection.
 XX Mus sp.
 OS Synthetic.
 XX WO9817682-A1.
 PN 30-APR-1998.
 PD 17-OCT-1997; 97WO-US19175.
 PF 18-OCT-1996; 96US-0733505.
 PR (UNIM) UNIV WASHINGTON.
 PA Korsmeyer SJ;
 PI WPI: 1998-261422/23.
 DR N-PSDB; MAV27836.
 XX New mutant BAD polypeptide with phosphorylatable serine replaced -
 PT useful for, e.g. treating reduced apoptosis such as in cancer or
 PT viral infection
 PS Claim 7; Page 60-61; 95pp; English.
 XX The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
 CC death regulator) proteins, having an amino acid other than Ser at
 CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
 CC present sequence represents a mutant BAD protein. Also described are: (1)
 CC fragments of mutant BAD protein able to decrease cell viability; (2)
 CC fusion proteins of mutant BAD with a heterologous polypeptide that
 CC increases intracellular delivery. Mutant BAD proteins are used to treat
 CC or prevent diseases associated with reduced apoptosis, e.g. cancer,
 CC viral infection, lymphoproliferation, arthritis, infertility,
 CC inflammation and autoimmune disease. Polynucleotide sequences encoding
 CC mutant BAD proteins can be used similarly by gene therapy or to produce
 CC transgenic animals for use as disease models or in drug screening. BAD
 CC proteins phosphorylated at specified Ser are used to screen for enhancers
 CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful
 CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,
 CC aging or ischemic cell death. The apoptotic status of cells is
 CC determined by measuring relative amounts of phosphorylated and non-
 CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
 CC greater death-promoting activity than wild-type BAD which can become
 CC phosphorylated on the specified Ser, forming a product that does not
 CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family
 CC proteins in the cytosol, thus promoting cell survival. The mutants with
 CC Ser substituted cannot bind 14-3-3.
 CC
 SQ Sequence 204 AA:
 Query Match 96.5%; Score 138; DB 19; Length 204;
 Best Local Similarity 100.0%; Pred. No. 2.8e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 NLMAAQRVGRRLRMSDEFGSFKGL 27
 DB 140 nlwaagrygrellrmsdefgsfkgl 165
 RESULT 12
 AAM58832 standard; protein; 204 AA.
 XX AAM58832;
 AC AAM58832;
 XX 23-JUL-1998 (first entry)
 DT Murine BAD protein.
 DE Murine BAD protein.
 XX BAD protein; Bcl-XL/Bcl-2 associated cell death regulator; 14-3-3;

KM serine phosphorylation; post-translational modification; apoptosis;
 KM signal transduction regulator; phosphoserine phosphatase; senescence;
 KM immunodeficiency disease; neurodegenerative disease; infertility;
 KM cancer; viral infection; lymphoproliferative condition; arthritis;
 KM inflammation; autoimmune diseases.
 XX Mus sp.
 OS WO9809643-A1.
 PN 12-MAR-1998.
 PD 09-SEP-1997; 97WO-US15871.
 PF 09-SEP-1996; 96US-0707868.
 PR (UNIM) UNIV WASHINGTON.
 PA Korsmeyer SJ;
 PI WPI: 1998-207049/18.
 DR Serine-phosphorylated Bcl-XL/Bcl-2 Associated cell Death regulator
 XX polypeptide - useful for modulation of apoptosis associated with,
 PT e.g. cancer and immunodeficiency diseases
 PT
 PS Claim 3; Fig 8; 61pp; English.
 XX This sequence represents a novel serine-phosphorylated protein, BAD
 CC (BCL-XL/BCL-2 associated cell death regulator). The serine residue is
 CC phosphorylated in a post-translational modification and allows binding
 CC to the 14-3-3 protein which is a signal transduction regulator.
 CC Modulators of phosphorylated BAD, which act through inhibition/activation
 CC of a phosphoserine phosphatase, are useful for preventing/treating
 CC increased/decreased apoptosis in a cell. The increased apoptosis may
 CC result from immunodeficiency diseases, senescence, neurodegenerative
 CC disease, ischemic cell death, reperfusion cell death, infertility and
 CC wound-healing. Decreased apoptosis may result from cancer, viral
 CC infection, lymphoproliferative conditions, arthritis, infertility,
 CC inflammation and autoimmune diseases. Measuring the amount of
 CC phosphorylated compared to unphosphorylated BAD polypeptide and/or total
 CC BAD in a cell is useful for determining the apoptotic state of a cell.
 CC
 SQ Sequence 204 AA:
 Query Match 96.5%; Score 138; DB 19; Length 204;
 Best Local Similarity 100.0%; Pred. No. 2.8e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 NLMAAQRVGRRLRMSDEFGSFKGL 27
 DB 140 nlwaagrygrellrmsdefgsfkgl 165
 RESULT 13
 AAB70369 standard; protein; 204 AA.
 XX AAB70369;
 AC AAB70369;
 XX 02-MAY-2001 (first entry)
 DT Longer murine BAD mutant amino acid sequence SEQ ID NO:2.
 DE Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;
 XX immunostimulant; neuroprotective; nootropic; antischismic; vulnary;
 KM cytostatic; antiviral; antiinflammatory; wound healing;
 KM immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;
 KM immunodeficiency disease; neurodegenerative disease; viral infection;
 KM ischemic cell death; reperfusion cell death; arthritis; infertility;
 KM lymphoproliferative condition; inflammation; autoimmune disease.

XX BBC6 gene; cell death; cell cycle; Bcl2; human.
 KW Homo sapiens.
 OS
 XX US5663316-A.
 PN
 XX 02-SEP-1997.
 PD
 XX 18-JUN-1996; 96US-0665617.
 PF
 XX 18-JUN-1996; 96US-0665617.
 PR
 XX (CLON-) CLONTECH LAB INC.
 PA
 XX
 XX
 PI Xudong Y;
 PI
 XX
 DR WPI; 1997-447980/41.
 DR N-PSDB; AAT91361.
 XX
 XX
 PT Isolated BBC6 gene - encodes a protein that regulates cell death
 PT through interaction with Bcl-2
 XX
 PS Claim 1; Column 11-12; 7pp; English.
 XX
 CC The present sequence represents a protein of 166 amino acids. The
 CC sequence is disclosed as being a protein called BBC6 which regulates
 CC cell death through interaction with Bcl-2. The DNA may be used for the
 CC production of the recombinant protein, which can be used in unspecified
 CC therapeutic or diagnostic procedures, as a molecular weight marker, and
 CC to raise antibodies that can be used in unspecified diagnostic or
 CC therapeutic applications and to reduce or eliminate the biological
 CC activity of the BBC6 protein in vivo.
 XX
 SQ Sequence 166 AA;

Query Match 79.7%; Score 114; DB 18; Length 166;
 Best Local Similarity 91.7%; Pred. No. 1.1e-09;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 NIMAAQRYGRELRLRMDEFGSFK 25
 Db 101 nlwaagrygrelrlrmsdelvdsik 124

Search completed: September 20, 2002, 10:35:59
 Job time: 427 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 20, 2002, 10:37:21 ; Search time 75.64 Seconds
(without alignments)
8.719 Million cell updates/sec

Title: US-09-544-664-56

Perfect score: 143

Sequence: 1 KNIMAAQRYGRELKRMSEDFECSFKGL 27

Scoring table:

Gap 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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3: /cgn2.6/ptodata/2/1aa/6A.COMB.pep: *
4: /cgn2.6/ptodata/2/1aa/6B.COMB.pep: *
5: /cgn2.6/ptodata/2/1aa/PCTUS.COMB.pep: *
6: /cgn2.6/ptodata/2/1aa/backfilltest.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	138	96.5	204	1 US-08-333-565-2	Sequence 2, Appl 1
2	138	96.5	204	2 US-08-661-479-2	Sequence 2, Appl 1
3	138	96.5	204	2 US-08-733-505A-1	Sequence 1, Appl 1
4	138	96.5	204	2 US-08-733-505A-12	Sequence 12, Appl 1
5	138	96.5	204	2 US-08-733-505A-13	Sequence 13, Appl 1
6	138	96.5	204	2 US-08-733-505A-14	Sequence 14, Appl 1
7	135	94.4	204	2 US-08-717-123-3	Sequence 3, Appl 1
8	114	79.7	166	1 US-08-665-617-2	Sequence 2, Appl 1
9	114	79.7	166	2 US-08-717-123-2	Sequence 2, Appl 1
10	114	79.7	166	3 US-08-985-335-1	Sequence 1, Appl 1
11	114	79.7	168	3 US-08-985-335-7	Sequence 7, Appl 1
12	114	79.7	168	4 US-09-410-372-1	Sequence 1, Appl 1
13	114	79.7	168	4 US-09-410-372-7	Sequence 7, Appl 1
14	113	79.0	23	1 US-08-333-565-10	Sequence 10, Appl 1
15	113	79.0	23	1 US-08-661-479-10	Sequence 10, Appl 1
16	102	71.3	59	2 US-08-733-505A-55	Sequence 55, Appl 1
17	102	71.3	59	2 US-08-733-505A-56	Sequence 56, Appl 1
18	102	71.3	59	2 US-08-733-505A-57	Sequence 57, Appl 1
19	102	71.3	59	2 US-08-733-505A-58	Sequence 58, Appl 1
20	86	60.1	16	1 US-08-333-565-56	Sequence 26, Appl 1
21	86	60.1	16	2 US-08-661-479-26	Sequence 26, Appl 1
22	61	42.7	11	2 US-08-733-505A-34	Sequence 69, Appl 1
23	61	42.7	11	2 US-08-706-741B-69	Sequence 69, Appl 1
24	61	42.7	11	2 US-08-924-695A-69	Sequence 40, Appl 1
25	51	35.7	66	2 US-08-867-087B-40	Sequence 3, Appl 1
26	46	32.2	946	3 US-09-074-579-3	Sequence 3, Appl 1
27	46	32.2	946	4 US-09-388-774-3	Sequence 3, Appl 1

28	44	30.8	263	4	US-09-651-656-27	Sequence 27, Appl 1
29	43	30.1	81	1	US-08-497-312-19	Sequence 19, Appl 1
30	43	30.1	213	3	US-08-718-738-18	Sequence 18, Appl 1
31	43	30.1	213	4	US-09-221-844-18	Sequence 18, Appl 1
32	43	30.1	380	1	US-08-153-848-40	Sequence 40, Appl 1
33	43	30.1	380	3	US-09-299-845A-40	Sequence 40, Appl 1
34	43	30.1	380	4	US-09-088-337B-40	Sequence 40, Appl 1
35	43	30.1	380	5	PCT-0593-11153-40	Sequence 40, Appl 1
36	42	29.4	322	4	US-09-359-161-7	Sequence 7, Appl 1
37	42	29.4	348	2	US-08-597-080-170	Sequence 170, Appl 1
38	42	29.4	348	2	US-08-997-362-170	Sequence 170, Appl 1
39	42	29.4	348	4	US-09-095-855-170	Sequence 170, Appl 1
40	42	29.4	348	4	US-09-324-542-170	Sequence 170, Appl 1
41	42	29.4	393	2	US-08-997-080-94	Sequence 94, Appl 1
42	42	29.4	393	2	US-08-997-362-94	Sequence 94, Appl 1
43	42	29.4	393	3	US-08-873-970-94	Sequence 94, Appl 1
44	42	29.4	393	3	US-09-095-855-94	Sequence 94, Appl 1
45	42	29.4	393	4	US-09-324-542-94	Sequence 94, Appl 1

ALIGNMENTS

```

RESULT 1
US-08-333-565-2
; Sequence 2, Application US/0833565
; Patent No. 5622852
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
; NUMBER OF INVENTIONS: 59
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend Knoutie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/333,565
; FILING DATE: 31-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000700
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..204
; OTHER INFORMATION:
; OTHER INFORMATION: of mouse BAD."
US-08-333-565-2

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Query Match 96.5%; Score 138; DB 1; Length 204;
Best Local Similarity 100.0%; Pred. No. 7e-14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-733-505A-12

Query Match 96.5%; Score 138; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 7e-14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NLMAORYGRELIRMSDEFGSFKGL 27
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DB 140 NLMAORYGRELIRMSDEFGSFKGL 165

RESULT 5
US-08-733-505A-13
Sequence 13, Application US/08733505A
Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-6092
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-733-505A-13

Query Match 96.5%; Score 138; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 7e-14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NLMAORYGRELIRMSDEFGSFKGL 27
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DB 140 NLMAORYGRELIRMSDEFGSFKGL 165

RESULT 6

US-08-733-505A-14
Sequence 14, Application US/08733505A
Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-733-505A-14

Query Match 96.5%; Score 138; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 7e-14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NLMAORYGRELIRMSDEFGSFKGL 27
|||||
DB 140 NLMAORYGRELIRMSDEFGSFKGL 165

RESULT 7
US-08-717-123-3
Sequence 13, Application US/08717123
Patent No. 5965703
GENERAL INFORMATION:
APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
TITLE OF INVENTION: Acids and Methods of Use
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/717,123
FILING DATE: 20-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-717-123-3

Query Match 94.4%; Score 114; DB 2; Length 204;
Best Local Similarity 96.2%; Pred. No. 2e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 NLMAAQRGRELRRMSDEFGSGKGL 27
|||||

DB 140 NLMAAQRGRELRRMTDFEGSGKGL 165

RESULT 8
US-08-665-617-2
Sequence 2, Application US/08665617
Patent No. 5663316
GENERAL INFORMATION:
APPLICANT: Xudong, Yin
TITLE OF INVENTION: Gene and Protein for Regulation of Cell Death
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,617
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: CL-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-665-617-2

Query Match 79.7%; Score 114; DB 1; Length 166;
Best Local Similarity 91.7%; Pred. No. 2.8e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NLMAAQRGRELRRMSDEFGSGK 25

DB 101 NLMAAQRGRELRRMSDFVDSFK 124
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RESULT 9
US-08-717-123-2
Sequence 2, Application US/08717123
Patent No. 5965703
GENERAL INFORMATION:
APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilmann
TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
TITLE OF INVENTION: Acids and Methods of Use
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/717,123
FILING DATE: 20-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 1929
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-717-123-2

Query Match 79.7%; Score 114; DB 2; Length 168;
Best Local Similarity 91.7%; Pred. No. 2.8e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NLMAAQRGRELRRMSDEFGSGK 25
|||||

DB 103 NLMAAQRGRELRRMSDFVDSFK 126

RESULT 10
US-08-985-335-1
Sequence 1, Application US/08985335
Patent No. 6080847
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purni
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA

COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,335
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SYNORAB01
CLONE: 358673
US-08-985-335-1

Query Match 79.7%; Score 114; DB 3; Length 168;
Best Local Similarity 91.7%; Pred. No. 2.8e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NLMAORYGRELRRMSDEFBSFK 25
Db 103 NLMAORYGRELRRMSDEFVDSFK 126

RESULT 11
US-08-985-335-7
Sequence 7, Application US/08985335
Patent No. 6080847
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
PROLIFERATION
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,335
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1683637
US-08-985-335-7

Query Match 79.7%; Score 114; DB 3; Length 168;
Best Local Similarity 91.7%; Pred. No. 2.8e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NLMAORYGRELRRMSDEFBSFK 25
Db 103 NLMAORYGRELRRMSDEFVDSFK 126

RESULT 12
US-09-410-372-1
Sequence 1, Application US/09410372
Patent No. 6281334
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
PROLIFERATION
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/410,372
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985,335
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SYNORAB01

CLONE: 358673
US-09-410-372-1

Query Match 79.7%; Score 114; DB 4; Length 168;
Best Local Similarity 91.7%; Pred. No. 2.8e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 N1MAAORYGRELRLMSDFEGSK 25
DB 103 N1MAAORYGRELRLMSDFEGSK 126

RESULT 13
US-09-410-372-7
Sequence 7, Application US/09410372
Patent No. 6281334
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purni
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/410,372
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985,335
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1683637
US-09-410-372-7

Query Match 79.7%; Score 114; DB 4; Length 168;
Best Local Similarity 91.7%; Pred. No. 2.8e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 N1MAAORYGRELRLMSDFEGSK 25
DB 103 N1MAAORYGRELRLMSDFEGSK 126

RESULT 14

US-08-333-565-10
Sequence 10, Application US/08333565
Patent No. 5622852
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,565
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-333-565-10

Query Match 79.0%; Score 113; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 4.5e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 N1MAAORYGRELRLMSDFEG 22
DB 3 N1MAAORYGRELRLMSDFEG 23

RESULT 15
US-08-661-479-10
Sequence 10, Application US/08661479
Patent No. 5834209
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,479

FILED DATE: 11-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/333,565
FILING DATE: 31-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-661-479-10

Query Match 79.08; Score 113; DB 2; Length 23;
Best Local Similarity 100.08; Pred.No. 4.5e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 NLMAAORYGRELRRMSDEFEFG 22
Db 3 NLMAAORYGRELRRMSDEFEFG 23

Search completed: September 20, 2002, 10:37:21
Job time: 409 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 20, 2002, 10:39:13 : Search time 95.59 seconds
(without alignments)
27.141 Million cell updates/sec

Title: US-09-544-664-56

Sequence: 1 KNLMAQRGRRLRMSDFEGSFKGL 27

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

1: PIR1:
2: PIR2:
3: PIR3:
4: PIR4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	138	96.5	204	2	bad protein - mouse
2	54	37.8	946	2	inter-alpha-trypsin
3	53	37.1	223	2	hypothetical prote
4	53	37.1	946	2	inter-alpha-inhibi
5	52	36.4	370	2	2-dehydro-3-deoxyp
6	51	35.7	232	2	floral homeotic pr
7	50	35.0	374	2	sermidine/putresc
8	49	35.0	516	2	probable threonine
9	48.5	33.9	134	2	conserved hypotnet
10	48.5	33.9	134	2	19 kappa chain - h
11	48.5	33.9	134	2	transferrin prote
12	48	33.6	206	2	oxidoreductase, so
13	48	33.6	220	2	threonine synthase
14	48	33.6	526	2	threonine synthase
15	47.5	33.2	334	2	oxalacetate decar
16	47	32.9	597	2	oxoglutarate dehyd
17	47	32.9	967	2	hypothetical prote
18	47	32.9	5138	2	anexin p33 - malz
19	46.5	32.5	314	2	hypothetical prote
20	46.5	32.5	435	2	hypothetical prote
21	46.5	32.5	1140	2	hypothetical prote
22	46	32.2	165	2	chlorocyturin chai
23	46	32.2	339	2	probable polyamine
24	46	32.2	946	1	inter-alpha-trypsin
25	46	32.2	1164	2	hypothetical prote
26	45.5	31.8	1378	2	conserved RNA p
27	45.5	31.8	261	2	neuropeptide pol-R
28	45.5	31.8	287	2	probable secreted
29	45.5	31.8	327	2	probable secreted

30	45.5	31.8	327	2	AF2859	conserved hypotnet
31	45.5	31.8	562	2	C71473	hypothetical prote
32	45.5	31.8	905	2	G83314	NADH dehydrogenase
33	45	31.5	273	2	S06736	photosystem II oxy
34	45	31.5	273	2	AG2287	manganese-stabiliz
35	45	31.5	295	2	F83201	conserved hypotnet
36	45	31.5	346	2	H95406	sodium ion pump ox
37	45	31.5	591	2	B44465	conserved hypotnet
38	45	31.5	591	2	AB0509	oxalacetate decar
39	45	31.5	591	2	AE0909	oxalacetate decar
40	45	31.5	596	2	A28088	probable membrane
41	45	31.5	715	2	S52675	env polypeptide
42	45	31.5	864	1	VOL7G4	hypothetical prote
43	45	31.5	1199	2	T23005	hypothetical prote
44	45	31.5	1217	2	T22672	hypothetical prote
45	45	31.5	1263	2	T19472	hypothetical prote

ALIGNMENTS

RESULT 1
bad protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 05-Nov-1999
C:Accession: A55671
R:King, E.; Zhai, U.; Jockel, J.; Boase, L.H.; Thompson, C.B.; Korsmeyer, S.J.
C:Title: Bad, a heterodimeric partner for Bcl-x-L and Bcl-2, displaces Bax and promot
A:Reference: A55671
A:Accession: A55671; MUID:95156361
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-204 <100%>
A:Cross-references: GB:137296; MID:9639778; PIDN:AAA64465.1; PID:9639779
C:Keywords: heterodimer

Query Match 96.5% Score 138; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 9.4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 2 KNLMAQRGRRLRMSDFEGSFKGL 27
|||||
RESULT 2
JC5575
inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster
C:Species: Mesocricetus auratus (golden hamster)
C:Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 20-Jun-2000
C:Accession: JC5575; PC4485
R:Nakatani, T.; Suzuki, Y.; Yamamoto, T.; Sinojima, H.
J. Biochem. 122, 71-82, 1997
A:Title: Molecular cloning and sequencing of cDNAs encoding three heavy-chain precurs
sin inhibitor heavy chain family.
A:Reference number: JC5574; MUID:97420688
A:Accession: JC5575
A:Molecule type: mRNA
A:Residues: 1-946 <NKA>
A:Cross-references: DDBJ:D89286; NID:91694689; PIDN:BA13939.1; PID:91694690
A:Experimental source: liver
A:Accession: PC4485
A:Molecule type: protein
A:Residues: 55-64;140-146;151-156;424-447;500-528;577-605 <NKA>
C:Comment: In the plasma three inter-alpha-trypsin inhibitor heavy chains 1, 2 and 3
that the complexes play important role for pancreatic cancer.
C:Superfamily: inter-alpha-trypsin inhibitor complex component II
F:261-264,717-916/Disulfide bonds: #status predicted

Query Match 37.8% Score 54; DB 2; Length 946;
Best Local Similarity 34.6%; Pred. No. 10;
Matches 9; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

OY 2 NLMNAORYGRELRLKMSDEFGCSFKGL 27
||| | | ||| |
DB 212 NWVIELQGMRFLLHVPDFTECHFOGV 237

RESULT 3
D70760
hypothetical protein RV2014 - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
R:Accession: D70760
R:ColE, S.T.: Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
; Connor, R.; Davies, R.; Devlin, K.; Fellwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Mature 393, 537-544, 1998
A:Authors: Saiter, R.; Saltsman, J.E.; Taylor, K.; Whitehead, S.; Barrett, B.G.
A>Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; PMID:98295987
A:Accession: D70760
A>Status: Preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: cDNA
A:Residues: 1-223 <CDS>
A:Cross-references: GB:Z740Z5; GB:ALJ23456; NID:g3261586; PIDN:CAA98415.1; PID:e1299911
C:Experimental source: Strain H37RV
C:Genetics:
A:Gene: RV2014

Query Match 37.1% Score 53; DB 2; Length 223;
Best Local Similarity 58.8%; Pred. No. 3-2;
Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 2 NLMNAORYGRELRLKMSD 18
|||| | | : |
DB 165 NLMADRYVRALRGHD 181

RESULT 4
S54354
Inter-alpha-inhibitor H2 chain - mouse
C:Species: Mus musculus (house mouse)
C>Date: 15-Jul-1999 #sequence_revision 01-Sep-1995 #text_change 20-Aug-1999
C:Accession: S54354
R:Chan, P.; Risler, J.L.; Requenez, G.; Sallier, J.P.
Biochem. J. 306, 505-512, 1995
A>Title: The three heavy-chain precursors for the Inter-alpha-inhibitor family in mouse
A:Reference number: S54353; PMID:95194326
A:Accession: S54354
A>Status: Preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Cross-references: EMBL:X70392; NID:9695633; PIDN:CAA49842.1; PID:g695634
C:Superfamily: Inter-alpha-trypsin inhibitor complex component II

Query Match 37.1% Score 53; DB 2; Length 946;
Best Local Similarity 34.6%; Pred. No. 14;
Matches 9; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

OY 2 NLMNAORYGRELRLKMSDEFGCSFKGL 27
||| | | ||| |
DB 212 NWVIELQGMRFLLHVPDFTECHFOGV 237

RESULT 5
S58185
2-dehydro-3-deoxyphosphonate aldolase (EC 4.1.2.15) ARO4 - yeast (*Saccharomyces cerevisiae*)
N:Alternate names: 3-deoxy-D-arabino-heptulosonate-7-phosphate synthase; DAHP synthase;
C:Species: *Saccharomyces cerevisiae*

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #next_change 22-Jun-1999
C:Accession: S38185; #sequence_revision 31-Dec-1993 #next_change 22-Jun-1999
R:Polignou, F.; Bileau, N.; Aigle, M.; Crouzet, M.
Yeast 9, 1131-1137, 1993
A:Title: The complete sequence of a 6794 bp segment located on the right arm of chrom
A:Accession number: S38185; MOID:94078675
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-370 <DOI>
A:Cross-references: GB:120296; PIDN:AAA65607.1; PID: g311102
R:Aljinovic, G.; Pohl, F.M.; Pohl, T.M.
submitted to the Protein Sequence Database, August 1994
A:Reference number: S45906
A:Accession: S46126
A:Molecule type: DNA
A:Residues: 1-370 <ALI>
A:Cross-references: EMBL:236118; NID:9536664; PIDN:CAA65212.1; PID: g536665; MIPS:YBR2
R:Aigle, M.; Bailez, M.C.; Barth, C.; Bileau, N.; Crouzet, M.; Dolignon, F.
submitted to the Protein Sequence Database, August 1994
A:Reference number: S45940
A:Accession: S46130
A:Molecule type: DNA
A:Residues: 1-370 <DNA>
A:Cross-references: EMBL:236118; NID:9536664; PIDN:CAA65212.1; PID: g536665; MIPS:YBR2
R:Kuenzler, M.; Paravicini, G.; Egli, C.M.; Iminger, S.; Braus, G.H.
Gene 113, 67-74, 1992
A:Title: Cloning, primary structure and regulation of the ARO4 gene, encoding the tyr
A:Reference number: JN0322; MOID:92225349
A:Accession: JN0322
A:Molecule type: DNA
A:Residues: 1-204, 208-370 <KUE>
A:Cross-references: EMBL:X61107
R:Kuenzler, M.; Balmelli, T.; Egli, C.M.; Paravicini, G.; Braus, G.H.
J. Bacteriol. 175, 5548-5558, 1993
A:Title: Cloning, primary structure, and regulation of the HIS7 gene encoding a bilin
A:Reference number: A48651; MOID:93374850
A:Accession: B48651
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 352-370 <KU2>
A:Cross-references: GB:X61107
C:Comment: This enzyme catalyzes the condensation of phosphoenolpyruvate and D-erythr
C:Genetics:
A:Gene: SGD:ARO4
A:Cross-references: SGD:S0000453; MIPS:YBR249C
A:Map Position: 2R
C:Function:
A:Description: aldehyde-lyase; carbon-carbon lyase
A:Pathway: aromatic amino acid biosynthesis; shikimate pathway
A:Note: first step in shikimate pathway
C:Superfamily: Phospho-2-dehydro-3-deoxyheptonate aldolase
C:Keywords: aldehyde-lyase; aromatic amino acid biosynthesis; carbon-carbon lyase; cy

Query Match 36 48; Score 52; DB 2; Length 370;
Best Local Similarity 47.68; Pred. No. 7.5;
Matches 10; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
CY 2 NLMANRGRLRMSDEEP 22
:|||||:|||||:
Db 80 DLEAKDVALRKLSDELKG 100

RESULT 6
A42095
L:total homeotic protein APETALA3 (AP3) - Arabidopsis thaliana
N:Alternate names: homeotic protein APETALA3; MAD5-box regulatory protein AP3
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C:Accession: A42095; S52633; T47593
R:Jack, T.; Brockman, L.L.; Meyerowitz, E.M.
Cell 66, 683-697, 1992

C:Genetics:
A:Gene: ATSP:F27B13.80

A:Map position: 4

A:Genome: nuclear

C:Keywords: carbon-oxygen lyase; chloroplast

F:1-39/Domain: transit peptide (chloroplast) #status predicted <TNP>

F:40-526/Product: threonine synthase #status experimental <MAT>

Query Match

33.6%; Score 48; DB 2; Length 526;

Best Local Similarity 35.3%; Pred. No. 42;

Matches 12; Conservative 6; Mismatches 8; Indels 8; Gaps 1;

QY 2 NLMAAQRVGRRLRMSD-----EFEGSPKGL 27

DB 172 NLFWAERFGKFLGMNDLWKKHCGISHTGSFKDL 205

RESULT 15

A39172 Antho-RFamide neuropeptide 19 repeat precursor - sea anemone (Calliactis parasitica)

C:Species: Calliactis parasitica

C:Date: 07-Feb-1992 #sequence_revision 07-Feb-1992 #text_change 21-Jul-2000

C:Accession: A39172

R:Darmer, D.; Schmutzler, C.; Diekhoff, D.; Grimelikhuijzen, C.J.P.

Proc. Natl. Acad. Sci. U.S.A. 88, 2555-2559, 1991

A:Title: Primary structure of the precursor for the sea anemone neuropeptide Antho-RFamide

A:Reference number: A39172; MUID:91172845

A:Accession: A39172

A:Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-334 <DAR>

A:Cross-references: GB:M59166; NID:9156133; PIDN:AAA27878.1; PID:9156134

C:Keywords: neuropeptide

Query Match

33.2%; Score 47.5; DB 2; Length 334;

Best Local Similarity 44.0%; Pred. No. 31;

Matches 11; Conservative 3; Mismatches 10; Indels 1; Gaps 1;

QY 1 KNLMAAQRVGRRLRMSDPEEGSF 24

DB 89 KRRVPERIGREFGGRGREFGGRF 113

Search completed: September 20, 2002, 10:39:13
Job time: 485 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 20, 2002, 11:04:35 ; Search time 44.99 seconds
(without alignments)
23.237 Million cell updates/sec

Title: US-09-544-664-56

Perfect score: 143
Sequence: 1 KNLMAQRYGRELIRMSDEEGSRKGL 27

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Database : SwissProt_40:*

Print. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	138	96.5	204	1	BAD_MOUSE
2	138	96.5	205	1	BAD_MOUSE
3	114	79.7	168	1	BAD_MOUSE
4	54	37.8	946	1	ITH2_MESAU
5	53	37.1	946	1	ITH2_MOUSE
6	52	36.4	370	1	AROG_YEAST
7	51	35.7	232	1	AP3_ARATH
8	49	34.3	453	1	RMUC_PSEPE
9	48	33.6	205	1	RAS3_RHTRA
10	48	33.6	220	1	6PGL_THENA
11	48	33.6	519	1	THRC_SOLIU
12	48	33.6	526	1	THRC_ARATH
13	47.5	33.2	334	1	FMRA_CALPA
14	47	32.9	198	1	BIM_HUMAN
15	46.5	32.5	429	1	FMRI2_ANTEL
16	46.5	32.5	945	1	FMRI2_ANTEL
17	46	32.2	946	1	FMRI2_HUMAN
18	46	32.2	1378	1	RPOB_CAME
19	45.5	31.8	287	1	PRFA_POLPE
20	45	31.5	273	1	PSBO_ANASP
21	45	31.5	328	1	SNF4_KLUDA
22	45	31.5	590	1	DCOA_SALTY
23	45	31.5	595	1	DCOA_KLEPN
24	45	31.5	653	1	HT2A_HUMAN
25	45	31.5	865	1	ENV_STVAT
26	45	31.5	1557	1	ENV_STVAT
27	44.5	31.1	907	1	LMU1_CAEEL
28	44.5	31.1	907	1	NUOG_ECOLI
29	44	30.8	196	1	NUOG_SALTY
30	44	30.8	196	1	BIM_MOUSE
31	44	30.8	262	1	BIM_RAT
32	44	30.8	629	1	END8_ECOLI
33	44	30.8	768	1	ENV_STVAT

34	44	30.8	877	1	ENV_STVAT	P27977 simian immu
35	43.5	30.4	217	1	UREF_SYNY3	P73327 synchocyst
36	43.5	30.4	1014	1	UVRA_STRCO	O92507 streptomyc
37	43.5	30.4	1200	1	DPGL_XENIA	O91684 xenopus lae
38	43	30.1	377	1	APJ_MOUSE	O9W08 mus musculu
39	43	30.1	380	1	APJ_HUMAN	P35414 homo sapien
40	43	30.1	380	1	APJ_MACMU	O97666 macaca mula
41	43	30.1	453	1	DPAP_MOUSE	P47739 mus musculu
42	43	30.1	463	1	Y030_NPVAC	P41434 autographa
43	43	30.1	578	1	ACEK_ECOLI	P11071 escherichia
44	43	30.1	583	1	ACEK_SALTY	P51067 salmonella
45	43	30.1	693	1	MDLI_YEAST	P33310 saccharomyc

ALIGNMENTS

RESULT 1
BAD_MOUSE STANDARD: PRT: 204 AA.
ID BAD_MOUSE
AC Q61337;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Bcl2-antagonist of cell death (BAD) (Bcl-2 binding component 6) (Bcl-xL/Bcl-2 associated death promoter).
DE BAD OR BIRC6.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, and Thymus;
RX MEDLINE=95136361; PubMed=7834748;
RA Yang E., Zha J., Jockel J., Boise L.H., Thompson C.B., Korsmeyer S.J.;
RT "Bad, a heterodimeric partner for Bcl-XL and Bcl-2, displaces Bax and promotes cell death.";
RL Cell 80:285-291(1995).
RN [2]
RP PHOSPHORYLATION AND MUTAGENESIS OF SER-112 AND SER-136.
RX MEDLINE=98022383; PubMed=9381178;
RA Del Peso L., Gonzalez-Garcia M., Page C., Herrera R., Nunez G.;
RT "Interleukin-3-induced phosphorylation of BAD through the protein kinase Akt.";
RL Science 278:687-689(1997).
RN [3]
RP MUTAGENESIS OF SERINE RESIDUES.
RX MEDLINE=20403302; PubMed=10949026;
RA Datta S.R., Katsov A., Hu L., Petros A., Pesik S.W., Yaffe M.B., Greenberg M.E.;
RT "14-3-3 proteins and survival kinases cooperate to inactivate BAD by Bcl-2 domain phosphorylation.";
RL Mol. Cell 6:41-51(2000).
CC -1- FUNCTION: Promotes cell death. Successfully competes for the binding to Bcl-x(L). Bcl-2 and Bcl-w, thereby affecting the level of heterodimerization of these proteins with BAX. Can reverse the death repressor activity of Bcl-x(L), but not that of Bcl-2. Appears to act as a link between growth factor receptor signaling and the apoptotic pathways.
CC -1- SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-x(L), Bcl-2 and Bcl-w. Also binds protein S100A10 (by similarity). The Ser-112/Ser-136 phosphorylated form binds 14-3-3 proteins.
CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon phosphorylation, locates to the cytoplasm.
CC -1- DOMAIN: Inactive Bcl-2 domain is required by BAX, BID, BAK, BAD AND BAX for their pro-apoptotic activity and for their interaction with anti-apoptotic members of the Bcl-2 family.
CC -1- PTM: Phosphorylated on Ser-112 in response to survival stimuli. Subsequent phosphorylation on Ser-136 promotes heterodimerization with 14-3-3 proteins. This interaction then facilitates the phosphorylation at Ser-155, a site within the BH3 domain, leading to the release of Bcl-x(L) and the promotion of cell survival.

CC Ser-136 is the major site of AKT/PKB phosphorylation. Ser-155 the
 CC major site of cAMP kinase A (CAPK) phosphorylation.
 CC -1- SIMILARITY: CONTAINS A BCL-3 HOMOLOG DOMAIN 3 (BH3).
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
 CC -----
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 CC or send an email to license@isb-sdb.ch).
 CC -----
 CC EMBL: L37296; AA64465.1; -
 CC MGD: MGI:1096330; Bad.
 CC InterPro: IPR000712; Bcl-2.
 CC PROSITE: PS01259; BH3; FALSE_NEG.
 CC Apoptosis: Phosphorylation.
 CC DOMAIN 147 161 BH3.
 CC MOD_RES 112 112 PHOSPHORYLATION (BY CAPK AND PKB).
 CC MOD_RES 136 136 PHOSPHORYLATION (BY CAPK AND PKB).
 CC MOD_RES 155 155 PHOSPHORYLATION (BY CAPK AND PKB).
 CC MUTAGEN 112 112 S->A: NO PHOSPHORYLATION.
 CC MUTAGEN 136 136 S->A: NO PHOSPHORYLATION.
 CC MUTAGEN 155 155 S->A: NO PHOSPHORYLATION; INTERACTS WITH
 CC BCL-X(L).
 CC SEQUENCE 204 AA: 22080 MW: 6C2BA910205053F7 CRC64;
 SO
 Query Match 96.5%; Score 138; DB 1; Length 204;
 Best Local Similarity 100.0%; Pred. No. 1,2e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 NLMAAQRGRGLRMSDEFGSFKGL 27
 DB 140 NLMAAQRGRGLRMSDEFGSFKGL 165
 ID ||||||||||||||||||||
 AC 035147; 070256; 09JHX1; PRT; 205 AA.
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Bcl2-antagonist of cell death (BAD) (Bcl-2 binding component
 DE 6) (Bcl-xL/Bcl-2 associated death promoter).
 GN BAD
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN RP SEQUENCE FROM N.A., AND MUTAGENESIS OF SER-113 AND SER-137.
 RC TISSUE-Ovary;
 RX MEDLINE=98034386; PubMed=9369453;
 RA Hsu S.Y., Kaipia A., Zhu L., Hsueh A.J.W.,
 RT "Interference of BAD (Bcl-xL/Bcl-2-associated death promoter)-induced
 RT apoptosis in mammalian cells by 14-3-3 isoforms and p11."
 RL Mol. Endocrinol. 11:1858-1867(1997).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Brain;
 RX MEDLINE=98194755; PubMed=9535132;
 RA D'Agata V., Magro G., Travali S., Musco S., Cavallaro S.,
 RT "Cloning and expression of the programmed cell death regulator BAD in
 RT the rat brain."
 RL Neurosci. Lett. 243:137-140(1998).
 RL [3]
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
 RC TISSUE-Brain;
 RX MEDLINE=21109372; PubMed=11161472;
 RA Hamner S., Arumae U., Yu L.-Y., Sun Y.-F., Saarna M., Lindholm D.;

RT "Functional characterization of two splice variants of rat BAD and
 RT their interaction with Bcl-w in sympathetic neurons."
 RL Mol. Cell. Neurosci. 17:97-106(2001).
 CC -1- FUNCTION: Promotes cell death. Successfully competes for the
 CC binding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level
 CC of heterodimerization of these proteins with BAX. Can reverse the
 CC death repressor activity of Bcl-x(L), but not that of Bcl-2 (By
 CC similarity). Appears to act as a link between growth factor
 CC receptor signaling and the apoptotic pathways.
 CC -1- SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-
 CC x(L), Bcl-2 and Bcl-w. Also binds protein S100A10. The Ser-
 CC 113/Ser-137 phosphorylated form binds 14-3-3 proteins
 CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon
 CC phosphorylation, locates to the cytoplasm (By similarity).
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms: alpha (shown here) and beta; are
 CC produced by alternative splicing. They differ only in their C-
 CC terminal regions.
 CC -1- TISSUE SPECIFICITY: Expressed in all tissues tested, including
 CC brain, liver, spleen and heart. In the brain, restricted to
 CC epithelial cells of the choroid plexus. Isoform alpha is the more
 CC abundant form.
 CC -1- DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND
 CC BAX for their pro-apoptotic activity and for their interaction
 CC with anti-apoptotic members of the Bcl-2 family.
 CC -1- PTM: Phosphorylated on Ser-113 in response to survival stimuli.
 CC Subsequent phosphorylation on Ser-137 promotes heterodimerization
 CC with 14-3-3 proteins. This interaction then facilitates the
 CC phosphorylation at Ser-156, a site within the BH3 domain, leading
 CC to the release of Bcl-x(L) and the promotion of cell survival.
 CC Ser-137 is the major site of AKT/PKB phosphorylation, Ser-156 the
 CC major site of protein kinase A (CAPK) phosphorylation (By
 CC similarity).
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
 CC -1- SIMILARITY: CONTAINS A BCL-3 HOMOLOG DOMAIN 3 (BH3).
 CC -----
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 CC or send an email to license@isb-sdb.ch).
 CC -----
 CC EMBL: AF003323; AAC53374.1; -
 CC EMBL: AF031227; AAC15100.1; -
 CC EMBL: AF279910; AAF91427.1; -
 CC EMBL: AF279911; AAF91428.1; -
 CC InterPro: IPR000712; Bcl-2.
 CC PROSITE: PS01259; BH3; FALSE_NEG.
 CC Apoptosis: Phosphorylation; Alternative splicing.
 CC DOMAIN 148 162 BH3.
 CC MOD_RES 113 113 PHOSPHORYLATION (BY CAPK AND PKB) (BY
 CC SIMILARITY).
 CC MOD_RES 137 137 PHOSPHORYLATION (BY CAPK AND PKB) (BY
 CC SIMILARITY).
 CC MOD_RES 156 156 PHOSPHORYLATION (BY CAPK AND PKB) (BY
 CC SIMILARITY).
 CC VARSPIC 166 205 LPRKSAQTATQKROSASWTRIIQSMWDRNLKGGSTPSQ
 CC -> EELTVSEVLEIPVRAIMEGMPIMFSQSPHLPPTPP
 CC WITH 14-3-3 PROTEINS.
 CC S->A: NO EFFECT ON HETERODIMERIZATION
 CC WITH 14-3-3 PROTEINS.
 CC S->A: NO HETERODIMERIZATION WITH 14-3-3
 CC PROTEINS. NO EFFECT ON HETERODIMERIZATION
 CC WITH BCL2 NOR WITH PROTEIN P11.
 CC SDAGGR -> ERGRKK (IN REF. 1).
 CC CONFLICT 29 34 7AFA71DAE9CFAA81 CRC64;
 SO SEQUENCE 205 AA: 22228 MW: 7AFA71DAE9CFAA81 CRC64;
 Query Match 96.5%; Score 138; DB 1; Length 205;
 Best Local Similarity 100.0%; Pred. No. 1,2e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY      2 NMAAORTGRELKMSDEFECSFKCL 27
DB      141 NMAAORTGRELKMSDEFECSFKCL 166

RESULT  3
BAD_HUMAN
ID      BAD_HUMAN          STANDARD:      PRT:      168 AA.
AC      092934; 014803; (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 40, Last sequence update)
DT      01-OCT-2001 (Rel. 41, Last sequence update)
DE      16-NOV-2002 (Rel. 41, Last sequence update)
DE      Bcl-2 antagonist of cell death (BAD) (Bcl-2 binding component
GN      BAD OR BCL2 OR BCL2L8.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;

RN      (1)
RP      SEQUENCE FROM N.A.
RA      Yin D.X., Li Z., Huang B., Chen S., Zhou H.;
RT      "A human protein that interacts with Bcl-2 and have homology to mouse
RT      BAD."
RL      Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
RN      (2)
RP      SEQUENCE FROM N.A., AND PHOSPHORYLATION BY RAF-1.
RX      MEDLINE=97083574; PubMed=8929532;
RA      Wang H.-G., Rapp U.R., Reed J.C.;
RT      "Bcl-2 targets the protein kinase Raf-1 to mitochondria."
RL      Cell 87:629-638(1996).
RN      (3)
RP      SEQUENCE FROM N.A.
RA      Takayama S., Reed J.C.;
RT      Submitted (OCT-1997) to the EMBL/Genbank/DBJ databases.
RN      (4)
RP      SEQUENCE FROM N.A., AND DIMERIZATION.
RC      TISSUE=bone marrow;
RX      MEDLINE=98049554; PubMed=9388232;
RA      Ohtsuka S., Diaz J.-L., Horne W., Chang J., Wang Y., Wilson G.,
RT      Chang S., Weeks S., Fritz L.C., Oltersdorf T.;
RT      "Dimerization properties of human BAD."
RL      J. Biol. Chem. 272:30866-30872(1997).
RN      (5)
RP      SEQUENCE FROM N.A.
RC      TISSUE=Lung;
RA      Strausberg R.;
RL      Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.
RN      (6)
RP      STRUCTURE BY NMR OF 103-127.
RX      MEDLINE=21073561; PubMed=11206074;
RA      Petros A.M., Nettesheim D.G., Wang Y., Olejniczak E.T., Meadows R.P.,
RA      Mack J., Swift K., Matayoshi E.D., Zhang H., Thompson C.B.,
RA      Resik S.W.;
RT      "Rationale for Bcl-xL/Bad peptide complex formation from structure,
RT      mutagenesis, and biophysical studies."
RL      Protein Sci. 9:2528-2534(2000).
CC      -1- FUNCTION: Promotes cell death. Successfully competes for the
CC      binding to Bcl-x(L). Bcl-2 and Bcl-w, thereby affecting the level
CC      of heterodimerization of these proteins with BAX. Can reverse the
CC      death repressor activity of Bcl-x(L), but not that of Bcl-2 (By
CC      similarity). Appears to act as a link between growth factor
CC      receptor signaling and the apoptotic pathways.
CC      -1- SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-
CC      x(L), Bcl-2 and Bcl-w. Also binds protein S100A10 (By similarity).
CC      The Ser-75/Ser-99 phosphorylated form binds 14-3-3 proteins (By
CC      similarity).
CC      -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon
CC      phosphorylation, localizes to the cytoplasm.
CC      -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
CC      -1- DOMAIN: Interacts Bcl-2 domain is required by Bcl-2, BAX, BAD AND
CC      BAX for their pro-apoptotic activity and for their interaction
CC      with anti-apoptotic members of the Bcl-2 family.

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CC      -1- PTH: Phosphorylated on Ser-75 in response to survival stimuli.
CC      Subsequent phosphorylation on Ser-99 promotes heterodimerization
CC      with 14-3-3 proteins. This interaction then facilitates the
CC      phosphorylation at Ser-118, a site within the BH3 domain, leading
CC      to the release of Bcl-x(L) and the promotion of cell survival.
CC      Ser-99 is the major site of AKT/PKB phosphorylation. Ser-118 the
CC      major site of protein kinase A (CAK) phosphorylation (by
CC      similarity).
CC      -1- SIMILARITY: CONTAINS 1 BCL-3 HOMOLOGOUS DOMAIN 3 (BH3).
CC      -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; U66879; AAB36516.1; -
DR      EMBL; AF021792; AAB72092.1; -
DR      EMBL; AF031523; AAB88124.1; -
DR      EMBL; BC001901; AAB01901.1; -
DR      PDB; 1G5J; 07-FEB-01.
DR      MIM; 603167; -
DR      InterPro; IPR000712; Bcl-2.
DR      PROSITE; PS01259; BH3; FALSE-NEG.
KW      Apoptosis; Phosphorylation; 3D-structure.
FT      DOMAIN 110 124
FT      MOD_RES 75 75
FT      MOD_RES 99 99
FT      MOD_RES 118 118
FT      MOD_RES 124 124
FT      CONFLICT 64 91
FT      CONFLICT 91 91
SQ      SEQUENCE 168 AA; 18392 MW; 69FB8D27DDEE3241 CRC64;
AGAVEIRSRHSSTIPAGTEDESGEERS -> RMCGGDPES
POLIPRGDGGRRRDGGGAG (IN REF. 1).

Query Match          79.7%; Score 114; DB 1; Length 168;
Best Local Similarity 91.7%; Pred. No. 4e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      2 NMAAORTGRELKMSDEFECSFK 25
DB      103 NMAAORTGRELKMSDEFECSFK 126

RESULT  4
ITP2_MESAU
ID      ITP2_MESAU          STANDARD:      PRT:      946 AA.
AC      P97279;
DT      15-JUL-1998 (Rel. 36, Created)
DT      15-JUL-1998 (Rel. 36, Last sequence update)
DE      01-NOV-2002 (Rel. 41, Last sequence update)
DE      Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITI heavy
DE      chain H2) (HC2).
GN      ITH2.
OS      Mesocricetus auratus (Golden hamster).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC      Mesocricetus.
OX      NCBI_TaxID=10036;

RN      (1)
RP      SEQUENCE FROM N.A.
RC      TISSUE=Liver;
RX      MEDLINE=97420688; PubMed=9276673;
RA      Nakatani T., Suzuki Y., Yamamoto T., Sinohara H.;
RT      "Molecular cloning and sequencing of cDNAs encoding three heavy-chain
RT      precursors of the inter-alpha-trypsin inhibitor in Syrian hamster:
RT      implications for the evolution of the inter-alpha-trypsin inhibitor
RT      heavy chain family."

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RL J. Biochem. 122:71-82(1997).

RN [2]

RP SEQUENCE OF 55-64; 140-146; 151-156; 424-447; 500-528 AND 577-605, AND SUBUNITS.

RC TISSUE-PLASMA.

RA Yamamoto T., Yamamoto K., Sinochata H.;

RT Inter-alpha-trypsin inhibitor and its related proteins in Syrian hamster urine and plasma."

RL J. Biochem. 120:145-152(1996).

CC -1- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN, INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY SIMILARITY).

CC -1- SUBUNIT: 1-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN, BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2 AND BIKUNIN. INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND BIKUNIN. AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.

CC -1- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN 4-SULFATE BRIDGE TO THEIR C-TERMINAL ASPARTATE (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE ITIH FAMILY.

CC -1- SIMILARITY: CONTAINS 1 VMFA DOMAIN.

CC -----

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CC -----

CC EMBL: D89286; BAA13939.1; -

DR InterPro: IPR002035; VMFA.

DR Pfam: PF00092; vma: 1.

DR SMART: SM00327; vma: 1.

DR PROSITE: PS50234; VMFA: 1.

KW Serine protease inhibitor; Repeat; Signal; Multigene family;

KW Glycoprotein.

FT FT 1 18 POTENTIAL.

FT FT 19 54 BY SIMILARITY.

FT FT 55 702 INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN

FT FT CHAIN H2.

FT FT PROPEP 703 946 BY SIMILARITY.

FT FT DOMAIN 308 468 VMFA.

FT FT CARBOHYD 118 118 N-LINKED (GLCNAc. . .) (POTENTIAL).

FT FT CARBOHYD 263 263 N-LINKED (GLCNAc. . .) (POTENTIAL).

FT FT CARBOHYD 445 445 N-LINKED (GLCNAc. . .) (POTENTIAL).

FT FT CARBOHYD 578 578 N-LINKED (GLCNAc. . .) (POTENTIAL).

FT FT BINDING 702 702 CHONDROITIN 4-SULFATE, CROSS-LINK SITE (BY SIMILARITY).

FT FT CONFLICT 510 510 V -> Y (IN REF. 2).

FT FT CONFLICT 595 595 E -> I (IN REF. 2).

FT FT SEQUENCE 946 AA; 106580 MW; CA8BF563458E7B2E CRC64;

OY 2 NMAAORYGRLRMSEDFGSKGL 27

DB 212 NWAVIEFGRLFLVDPTEGFGV 237

Query Match 37.8%; Score 54; DB 1; Length 946;

Best Local Similarity 34.6%; Pred. No. 3;

Matches 9; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

RESULT 5

ID ITH2.MOUSE STANDARD: PRT; 946 AA.

AC 061703;

DT 15-JUL-1998 (rel. 36, Created)

DT 15-JUL-1998 (rel. 36, Last sequence update)

DE Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITI heavy chain H2).

GN ITH2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OC NCBI_Taxid=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6N; TISSUE=Liver;

RA MEDLINE=95194326; PubMed=7334067;

RA Chan P., Risler J.-L., Raguenez G., Saller J.-P.;

RT "The three heavy-chain precursors for the inter-alpha-inhibitor family in mouse: new members of the multicopper oxidase protein group with differential transcription in liver and brain."

RL Biochem. J. 306:505-512(1995).

CC -1- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN, INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY SIMILARITY).

CC -1- SUBUNIT: 1-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN, BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2 AND BIKUNIN. INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND BIKUNIN. AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.

CC -1- TISSUE SPECIFICITY: EXPRESSED IN BOTH LIVER AND BRAIN.

CC -1- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN 4-SULFATE BRIDGE TO THEIR C-TERMINAL ASPARTATE (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE ITIH FAMILY.

CC -1- SIMILARITY: CONTAINS 1 VMFA DOMAIN.

CC -----

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CC -----

CC EMBL: X70392; CAA49842.1; -

DR MGD: MGI:96619; Itih2.

DR InterPro: IPR002035; VMFA.

DR Pfam: PF00092; vma: 1.

DR SMART: SM00327; vma: 1.

DR PROSITE: PS50234; VMFA: 1.

KW Serine protease inhibitor; Repeat; Signal; Multigene family;

KW Glycoprotein.

FT FT 1 18 POTENTIAL.

FT FT 19 54 BY SIMILARITY.

FT FT 55 702 INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN

FT FT CHAIN H2.

FT FT PROPEP 703 946 BY SIMILARITY.

FT FT DOMAIN 308 468 VMFA.

FT FT CARBOHYD 118 118 N-LINKED (GLCNAc. . .) (POTENTIAL).

FT FT CARBOHYD 263 263 N-LINKED (GLCNAc. . .) (POTENTIAL).

FT FT CARBOHYD 445 445 N-LINKED (GLCNAc. . .) (POTENTIAL).

FT FT BINDING 702 702 CHONDROITIN 4-SULFATE, CROSS-LINK SITE (BY SIMILARITY).

FT FT SEQUENCE 946 AA; 105927 MW; 40DB6716433ED9DC CRC64;

OY 2 NMAAORYGRLRMSEDFGSKGL 27

DB 212 NWAVIEFGRLFLVDPTEGFGV 237

Query Match 37.1%; Score 53; DB 1; Length 946;

Best Local Similarity 34.6%; Pred. No. 4.2;

Matches 9; Conservative 5; Mismatches 12; Indels 0; Gaps 0;


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RESULT 6
AOC_YEAST STANDARD: PRT: 370 AA.
ID AOC_YEAST
AC P32449:
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Phospho-2-dehydro-3-deoxyheptanate aldolase, tyrosine-inhibited
DE (EC 4.1.2.15) (Phospho-2-keto-3-deoxyheptanate aldolase) (DHP
DE synthetase) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase).
OS ARO4 OR YBR249C OR YBR1701.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycos.
OX NCBI_TaxID=4932;

RP SEQUENCE FROM N.A.
MEDLINE=9225349; PubMed=1348717;
RA Kuenzler M., Paravicini G., Egli C., Irniger S., Brans G.H.;
RT Cloning, primary structure and regulation of the ARO4 gene, encoding
RT the tyrosine-inhibited 3-deoxy-D-arabino-heptulosonate-7-phosphate
RT synthase from Saccharomyces cerevisiae.*;
RN Gene 113:67-74(1992).
RL [2]
RP REVISIONS TO 205-207.
RA Kuenzler M.;
RL Submitted (NOV-1993) to the EMBL/Genbank/DBJ databases.
RP SEQUENCE FROM N.A.
RC STRAIN=5288C;
RX MEDLINE=94076675; PubMed=8256522;
RA Daignon F., Billeau N., Aigle M., Crouzet M.;
RT "The complete sequence of a 6794 bp segment located on the right arm
RT of chromosome II of Saccharomyces cerevisiae. Finding of a putative.
RT QTPase in a yeast."*
RN Yeast 9:1131-1137(1993).
RL [4]
RP SEQUENCE FROM N.A.
RC STRAIN=5288C;
RA Aljinovic G., Pohl F.M., Pohl T.M.;
RL Submitted (AUG-1994) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: STEREOSPECIFIC CONDENSATION OF PHOSPHENOLPYRUVATE (PEP)
CC AND D-ERYTHROSE-4-PHOSPHATE (E4P) GIVING RISE TO 3-DEOXY-D-
CC ARABINO-HEPTULOSONATE-7-PHOSPHATE (DHP).
CC -1- CATALYTIC ACTIVITY: 2-dehydro-3-deoxy-D-arabino-heptanate 7-
CC phosphate + phosphate -> phosphoenolpyruvate + D-erythrose 4-
CC phosphate + H(2)O.
CC -1- ENZYME REGULATION: INHIBITED BY TYROSINE.
CC -1- PATHWAY: FIRST STEP IN THE BIOSYNTHESIS OF CHORISMATE WITHIN
CC THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE PATHWAY).
CC -1- INDUCTION: BY AMINO ACID STARVATION
CC -1- SIMILARITY: BELONGS TO CLASS-I DHP SYNTHETASE FAMILY.
CC -----
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CC -----
DR EMBL: X61107; CAA43419.1;
DR EMBL: L20236; AAA65607.1;
DR EMBL: L26118; CAA85212.1;
DR PIR: S38185; S38185.
DR HSP: P00866; I087.
DR SBD: S0000453; ARO4.
DR InterPro: IPR001185; DHP_synth_1.
DR Pfam: PF00793; DHP_synth_1; 1.
DR ProDom: PD005060; DHP_synth_1; 1.
KW Aromatic amino acid biosynthesis; Lyase; Multigene family.

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SQ SEQUENCE 370 AA: 39749 MW: 594ED48F24175979 CRC64;
Query Match 36.48; Score 52; DB 1; Length 370;
Best Local Similarity 47.68; Pred. No. 2.1;
Matches 10; Conservative 5; Mismatches 6; Indels 0; Gaps 0.
OY 2 NLMAQRYGRELKMSDFEG 22
DB 80 DLEMADEYALRLKLSDELK 100

RESULT 7
AP3_ARATH STANDARD: PRT: 232 AA.
ID AP3_ARATH
AC P35632; O39003;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Floral homeotic protein APETALA3.
DE AP3 OR AT3G54340 OR T12E18.30.
OS Arabidopsis thaliana (Mouse-ear cress). Embryophyta; Tracheophyta;
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RL [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Petal;
RX MEDLINE=92154682; PubMed=1346756;
RA Jack T., Brockman L.V., Meyerowitz E.M.;
RT "The homeotic gene APETALA3 of Arabidopsis thaliana encodes a MADS
RT box and is expressed in petals and stamens."*
RN Cell 68:683-697(1992).
RL [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV LANDSBERG ERCTA;
RX MEDLINE=95036018; PubMed=794893;
RA Okamoto H., Yano A., Shirasahi H., Okada K., Shimura Y.;
RT "Genetic complementation of a floral homeotic mutation, apetalas3,
RT with an Arabidopsis thaliana gene homologous to DERICENS of
RT Antirrhinum majus."*
RN Plant Mol. Biol. 26:465-472(1994).
RL [3]
RP SEQUENCE FROM N.A.
RC STRAIN=VARIOUS STRAINS;
RX MEDLINE=99126449; PubMed=9927474;
RA Purugganan M.D., Suddith J.I.;
RT "Molecular population genetics of floral homeotic loci. Departures
RT from the equilibrium-neutral model at the APETALA3 and PISTILLATA
RT genes of Arabidopsis thaliana."*
RN Genetics 151:839-848(1999).
RL [4]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, COLUMBIA;
RX MEDLINE=21016720; PubMed=11130713;
RA Salanoubat M., Lemcke K., Rieger M., Ansoerge W., Unsel'd M.,
RA Farmanou B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
RA Delserny N., Boultiry M., Grivell L.A., Mache R., Puigdomenech P.,
RA De Simone V., Choisyne N., Artiguenave F., Robert C., Brotier P.,
RA Wincker P., Catolico J., Weissenbach J., Saurin W., Quetier F.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wurmbach E., Drzonek H., Erfle H., Jordan R., Bangert S.,
RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,
RA Conrad A., Horsticher K., Kauer G., Loehner T.-H., Nordiek G.,
RA Reichelt J., Schaefer M., Schoen O., Barques M., Terol J., Clement J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwalder B., Duchemin D.,
RA Cooke P., Landie M., Berger-Lauco C., Punelle B., Masny D.,
RA de Haan W., Maarse A.C., Alcaraz J.-P., Cortes A., Casacubeta E.,
RA Montfort A., Argitirov A., Flores M., Liqiori R., Vitala D., Mendes H.-W.,
RA Mannheim G., Haase D., Schopf H., Rued S., Zaccaria P., Jenkins J.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,

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RA Rooney T., Rizzo M., Wals A., Uteperback T., Fujii C.Y., Shea T.P.,
RA Crensy T.H., Haas B., Malt R., Wu D., Peterson J., Van Aken S.,
RA Pal G., Miltner J., Sellers P., Gill J.E., Feldhym T.V.,
RA Prus D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
RA Fraser C.M., Kaneo T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Idegawa K., Kawashima K., Kishida A.,
RA Nakayama C., Kohara M., Matsumoto M., Matsuno A., Moraki A.,
RA Nakayama A., Yamada N., Shino S., Terauchi C., Wada T.,
RA "Sequence and analysis of chromosome 3 of the plant Arabidopsis
RA thaliana" (820-B22/2000).
RL Nature 408:820-B22(2000).
CC -1- FUNCTION: TRANSCRIPTION FACTOR INVOLVED IN THE GENETIC CONTROL OF
CC FLOWER DEVELOPMENT.
CC -1- SUBUNIT: FORMS AN HETERODIMER WITH PISTILLATA.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN PETALS AND STAMENS.
CC -1- MISCELLANEOUS: MUTATIONS IN AP3 CAUSE TRANSFORMATION OF PETALS
CC INTO SEEDS AND STAMINA INTO CARPELS.
CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC -1- SIMILARITY: CONTAINS A PROBABLE DIMERIZATION DOMAIN FOUND IN
CC SRF-TYPE TRANSCRIPTION FACTORS (K-BOX).
CC CC
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CC CC
DR EMBL: M66357; AAA3740.1; -
DR EMBL: D21125; BAA04665.1; -
DR EMBL: AF115799; MADS1888.1; -
DR EMBL: AF115800; MADS1889.1; -
DR EMBL: AF115802; MADS1891.1; -
DR EMBL: AF115804; MADS1893.1; -
DR EMBL: AF115811; MADS1900.1; -
DR EMBL: AF115814; MADS1903.1; -
DR EMBL: AF115821; MADS1905.1; -
DR PIR: A42095; M42095.
DR HSSP: P11746; 1MMN.
DR TRANSFAC: T01776; -
DR InterPro: IPR002487; K-box.
DR InterPro: IPR002100; MADS-box.
DR Pfam: PF01486; K-box; 1.
DR Pfam: PF00319; SRF-TF; 1.
DR PRINTS: PR00404; MADSDOMAIN.
DR SMART: SM00432; MADS; 1.
DR PROSITE: PS00350; MADS_BOX_1; 1.
DR PROSITE: PS00066; MADS_BOX_2; 1.
DR Transcription regulation: DNA-binding; Activator; Nuclear protein;
DR Developmental protein.
KW DOMAIN 3 57 MADS.
KW DOMAIN 93 165 K-BOX.
FT DOMAIN 199 199 A -> R (IN REF. 2).
FT CONFLICT 232 AA: 27341 MW: 669070319F9857C3 CRC64;
SQ SEQUENCE

```

DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE DNA recombination protein rmc homolog.
GN RMC OR PA1031.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas
OX NCBI_TaxID=287;
PP [[1]]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAOI:
RA MEDLINE=20437537; PubMed=10984043;
RA Stever C.K., Pham K.-O.T., Ertin A.L., Mizoguchi S.D., Warren P.,
RA Hickory C.J., Brinkman F.S.L., Hutnagle W.O., Kowalik D.U., Laaron M.,
RA Brody R.L., Coulter S.N., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Smeltz K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saler M.H., Hancock R.E.W., Loty S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAOI, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
CC - FUNCTION: Involved in DNA recombination (By similarity).
CC - SIMILARITY: BELONGS TO THE RMC FAMILY.
CC -----
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CC -----
DR EMBL: AE004535; AACG04420.1; -
DR InterPro: IPR003798; DUF195.
DR Pfam: PR02645; DUF195.1
KW DNA recombination; Coiled coil; Complete proteome.
FT DOMAIN 16 COILED COIL (POTENTIAL),
FT SEQUENCE 453 AA: 51539 MW: 1E7EA97B82EC5E4B CRC64;
SQ

Query Match 34.3%; Score 49; DB 1; Length 453;
Best Local Similarity 55.6%; Pred. No. 7.3;
Matches 10; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

QY 4 WAAORYGR-ELRRMSDE 19
DB 65 WASERGGREELRLRLASE 82
[[::]] [[::]] [[::]]

RESULT 9
RAS3_RHIRA ID RAS3_RHIRA STANDARD; PRT: 205 AA.
AC P2280;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ras-like protein 3.
GN RAS3.
OS Rhizomucor racemosus (Mucor citrinelloides f. lusitanicus).
OC Eukaryota; Fungi; Zygomycota; zygomycetes; Mucorales; Mucoraceae;
OC Mucor.
OX NCBI_TaxID=4841;
PP [[1]]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12109;
RA MEDLINE=91061774; PubMed=1701021;
RA Casale M.L., McConnell D.G., Wang S.-Y., Lee Y.-J., Linz J.E.;
RA "Expression of a gene family in the dimorphic fungus Mucor racemosus
RA which exhibits striking similarity to human ras genes."
RL Mol. Cell. Biol. 10:6654-6663(1990).
RT - ENZYME REGULATION: ALTERNATE BETWEEN AN INACTIVE FORM BOUND TO GDP
AND AN ACTIVE FORM BOUND TO GTP. ACTIVATED BY A GUANINE

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CC
DR      EMBL; AE001772; AAD36230.1; -
DR      TIGR; TM154; -
DR      InterPro: IPR000457; Glucosamine_isoc.
DR      Pfam; PF01182; Glucosamine_isoc. 1.
KW      Hydrolase; Complete proteome.
SQ      SEQUENCE 220 AA; 25325 MW; 980FD07E0E1E60C3 CRC64;
OY      5 AADRYGHELRMRSDEREGSGKL 27
Db      111 ACERYEREIRSATDPDLALIGM 133
RESULT 11
THRC_SOLTU
ID      THRC_SOLTU STANDARD; PRT; 519 AA.
AC      Q9WT28;
DT      01-MAR-2002 (Rel. 41, Created)
DT      01-MAR-2002 (Rel. 41, Last sequence update)
DT      01-MAR-2002 (Rel. 41, Last annotation update)
DE      Threonine synthase, chloroplast precursor (EC 4.2.99.2) (TS).
OS      Solanum tuberosum (Potato).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC      Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX      NCBI_TaxID=4113;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Casazza P., Kaiser S., Willmitzer L., Hoeffgen R., Hesse H.;
RT      "Isolation and characterization of a cDNA encoding threonine synthase
RT      from Solanum tuberosum."
RL      Submitted (MUG-1998) to the EMBL/GenBank/DDBJ databases.
CC      -1- CATALYTIC ACTIVITY: O-phospho-L-homoserine + H(2)O -> L-threonine +
CC      phosphate.
CC      -1- COFACTOR: Pyridoxal phosphate (By similarity).
CC      -1- ENZYME REGULATION: Allosterically activated by S-adenosyl-
CC      methionine (SAM) (By similarity).
CC      -1- PATHWAY: Threonine biosynthesis; last step.
CC      -1- SUBUNIT: Homodimer (By similarity).
CC      -1- SUBCELLULAR LOCATION: Chloroplast (By similarity).
CC      -1- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
CC
CC      -----
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CC
DR      EMBL; AF082894; AAF74984.1; -
DR      InterPro: IPR001926; B6_enzyme_beta.
DR      Pfam; PF00291; PALP; 1.
DR      PROSITE; PS00165; DEHYDRATASE_SER_PRR; 1.
KW      Threonine biosynthesis; Lyase; Pyridoxal phosphate; Allosteric enzyme;
KW      Chloroplast; Transist peptide.
FT      TRANSIT 1 40
FT      CHAIN 41 519 CHLOROPLAST (BY SIMILARITY).
FT      BINDING 196 196 THREONINE SYNTHASE.
FT      BINDING 196 196 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ      SEQUENCE 519 AA; 57412 MW; 114C0979CD231464 CRC64;

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Db 172 NLWAEFGKFLGMDIMVHKHSHTGSKDL 205

RESULT 13

PMRA_CALPA STANDARD: PRT: 334 AA.

AC 001133;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Antho-Rhamide neuropeptides precursor.

OS Calliacis parasitica (See anemone).

OC Eukaryota: Metazoa: Cnidaria: Anthozoa: Zoantharia: Actinaria;

OC Nematodeae: Hormathiidae: Calliactis.

OC NCBI_TaxID=6114;

OX [1]

PN SEQUENCE FROM N.A.

RX MEDLINE=91172845; PubMed=1706527.

RA Diermer D., Schmutzler C., Diekhoff D., Grimmelikhuijzen C.J.P.:

RT Primary structure of the precursor for the sea anemone neuropeptide

RU Antho-Rhamide (<Glu-Gly-Arg-Phe-NH₂>).

CC Proc. Natl. Acad. Sci. U.S.A. 98:2555-2559(1991).

CC - FUNCTION: NOT KNOWN BUT IT COULD ACT AS A TRANSMITTER AT

CC NEUROMUSCULAR SYNAPSES.

CC - TISSUE SPECIFICITY: NEURONS ASSOCIATED WITH SMOOTH MUSCLE FIBERS.

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CC -----

DR EMBL: M59166; AAA27878.1; -

DR PIR: A39172; A39172.

DR InterPro: IPR002544; FARP.

DR Pfam: PF01581; FARP; 15.

KW Neuropeptide; Amidation; Repeat; Signal.

FT SIGNAL 1 26

FT PEPTIDE 117 120 ANTHO-RHAMIDE.

FT PEPTIDE 126 129 ANTHO-RHAMIDE.

FT PEPTIDE 135 138 ANTHO-RHAMIDE.

FT PEPTIDE 143 146 ANTHO-RHAMIDE.

FT PEPTIDE 152 155 ANTHO-RHAMIDE.

FT PEPTIDE 161 164 ANTHO-RHAMIDE.

FT PEPTIDE 170 173 ANTHO-RHAMIDE.

FT PEPTIDE 179 182 ANTHO-RHAMIDE.

FT PEPTIDE 188 191 ANTHO-RHAMIDE.

FT PEPTIDE 197 200 ANTHO-RHAMIDE.

FT PEPTIDE 206 209 ANTHO-RHAMIDE.

FT PEPTIDE 215 218 ANTHO-RHAMIDE.

FT PEPTIDE 224 227 ANTHO-RHAMIDE.

FT PEPTIDE 234 237 ANTHO-RHAMIDE.

FT PEPTIDE 243 246 ANTHO-RHAMIDE.

FT PEPTIDE 253 256 ANTHO-RHAMIDE.

FT PEPTIDE 263 266 ANTHO-RHAMIDE.

FT PEPTIDE 272 275 ANTHO-RHAMIDE.

FT PEPTIDE 281 284 ANTHO-RHAMIDE.

FT MOD_RES 120 120 PROVIDE AMIDE GROUP).

FT MOD_RES 129 130 PROVIDE AMIDE GROUP).

FT MOD_RES 138 139 PROVIDE AMIDE GROUP).

FT MOD_RES 146 147 PROVIDE AMIDE GROUP).

FT MOD_RES 155 156 PROVIDE AMIDE GROUP).

FT MOD_RES 164 165 PROVIDE AMIDE GROUP).

FT MOD_RES 173 174 PROVIDE AMIDE GROUP).

FT MOD_RES 182 183 PROVIDE AMIDE GROUP).

FT MOD_RES 191 191 PROVIDE AMIDE GROUP).

FT MOD_RES 200 200 PROVIDE AMIDE GROUP).

FT MOD_RES 209 209 PROVIDE AMIDE GROUP).

FT MOD_RES 218 218 PROVIDE AMIDE GROUP).

FT MOD_RES 227 227 PROVIDE AMIDE GROUP).

FT MOD_RES 237 237 PROVIDE AMIDE GROUP).

FT MOD_RES 246 246 AMIDATION (G-247 PROVIDE AMIDE GROUP).

FT MOD_RES 256 256 AMIDATION (G-257 PROVIDE AMIDE GROUP).

FT MOD_RES 266 266 AMIDATION (G-267 PROVIDE AMIDE GROUP).

FT MOD_RES 275 275 AMIDATION (G-276 PROVIDE AMIDE GROUP).

FT MOD_RES 284 284 AMIDATION (G-285 PROVIDE AMIDE GROUP).

SO SEQUENCE 334 AA: 39781 MW: 438E182C736EB583 CRC64;

Query Match 33.28; Score 47.5; DB 1; Length 334;

Best Local Similarity 44.08; Pred. No. 8.8;

Matches 11; Conservative 3; Mismatches 10; Indels 1; Gaps 1;

OY 1 KNLMAQRVGRGLR-RMSDEFEGSC 24

Db 89 KRRVYPGVGRGFRGFRGFRGFR 113

RESULT 14

BIM_HUMAN STANDARD: PRT: 198 AA.

AC 043521; 043522.

DT 18-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Bcl2-like protein 11 (Bcl2 interacting mediator of cell death).

GN BCL2L11 OR BIM.

OS Homo sapiens (Human).

OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;

OC Mammalia: Eutheria: Primates: Catarrhini: Hominiidae: Homo.

OC NCBI_TaxID=9606;

OX [1]

PN SEQUENCE FROM N.A. - FUNCTION, AND ALTERNATIVE SPLICING.

RP TISSUE=Peripheral blood, and spleen;

RC MEDLINE=98094360; PubMed=9430630;

RX O'Connor L., Strasser A., O'Reilly L.A., Hausmann G., Adams J.M.,

RA Cory S., Huang D.C.S., "Bim: a novel member of the Bcl-2 family that promotes apoptosis."

RU EMBO J. 17:364-393(1998).

CC - FUNCTION: INDUCES APOPTOSIS. ISOFORM BIML IS MORE POTENT THAN

CC ISOFORM BIMEL.

CC - SUBUNIT: FORMS HETERODIMERS WITH A NUMBER OF ANTIAPOPTOTIC BCL-2

CC PROTEINS INCLUDING MCL-1, BCL-2, BCL-XL, BFL-1, AND BHRF-1. DOES

CC NOT HETERODIMERIZE WITH PROAPOPTOTIC PROTEINS SUCH AS BAD, BOK,

CC BAX OR BAK (BY SIMILARITY).

CC - SUBCELLULAR LOCATION: ASSOCIATED WITH INTRACYTOSOLIC MEMBRANES

CC (BY SIMILARITY).

CC - ALTERNATIVE PRODUCTS: 2 ISOFORMS: BIMEL (SHOWN HERE) AND

CC BIML: ARE PRODUCED BY ALTERNATIVE SPLICING.

CC - DOMAIN: THE BHR3 DOMAIN IS REQUIRED FOR BCL-2 BINDING AND

CC CYTOTOXICITY.

CC - SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 3 (BHR3).

CC -----

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CC -----

DR EMBL: AF032457; AAC39593.1; -

DR EMBL: AF032458; AAC39594.1; -

DR MIM: 603827; -

DR InterPro: IPR000712; BCL-2.

DR PROSITE: PS01259; BHR3; FALSE_NEG.

KW Apoptosis; Alternative splicing; Membrane.

FT DOMAIN 148 162 BHR3.

FT VARSPIC 42 101 MISSING (IN ISOFORM BIML).

SO SEQUENCE 198 AA: 22171 MW: D75735E469CA6997 CRC64;

Query Match 32.98; Score 47; DB 1; Length 198;

Best Local Similarity 45.58; Pred. No. 5.8;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 20, 2002, 11:03:47 : Search time 172.19 seconds
(without alignments)
27.126 Million cell updates/sec

Title: US-09-544-664-56

Perfect score: 143
Sequence: 1 KNIMAAQRYGRELRLRMSDEFGSRKGL 27

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

Database :

SPTREMBL_19:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mbc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_protist:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_rviro:
16: sp_bacteriophage:
17: sp_archaeophages:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	60.8	146	13	0919N2 brachydanio
2	53	37.1	223	16	010843 mycobacteri
3	52.5	36.7	506	8	047148 menziesia c
4	52.5	36.7	506	8	063960 rhododendro
5	52.5	36.7	506	8	062972 rhododendro
6	52.5	36.7	506	8	062973 rhododendro
7	52.5	36.7	506	8	062974 rhododendro
8	52.5	36.7	506	8	062975 rhododendro
9	52.5	36.7	506	8	062977 rhododendro
10	52.5	36.7	506	8	062978 rhododendro
11	52.5	36.7	506	8	062980 rhododendro
12	52.5	36.7	506	8	062981 rhododendro
13	52.5	36.7	506	8	062982 rhododendro
14	52.5	36.7	506	8	062983 rhododendro
15	52.5	36.7	506	8	062984 rhododendro
16	52.5	36.7	506	8	062988 rhododendro

17	52.5	36.7	506	8	062989 rhododendro
18	52.5	36.7	506	8	062990 rhododendro
19	52.5	36.7	506	8	062991 rhododendro
20	52.5	36.7	506	8	062992 rhododendro
21	52.5	36.7	506	8	062993 menziesia m
22	52.5	36.7	506	8	047149 rhododendro
23	52.5	36.7	506	8	047152 rhododendro
24	52.5	36.7	506	8	047155 rhododendro
25	52.5	36.7	506	8	047168 menziesia p
26	52.5	36.7	506	8	047170 rhododendro
27	52.5	36.7	506	8	047171 rhododendro
28	52.5	36.7	506	8	047173 rhododendro
29	52.5	36.7	506	8	047174 tsusisophyll
30	52.5	36.7	507	8	047175 rhododendro
31	52.5	36.7	507	8	062985 rhododendro
32	52.5	36.7	507	8	062986 rhododendro
33	52.5	36.7	508	8	062979 rhododendro
34	51.5	36.0	506	8	047153 rhododendro
35	51.5	36.0	506	8	047160 rhododendro
36	51	35.7	231	10	09SEGO arabidopsis
37	51	35.7	232	10	09S7Q3 arabidopsis
38	51	35.7	232	10	09SQ22 arabidopsis
39	51	35.7	232	10	09SQ21 arabidopsis
40	51	35.7	232	10	09SQ20 arabidopsis
41	51	35.7	232	10	09SQ19 arabidopsis
42	51	35.7	232	10	09SQ18 arabidopsis
43	51	35.7	232	10	09SQ17 arabidopsis
44	51	35.7	232	10	09SQ16 arabidopsis
45	51	35.7	232	10	09SQ15 arabidopsis

ALIGNMENTS

RESULT 1

ID: 0919N2 PRELIMINARY: PRT: 146 AA.

AC 0919N2: 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)

DE BAD.

GN Brachydanio rerio (zebrafish) (Zebra danio).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;

OC Cypriniformes; Cyprinidae; Danio.

OX NCBI_TaxID=7955;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20373792; PubMed=10917738;

RA Inohara N., Nunez G.;

RT "Genes with homology to mammalian apoptosis regulators identified in

RT zebrafish."

RL Cell Death Differ. 7:509-510(2000).

DR EMBL: AF231017; AAF66962.2;

SQ SEQUENCE 146 AA; 16546 MW; 28A5650B5107ECB CRC64;

Query Match 60.8%; Score 87; DB 13; Length 146;

Best Local Similarity 65.2%; Pred. No. 4.2e-05;

Matches 15; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 3 LMAAQRGRELRLRMSDEFGSRK 25

DB 89 LMAAQRGRELRLRMSDEFGSRK 111

RESULT 2

ID: 010843 PRELIMINARY: PRT: 223 AA.

AC 010843: 01-NOV-1998 (TREMBlrel. 08, Created)

DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
 DE 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 GN HYPOTHEETICAL 24.1 KDA PROTEIN CY39.03C.
 GN RV2014 OR MTCY39.03C.
 OS Mycobacterium tuberculosis.
 CC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 CC Actinomycetales; Corynebacteriaceae; Mycobacterium.
 NCBI_TaxID=1773;
 OX
 RN
 RP
 SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RC MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skellon S., Squares S., Squares R.,
 RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;
 RT "Deciphering the Biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.";
 RL Nature 393:537-544(1998).
 CC -1 SIMILARITY: TO M.PARATUBERCULOSIS IS900.
 DR EMBL: 274025; CA98415.1; -;
 DR Tuberculist: RV2014; -;
 DR InterPro: IPR003346; Transposase-20.
 DR Pfam: PF02371; Transposase-20; 1;
 KW Hypothetical protein: Complete proteome.
 KW
 SQ SEQUENCE 223 AA; 24132 MW; 70456750017FEF37 CRC64;

Query Match 37.1%; Score 53; DB 16; Length 223;
 Best Local Similarity 58.8%; Pred. No. 6.8;
 Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
 OY 2 NLMAAQRXGRLRRMSD 18
 DB 165 NLMAADRYNRAIRAGHD 181
 ID 047148 PRELIMINARY; PRT; 505 AA.
 AC 047148;
 DT 01-JUN-1998 (TReMBLrel. 06, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE RIBOSOMAL MATURASE (FRAGMENT).
 GN
 GN Menziesia ciliacea]yx.
 OS
 CC Chloroplast.
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 CC Asteridae; Ericales; Ericaceae; Menziesia.
 NCBI_TaxID=49154;
 OX
 RN
 RP
 SEQUENCE FROM N.A.
 RA Kiron K.A.;
 RT Phylogenetics of Rhododendroideae (Ericaceae)";
 RT Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 RL EMBL: U61331; AAC15245.2; -;
 DR InterPro: IPR000442; Intron_maturase2.
 DR InterPro: IPR002866; MatK_N.
 DR Pfam: PF01348; Intron_maturase2; 1.
 DR Pfam: PF01824; MatK_N; 1.
 KW Chloroplast.
 KW
 SQ SEQUENCE 505 AA; 60233 MW; EEF5927AD2E57DE5 CRC64;

Query Match 36.7%; Score 52.5; DB 8; Length 505;
 Best Local Similarity 37.5%; Pred. No. 20;

Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;
 OY 1 KNLMAA-----ORYGRELRRMSDEFGSPK 25
 DB 390 KPVMAALSDSDIIEFGRIYRNLSHYSGSLK 421
 ID 063960 PRELIMINARY; PRT; 506 AA.
 AC 063960;
 DT 01-AUG-1998 (TReMBLrel. 07, Created)
 DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE RIBOSOMAL MATURASE.
 GN YCP14 OR MATK.
 OS Rhododendron tashiroi, and
 OS Rhododendron farinaceae.
 CC Chloroplast.
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 CC Asteridae; Ericales; Ericaceae; Rhododendron.
 NCBI_TaxID=75582, 75580;
 OX
 RN
 RP
 SEQUENCE FROM N.A.
 RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
 RA Yukawa T.;
 RL J. Jpn. Bot. 0:0-0(1998).
 DR EMBL: AB012749; BAA25870.1; -;
 DR EMBL: AB012745; BAA25866.1; -;
 DR InterPro: IPR000442; Intron_maturase2.
 DR InterPro: IPR002866; MatK_N.
 DR Pfam: PF01348; Intron_maturase2; 1.
 DR Pfam: PF01824; MatK_N; 1.
 KW Chloroplast.
 KW
 SQ SEQUENCE 506 AA; 60389 MW; DE0C07AE608B787 CRC64;

Query Match 36.7%; Score 52.5; DB 8; Length 506;
 Best Local Similarity 37.5%; Pred. No. 20;
 Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;
 OY 1 KNLMAA-----ORYGRELRRMSDEFGSPK 25
 DB 391 KPVMAALSDSDIIEFGRIYRNLSHYSGSLK 422
 ID 062972 PRELIMINARY; PRT; 506 AA.
 AC 062972;
 DT 01-AUG-1998 (TReMBLrel. 07, Created)
 DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE RIBOSOMAL MATURASE.
 GN
 GN Rhododendron ovatum.
 OS
 CC Chloroplast.
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 CC Asteridae; Ericales; Ericaceae; Rhododendron.
 NCBI_TaxID=49169;
 OX
 RN
 RP
 SEQUENCE FROM N.A.
 RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
 RA Yukawa T.;
 RT "Investigation of sectional Relationships in the Genus
 RT Rhododendron (Ericaceae) based on matK sequences.";
 RL J. Jpn. Bot. 0:0-0(1998).
 DR EMBL: AB012729; BAA25850.1; -;
 DR InterPro: IPR000442; Intron_maturase2.
 DR InterPro: IPR002866; MatK_N.
 DR Pfam: PF01348; Intron_maturase2; 1.

DR Pfam: PF01824; Matk_N: 1.
 KW Chloroplast.
 SQ SEQUENCE 506 AA; 60493 MW; D230E54B8C20FEF0 CRC64;

Query Match 36.7%; Score 52.5; DB 8; Length 506;
 Best Local Similarity 37.5%; Pred. No. 20;
 Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

QY 1 KNLMAA-----QRYGRELRRMSDFEGSFK 25
 DB 391 KPYMAALSDSDITERFGRIRYRNLSHYSGSLK 422

RESULT 6
 ID 062973 PRELIMINARY; PRT: 506 AA.
 AC 062973;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE RIBOSOMAL MATURASE.
 GN MATK.
 OS Rhododendron stamineum.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Ericales; Ericaceae; Rhododendron.
 OK NCBI_TaxID=75575;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
 RA Yukawa T.;
 RT Investigation of Sectional Relationships in the Genus
 RT Rhododendron(Ericaceae) based on matk Sequences.";
 RL J. Jpn. Bot. 0:0-(1998).
 DR EMBL: AB012730; BAA25851.1;
 DR InterPro: IPR000442; Intron_maturase2.
 DR InterPro: IPR002866; Matk_N.
 DR Pfam: PF01348; Intron_maturase2; 1.
 DR Pfam: PF01824; Matk_N; 1.
 KW Chloroplast.
 SQ SEQUENCE 506 AA; 60611 MW; 53FA36E7CD99483C CRC64;

Query Match 36.7%; Score 52.5; DB 8; Length 506;
 Best Local Similarity 37.5%; Pred. No. 20;
 Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

QY 1 KNLMAA-----QRYGRELRRMSDFEGSFK 25
 DB 391 KPYMAALSDSDITERFGRIRYRNLSHYSGSLK 422

RESULT 7
 ID 062974 PRELIMINARY; PRT: 506 AA.
 AC 062974;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE RIBOSOMAL MATURASE.
 GN MATK.
 OS Rhododendron albiflorum.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Ericales; Ericaceae; Rhododendron.
 OK NCBI_TaxID=49161;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
 RA Yukawa T.;

RT "Investigation of Sectional Relationships in the Genus
 RT Rhododendron(Ericaceae) based on matk Sequences.";
 RL J. Jpn. Bot. 0:0-(1998).
 DR EMBL: AB012731; BAA25852.1;
 DR InterPro: IPR000442; Intron_maturase2.
 DR InterPro: IPR002866; Matk_N.
 DR Pfam: PF01348; Intron_maturase2; 1.
 DR Pfam: PF01824; Matk_N; 1.
 KW Chloroplast.
 SQ SEQUENCE 506 AA; 60491 MW; 3CC930385B12DBC CRC64;

Query Match 36.7%; Score 52.5; DB 8; Length 506;
 Best Local Similarity 37.5%; Pred. No. 20;
 Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

QY 1 KNLMAA-----QRYGRELRRMSDFEGSFK 25
 DB 391 KPYMAALSDSDITERFGRIRYRNLSHYSGSLK 422

RESULT 8
 ID 062975 PRELIMINARY; PRT: 506 AA.
 AC 062975;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE RIBOSOMAL MATURASE.
 GN MATK.
 OS Rhododendron ponticum.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Ericales; Ericaceae; Rhododendron.
 OK NCBI_TaxID=49628;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
 RA Yukawa T.;
 RT Investigation of Sectional Relationships in the Genus
 RT Rhododendron(Ericaceae) based on matk Sequences.";
 RL J. Jpn. Bot. 0:0-(1998).
 DR EMBL: AB012732; BAA25853.1;
 DR InterPro: IPR000442; Intron_maturase2.
 DR InterPro: IPR002866; Matk_N.
 DR Pfam: PF01348; Intron_maturase2; 1.
 DR Pfam: PF01824; Matk_N; 1.
 KW Chloroplast.
 SQ SEQUENCE 506 AA; 60449 MW; 21DF700B071B5B8 CRC64;

Query Match 36.7%; Score 52.5; DB 8; Length 506;
 Best Local Similarity 37.5%; Pred. No. 20;
 Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

QY 1 KNLMAA-----QRYGRELRRMSDFEGSFK 25
 DB 391 KPYMAALSDSDITERFGRIRYRNLSHYSGSLK 422

RESULT 9
 ID 062977 PRELIMINARY; PRT: 506 AA.
 AC 062977;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE RIBOSOMAL MATURASE.
 GN MATK.
 OS Rhododendron luteum.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;


```

RESULT 13
ID 062982 PRELIMINARY; PRT: 506 AA.
AC 062982;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE RIBOSOMAL MATURASE.
OS Rhododendron niponicum.
OC Chloroplast.
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
CC Asterales; Ericales; Ericaceae; Rhododendron.
NCBI_TaxID=75577;
RN [1]
RP SEQUENCE FROM N.A.
RA Kutsahige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
RA Yukawa T.;
RT "Investigation of Sectional Relationships in the Genus
RT Rhododendron(Ericaceae) based on matk Sequences.";
RL J. Jpn. Bot. 0:0-0(1998).
DR EMBL; AB012739; BAA25860.1; -.
DR InterPro: IPR000442; Intron_maturase2.
DR InterPro: IPR002866; MatK_N.
DR Pfam: PF01348; Intron_maturas2; 1.
KM Pfam: PF01824; MatK_N; 1.
SQ CHLOROPLAST.
SEQUENCE 506 AA: 60419 MW; 1F95132CFAF6B40 CRC64;

Query Match 36.7%; Score 52.5; DB 8; Length 506;
Best Local Similarity 37.5%; Pred. No. 20;
Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

OY 1 KNLMAA-----QRYGRELRRMSDEFEGSFK 25
   | : ||| :||| | : | : |||
DB 391 KPVMALSDSDITERGRIRYNLSHYSSSLK 422

RESULT 14
ID 062983 PRELIMINARY; PRT: 506 AA.
AC 062983;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE RIBOSOMAL MATURASE.
OS Rhododendron primuliiflorum.
OC Chloroplast.
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
CC Asterales; Ericales; Ericaceae; Rhododendron.
NCBI_TaxID=75578;
RN [1]
RP SEQUENCE FROM N.A.
RA Kutsahige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
RA Yukawa T.;
RT "Investigation of Sectional Relationships in the Genus
RT Rhododendron(Ericaceae) based on matk Sequences.";
RL J. Jpn. Bot. 0:0-0(1998).
DR EMBL; AB012740; BAA25861.1; -.
DR InterPro: IPR000442; Intron_maturase2.
DR InterPro: IPR002866; MatK_N.
DR Pfam: PF01348; Intron_maturas2; 1.
KM Pfam: PF01824; MatK_N; 1.
SQ CHLOROPLAST.
SEQUENCE 506 AA: 60393 MW; DAAB47A759CFEC46 CRC64;

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Query Match 36.7%; Score 52.5; DB 8; Length 506;

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Best local Similarity 37.5%; Pred. No. 20;
Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

Oy 1 KNLMAA-----QRYGRELKRNDSDEFESSEK 25
   | : || | : : || | : : || |
Db 391 KPVMAALSDSDITERGRITRNLSHYSSGSK 422

RESULT 15
062984
ID 062984 PRELIMINARY; PRT: 506 AA.
AC 062984;
DT 01-AUG-1998 (TREMBLrel, 07, Created)
DT 01-AUG-1998 (TREMBLrel, 07, Last sequence update)
DT 01-DEC-2001 (TREMBLrel, 19, Last annotation update)
DE RHISOSOMAL MATURASE.
GN MATR.
OS Rhododendron ferrugineum (Alpenrose).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Assteridae; Ericales; Ericaceae; Rhododendron.
OX NCBI_TaxID=49622;
RN [1]
RP SEQUENCE FROM N.A.
RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
RA Yukawa T.;
RT "Investigation of Sectional Relationships in the Genus
RT Rhododendron (Ericaceae) based on matk Sequences.";
RL J. Jpn. Bot. 0:0-0(1998).
RL EMBL: AB012741; BAA25862.1; -.
DR InterPro: IPR000442; Intron_maturase2.
DR InterPro: IPR002866; Matk_N
DR pfam: PF01348; Intron_maturas2; 1.
DR pfam: PF01824; Matk_N; 1.
DR Chloroplast.
SW SEQUENCE 506 AA; 60534 MW; ADNA4B25E92A36E8 CRC64;

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Query Match      36.7%; Score 52.5; DB 8; Length 505;
Best Local Similarity 37.5%; Pred. NO. 20;
Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1
QY      1 KNLMA-----QRGRLELRNRSDFEESFK 25
          | : ||| : : ||| : : ||| : : |||
DB      391 KPVAALSSDILIRFGRITRNLSHYSSSLK 422

```

Search completed: September 20, 2002, 11:03:48
Job time: 1665 sec

PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for
 XX treating neurodegenerative disorders, stroke, or cancer -

PS Claim 18: Page 17: 74pp: English.

CC The invention relates to a peptide conjugate having the formula:
 CC (R-X)_n-peptide where n = 1-10; X = C=O, when the R-X group is attached
 CC to the N-terminus of the peptide, or a side chain of the peptide where
 CC the functional group of the side chain is NH₂ or OH; or X = O or NH,
 CC when the R-X group is attached to the C-terminus of the peptide, or a
 CC side chain of the peptide, where the side chain functional group is COOH
 CC or CONH₂; and R = 2-18C alkyl or alkoxy, 2-14C alkenyl containing one
 CC or two double bonds, cyclohexyl, cyclopentyl, cyclohexyl optionally
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain
 CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of
 CC the Bcl-2 domain of the cell death agonist Bad. The peptide conjugate is
 CC useful for modulating apoptosis in the cells of a subject, or for
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockade of
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2
 CC function. In particular, the peptide conjugate is useful for treating a
 CC subject afflicted with a cancer characterized by cancer cells that
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric, or
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
 CC conjugate is also useful for treating disorders characterized by
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.

CC Sequence 26 AA:

Query Match 100.0%; Score 138; DB 21; Length 26;

Best Local Similarity 100.0%; Pred. No. 1,4e-14;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLMAAQRGRELRRMSDEFEGSFKGL 26

DB 1 nlwaagrygrelrrmsdefegsfkyl 26

RESULT 2

AAB37002 standard; peptide: 26 AA.

AC AAB37002:

XX 28-FEB-2001 (first entry)

DE Bcl2 polypeptide BH3 domain peptide #2.

XX Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;

XX cardiac; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;

XX apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;

XX colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;

XX melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;

XX stroke; myocardial infarction.

XX Homo sapiens.

XX WO200059526-A1.

XX 12-OCT-2000.

XX 06-APR-2000: 2000MO-US09352.

XX 07-APR-1999: 99US-0128202.

XX (UJJE-) UNIV JEFFERSON THOMAS.

XX Huang Z, Wang J, Zhang Z, Shan S, Lu Z;

XX WPI: 2000-679325/66.

PT New peptide conjugates for modulating apoptosis or for inhibiting B
 XX cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for
 PT treating neurodegenerative disorders, stroke, or cancer -

PS Claim 18: Page 17: 74pp: English.

CC The invention relates to a peptide conjugate having the formula:
 CC (R-X)_n-peptide where n = 1-10; X = C=O, when the R-X group is attached
 CC to the N-terminus of the peptide, or a side chain of the peptide where
 CC the functional group of the side chain is NH₂ or OH; or X = O or NH,
 CC when the R-X group is attached to the C-terminus of the peptide, or a
 CC side chain of the peptide, where the side chain functional group is COOH
 CC or CONH₂; and R = 2-18C alkyl or alkoxy, 2-14C alkenyl containing one
 CC or two double bonds, cyclohexyl, cyclopentyl, cyclohexyl optionally
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain
 CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of
 CC the Bcl-2 domain of the cell death agonist Bad. The peptide conjugate is
 CC useful for modulating apoptosis in the cells of a subject, or for
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockade of
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2
 CC function. In particular, the peptide conjugate is useful for treating a
 CC subject afflicted with a cancer characterized by cancer cells that
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric,
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
 CC conjugate is also useful for treating disorders characterized by
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.

CC Sequence 26 AA:

Query Match 100.0%; Score 138; DB 21; Length 26;

Best Local Similarity 100.0%; Pred. No. 1,4e-14;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLMAAQRGRELRRMSDEFEGSFKGL 26

DB 1 nlwaagrygrelrrmsdefegsfkyl 26

RESULT 3

AAB37003 standard; peptide: 27 AA.

AC AAB37003:

XX 28-FEB-2001 (first entry)

DE Bcl2 polypeptide BH3 domain peptide #3.

XX Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;

XX cardiac; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;

XX apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;

XX colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;

XX melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;

XX stroke; myocardial infarction.

XX Homo sapiens.

XX WO200059526-A1.

XX 12-OCT-2000.

XX 06-APR-2000: 2000MO-US09352.

XX 07-APR-1999: 99US-0128202.

XX (UYJE-) UNIV JEFFERSON THOMAS.
 PA Huang Z, Wang J, Zhang Z, Shan S, Lu Z;
 PI WPI: 2000-679325/56.
 XX
 XX New peptide conjugates for modulating apoptosis or for inhibiting B
 PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for
 PT treating neurodegenerative disorders, stroke, or cancer
 XX
 XX Claim 18; Page 17; 74pp; English.
 PS
 CC The invention relates to a peptide conjugate having the formula:
 CC (R-X)n-peptide where n = 1-10; X = C=O, when the R-X group is attached
 CC to the N-terminus of the peptide, or a side chain of the peptide where
 CC the functional group of the side chain is NH₂ or OH; or X = O or NH,
 CC when the R-X group is attached to the C-terminus of the peptide, or a
 CC side chain of the peptide, where the side chain functional group is COOH
 CC or CONH₂; and R = 2-18C alkyl or alkoxy, 2-14C alkenyl optionally
 CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain
 CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of
 CC the B3 domain of the cell death agonist Bad. The peptide conjugate is
 CC useful for modulating apoptosis in the cells of a subject, or for
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2
 CC function in particular, the peptide conjugate is useful for treating a
 CC subject afflicted with a cancer characterized by cancer cells that
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric,
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
 CC conjugate is also useful for treating disorders characterized by
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
 CC
 XX Sequence 27 AA:
 SQ
 Query Match 100.0%; Score 138; DB 21; Length 27;
 Best Local Similarity 100.0%; Pred. No. 1,4e-14;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NMAAQRGRLRRMSDFEGSFKGL 26
 DB 1 nlwaagrygreilrmsdtegsfkgl 26
 RESULT 4
 AAB37056
 ID AAB37056 standard; peptide: 27 AA.
 AC AAB37056;
 DT 28-FEB-2001 (first entry)
 DE Bcl2 polypeptide B3 domain peptide #56.
 XX
 XX Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;
 KW cardiant; Bcl-2 superfamily; B3 domain; cell death agonist; Bad;
 KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;
 KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;
 KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
 KW stroke; myocardial infarction.
 XX
 XX Homo sapiens.
 OS
 PN WO200059526-A1.
 XX
 XX 12-OCT-2000.

XX 06-APR-2000; 2000MO-US09352.
 PF
 XX 07-APR-1999; 9905-0128202.
 PR
 XX (UYJE-) UNIV JEFFERSON THOMAS.
 XX
 XX Huang Z, Wang J, Zhang Z, Shan S, Lu Z;
 PI WPI: 2000-679325/56.
 XX
 XX New peptide conjugates for modulating apoptosis or for inhibiting B
 PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for
 PT treating neurodegenerative disorders, stroke, or cancer
 XX
 XX Claim 18; Page 19; 74pp; English.
 PS
 CC The invention relates to a peptide conjugate having the formula:
 CC (R-X)n-peptide where n = 1-10; X = C=O, when the R-X group is attached
 CC to the N-terminus of the peptide, or a side chain of the peptide where
 CC the functional group of the side chain is NH₂ or OH; or X = O or NH,
 CC when the R-X group is attached to the C-terminus of the peptide, or a
 CC side chain of the peptide, where the side chain functional group is COOH
 CC or CONH₂; and R = 2-18C alkyl or alkoxy, 2-14C alkenyl optionally
 CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain
 CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of
 CC the B3 domain of the cell death agonist Bad. The peptide conjugate is
 CC useful for modulating apoptosis in the cells of a subject, or for
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2
 CC function in particular, the peptide conjugate is useful for treating a
 CC subject afflicted with a cancer characterized by cancer cells that
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric,
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
 CC conjugate is also useful for treating disorders characterized by
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
 CC
 XX Sequence 27 AA:
 SQ
 Query Match 100.0%; Score 138; DB 21; Length 27;
 Best Local Similarity 100.0%; Pred. No. 1,4e-14;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NMAAQRGRLRRMSDFEGSFKGL 26
 DB 2 nlwaagrygreilrmsdtegsfkgl 27
 RESULT 5
 AAB37055
 ID AAB37055 standard; peptide: 28 AA.
 AC AAB37055;
 DT 28-FEB-2001 (first entry)
 DE Bcl2 polypeptide B3 domain peptide #55.
 XX
 XX Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;
 KW cardiant; Bcl-2 superfamily; B3 domain; cell death agonist; Bad;
 KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;
 KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;
 KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
 KW stroke; myocardial infarction.
 XX
 XX Homo sapiens.
 OS

XX WO200059526-A1.
 XX 12-OCT-2000.
 XX 06-APR-2000; 2000WO-US09352.
 XX 07-APR-1999; 99US-0128202.
 XX (UYJE-) UNIV JEFFERSON THOMAS.
 XX Huang Z, Wang J, Zhang Z, Shan S, Lu Z;
 XX WPI: 2000-679325/66.
 XX New peptide conjugates for modulating apoptosis or for inhibiting B
 XX cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for
 XX treating neurodegenerative disorders, stroke, or cancer
 XX
 XX Claim 18: Page 19; 74pp: English.
 XX
 CC The invention relates to a peptide conjugate having the formula:
 CC (R-X)_n-peptide where n = 1-10; X = C=O, when the R-X group is attached
 CC to the N-terminus of the peptide, or a side chain of the peptide where
 CC the functional group of the side chain is NH₂ or OH; or X = O or NH
 CC when the R-X group is attached to the C-terminus of the peptide, or a
 CC side chain of the peptide, where the side chain functional group is COOH
 CC or CONH₂; and R = 2-18C alkyl or alkoxy, 2-14C alkenyl containing one
 CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain
 CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent analogues
 CC of the peptide portion of the conjugate. The peptides represent analogues
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of
 CC the Bcl-2 domain of the cell death agonist Bad. The peptide conjugate is
 CC useful for modulating apoptosis in the cells of a subject, or for
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2
 CC function, in particular, the peptide conjugate is useful for treating a
 CC subject afflicted with a cancer characterized by cancer cells that
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric,
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
 CC conjugate is also useful for treating disorders characterized by
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
 CC
 SO Sequence 28 AA:
 Query Match 100.0%; Score 138; DB 21; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1,5e-10;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NLNMAORRGRELRMSDEFGSFKGL 26
 DB 2 nlwaagrygrrelrmsdefgsfkgl 27
 RESULT 6
 AAB70370
 ID AAB70370 standard; Protein: 162 AA.
 AC AAB70370;
 XX 02-MAY-2001 (first entry)
 XX Shorter murine BAD mutant amino acid sequence SEQ ID NO:3.
 DE Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;
 KW immunostimulant; neuroprotective; nootropic; antischlemic; vulnary;
 KW cystostatic; antiviral; antidiabetic; antiinflammatory; wound healing;
 KW immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;

KW immunodeficiency disease; neurodegenerative disease; viral infection;
 KW ischaemic cell death; reperfusion cell death; arthritis; interlility;
 KW lymphoproliferative condition; inflammation; autoimmune disease.
 OS Mus musculus.
 OS Synthetic.
 XX WO200110888-A1.
 XX 15-FEB-2001.
 XX 30-MAY-2000; 2000WO-US11864.
 XX 28-MAY-1999; 99US-0136783.
 XX (APOP-) APOPTOSIS TECHNOLOGY INC.
 XX Zhou X;
 XX WPI: 2001-138734/14.
 XX New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,
 XX useful for screening for candidate compounds which induce or inhibit
 XX apoptosis, comprises amino acid substitutions at Ser118, Ser155 or
 XX Ser113
 XX
 XX Claim 7; Page 148-149; 157pp: English.
 XX
 CC The present invention describes an isolated or synthetic polypeptide
 CC (I) comprising a less than full length amino acid sequence of a mutant
 CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its
 CC fragment, which contains amino acid substitutions at Ser118 or a murine
 CC BAD Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine
 CC BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective,
 CC antitumor, anticancer, vulnary, cystostatic, antiviral,
 CC antidiabetic, antiinflammatory and, immunosuppressive activities, and
 CC can be used as an apoptosis inducer or inhibitor. BAD polypeptides and
 CC polynucleotides can be used for screening candidate compounds and drugs
 CC for activity that promote cell survival or apoptosis. Other uses include
 CC inducing or inhibiting apoptosis in a cell. Candidate compounds
 CC identified and (mutant) BAD polypeptides are useful in treating
 CC immunodeficiency diseases, neurodegenerative diseases, ischemic cell
 CC death, reperfusion cell death, wound healing, cancer, viral infections,
 CC lymphoproliferative conditions, arthritis, interlility, inflammation and
 CC autoimmune diseases. The present sequence represents a specifically
 CC claimed shorter murine BAD mutant amino acid sequence from the present
 CC invention.
 CC
 SO Sequence 162 AA:
 Query Match 100.0%; Score 138; DB 22; Length 162;
 Best Local Similarity 100.0%; Pred. No. 1.1e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NLNMAORRGRELRMSDEFGSFKGL 26
 DB 98 nlwaagrygrrelrmsdefgsfkgl 123
 RESULT 7
 AAR95168
 ID AAR95168 standard; Protein: 204 AA.
 AC AAR95168;
 XX 06-JAN-1997 (first entry)
 XX bcl-x(l)/bcl-2 associated death promoter protein.
 DE Epitope; murine; bcl-x(l)/bcl-2 associated death promoter; Bad; stroke;
 KW polypeptide; bcl-x; cell death; regulate; BH1; BH2; apoptotic cell death;
 KW cytokine deprivation; IL-3 dependent cell line; immunodeficiency; AIDS.


```

XX  neurodegenerative disease; senescence; ischaemia; neoplasia.
XX  Mus musculus.
XX  Location/Qualifiers
FH  Key 147..149
FT Region /note="BH1 conserved amino acids"
FT Region 191..192
FT Domain /note="BH2 conserved amino acids"
FT Domain 38..61
FT Domain /note="PEST sequence"
FT Domain 111..130
FT Domain /note="PEST sequence"
XX  MW0613614-A1.
XX  09-MAY-1996.
XX  31-OCT-1995; 95MW-0514246.
XX  31-OCT-1994; 94US-0333655.
XX  (UNITW ) UNIV WASHINGTON.
XX  Korsmeyer SJ;
XX  WPI: 1996-251465/25.
XX  NP:PSDB; NAT29479.
XX  Polynucleotide encoding bcl-x(L)/bcl-2 associated death promoter
XX  useful to treat neoplasia and apoptosis and to identify agents
XX  inhibiting its binding to bcl-2 or bcl-x(L) to form heterodimers
XX  Claim 3; Fig 1; 130pp; English.
XX  This sequence represents the murine bcl-x(L)/bcl-2 associated death
XX  promoter (bad) gene. Bad is a 22.1 kD protein which interacts with
XX  bcl-2 and bcl-x proteins and regulates cell death. It has homology
XX  to the bcl-2-related family clustered in the BH1 and BH2 domain. Bad
XX  has been found to hybridise to bcl-x(L) and bcl-2 in yeast two-hybrid
XX  assays and in vivo in mammalian cells. Overexpressed Bad counteracts the
XX  death inhibitory activity of bcl-x(L), but is much less effective at
XX  counteracting the death inhibitory activity of bcl-2. Bad expression can
XX  accelerate apoptotic cell death induced by cytokine deprivation in an
XX  IL-3 dependent cell line expressing bcl-x(L) and its also counters the
XX  death repressor activity of bcl-x(L). Bad competes with Bax for binding
XX  to bcl-x(L). Bad may be used to identify agents which inhibit its binding
XX  to bcl-2 or bcl-x(L) to form heterodimers. Such agents may be
XX  used to treat neurodegenerative diseases, immunodeficiency diseases,
XX  e.g. AIDS, senescence or ischaemia.
XX  Sequence 204 AA.
XX
XX  Query Match 100.0%; Score 138; DB 17; Length 204;
XX  Best Local Similarity 100.0%; Pred. NO.1,4e-13;
XX  Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX  1 NEMAAQRYGELRNMSDEFESRGL 26
XX  140 nlwaagrygrelrmsdefesgyl 105
XX
XX  RESULT 8
XX  AA061315
XX  ID AAM61315 standard; Protein; 204 AA.
XX  AA061315;
XX  07-OCT-1998 (first entry)
XX  Murine BCL-XL/BCL-2 associated cell death regulator.
XX

```

KW	murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein
KM	murine substituted mutant; apoptosis; cancer; viral infection.
XX	
XX	Mus sp.
OS	
PN	W09817682-A1.
PN	
PD	30-APR-1998.
PD	
PF	17-OCT-1997; 97MO-US91975.
PR	18-OCT-1996; 96DS-0733505.
PA	(UNIM) UNIV WASHINGTON.
PI	Koismeyer SJ;
PI	
DR	WPI: 1998-261422/23.
DR	N-PSDB: AAV27833.
XX	
PT	New mutant BAD polypeptide with phosphorylatable serine replaced -
PT	useful for, e.g. treating reduced apoptosis such as in cancer or
PT	viral infection
PS	Claim 1; Fig 10; 95pp; English.
XX	
CC	The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
CC	death regulator) proteins, having an amino acid other than Ser at
CC	position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
CC	present sequence is the murine BAD protein. Also described are: (1)
CC	fragments of mutant BAD protein able to decrease cell viability; (2)
CC	fusion proteins of mutant BAD with a heterologous polypeptide that
CC	increases intracellular delivery. Mutant BAD proteins are used to treat
CC	or prevent diseases associated with reduced apoptosis, e.g. cancer,
CC	viral infection, lymphoproliferation, arthritis, infertility,
CC	inflammation and autoimmune disease. Polynucleotide sequences encoding
CC	mutant BAD proteins can be used similarly by gene therapy or to produce
CC	transgenic animals for use as disease models or in drug screening. BAD
CC	proteins phosphorylated at specified Ser are used to screen for enhancers
CC	and inhibitors of serine-phosphatase. Inhibitors are potentially useful
CC	in treatment of excessive apoptosis such as AIDS, neurodegeneration,
CC	aging or ischemic cell death. The apoptotic status of cells is
CC	determined by measuring relative amounts of phosphorylated and non-
CC	phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
CC	greater death-promoting activity than wild-type BAD which can become
CC	phosphorylated on the specified Ser, forming a product that does not
CC	heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family
CC	proteins in the cytosol, thus promoting cell survival. The mutants with
CC	Ser substituted cannot bind 14-3-3.
XX	
XX	Sequence 204 AA:
SO	
Query Match	100.0%; Score 138; DB 19; Length 204;
Best Local Similarity	100.0%; Pred. No. 1,4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
OY	1 NMAAORYGRELRRMSDEFGSPFGL 26
DB	140 nlmaagrygrelrrmsdelegsfvgl 165
RESULT 9	
AAW61316	AAW61316 standard; Protein: 204 AA.
XX	
XX	AAW61316:
XX	07-OCT-1998 (first entry)
XX	
DE	Mutant BCL-XL/BCL-2 associated cell death regulator #1.
XX	
KM	Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;

serine substituted mutant; apoptosis; cancer; viral infection.

Mus sp.
Synthetic.

MO9817682-A1.
30-APR-1998.

17-OCT-1997; 97MO-US19175.
18-OCT-1996; 96US-0733505.

(UNITV) UNITV WASHINGTON.

Korsmeyer SJ;
WPI: 1998-261422/23.
N-PSDB: AAV27834.

New mutant BAD polypeptide with phosphorylatable serine replaced -
useful for, e.g. treating reduced apoptosis such as in cancer or
viral infection

Claim 7; Page 59; 95pp; English.

The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
death regulator) proteins having an amino acid other than Ser at
position 112 and/or 116, relative to the murine BAD 204 aa sequence. The
present sequence represents a mutant BAD protein. Also described are: (1)
fragments of mutant BAD protein able to decrease cell viability; (2)
fusion proteins of mutant BAD with a heterologous polypeptide that
increases intracellular delivery. Mutant BAD proteins are used to treat
or prevent diseases associated with reduced apoptosis, e.g. cancer,
viral infection, lymphoproliferation, arthritis, infertility,
inflammation and autoimmune disease. polynucleotide sequences encoding
mutant BAD proteins can be used similarly by gene therapy or to produce
transgenic animals for use as disease models or in drug screening. BAD
proteins phosphorylated at specified Ser are used to screen for enhancers
and inhibitors of serine-phosphatase. Inhibitors are potentially useful
in treatment of excessive apoptosis such as AIDS, neurodegeneration,
aging or ischemic cell death. The apoptotic status of cells is
determined by measuring relative amounts of phosphorylated and non-
phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
greater death-promoting activity than wild-type BAD which can become
CC phosphorylated on the specified Ser, forming a product that does not
CC heterodimerise with BCL-2 or BCL-XL, but instead binds to 14-3-3 family
CC proteins in the cytosol, thus promoting cell survival. The mutants with
CC Ser substituted cannot bind 14-3-3.

Sequence 204 AA:

Query Match 100.0%; Score 138; DB 19; Length 204;
Best local similarity 100.0%; Pred. No. 1,4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NMAAQRGRLRMSPDEPGSKGL 26
Db 140 nlwaagrygrelrmadelegsfkgl 165
|||||

RESULT 10
ID AAW61317 standard; Protein; 204 AA.
XX AAW61317;
XX
XX
XX 07-OCT-1998 (first entry)
XX
XX Mutant BCL-XL/BCL-2 associated cell death regulator #2.
XX
XX Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;

serine substituted mutant; apoptosis; cancer; viral infection.

Mus sp.
Synthetic.

MO9817682-A1.
30-APR-1998.

17-OCT-1997; 97MO-US19175.
18-OCT-1996; 96US-0733505.

(UNITV) UNITV WASHINGTON.

Korsmeyer SJ;
WPI: 1998-261422/23.
N-PSDB: AAV27835.

New mutant BAD polypeptide with phosphorylatable serine replaced -
useful for, e.g. treating reduced apoptosis such as in cancer or
viral infection

Claim 7; Page 60; 95pp; English.

The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
death regulator) proteins, having an amino acid other than Ser at
position 112 and/or 116, relative to the murine BAD 204 aa sequence. The
present sequence represents a mutant BAD protein. Also described are: (1)
fragments of mutant BAD protein able to decrease cell viability; (2)
fusion proteins of mutant BAD with a heterologous polypeptide that
increases intracellular delivery. Mutant BAD proteins are used to treat
or prevent diseases associated with reduced apoptosis, e.g. cancer,
viral infection, lymphoproliferation, arthritis, infertility,
inflammation and autoimmune disease. polynucleotide sequences encoding
mutant BAD proteins can be used similarly by gene therapy or to produce
transgenic animals for use as disease models or in drug screening. BAD
proteins phosphorylated at specified Ser are used to screen for enhancers
and inhibitors of serine-phosphatase. Inhibitors are potentially useful
in treatment of excessive apoptosis such as AIDS, neurodegeneration,
aging or ischemic cell death. The apoptotic status of cells is
determined by measuring relative amounts of phosphorylated and non-
phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
greater death-promoting activity than wild-type BAD which can become
CC phosphorylated on the specified Ser, forming a product that does not
CC heterodimerise with BCL-2 or BCL-XL, but instead binds to 14-3-3 family
CC proteins in the cytosol, thus promoting cell survival. The mutants with
CC Ser substituted cannot bind 14-3-3.

Sequence 204 AA:

Query Match 100.0%; Score 138; DB 19; Length 204;
Best local similarity 100.0%; Pred. No. 1,4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NMAAQRGRLRMSPDEPGSKGL 26
Db 140 nlwaagrygrelrmadelegsfkgl 165
|||||

RESULT 11
ID AAW61318 standard; Protein; 204 AA.
XX AAW61318;
XX
XX
XX 07-OCT-1998 (first entry)
XX
XX Mutant BCL-XL/BCL-2 associated cell death regulator #3.
XX
XX Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein

OS Mus musculus.
 OS Synthetic.
 XX WO200110888-A1.
 XX 15-FEB-2001.
 PD 30-MAY-2000; 2000WO-US11864.
 PF 28-MAY-1999; 99US-0136783.
 XX (APOP-) APOPTOSIS TECHNOLOGY INC.
 PA Zhou X;
 PI WPI: 2001-138734/14.
 DR New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,
 XX useful for screening for candidate compounds which induce or inhibit
 PT apoptosis, comprises amino acid substitutions at Ser118, Ser155 or
 PT Ser113 -
 XX
 XX Claim 4: Page 148; 157pp: English.
 PS
 CC The present invention describes an isolated or synthetic polypeptide
 CC (I) comprising a less than full length amino acid sequence of a mutant
 CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its
 CC fragment, which contains amino acid substitutions at Ser118 of a human
 CC BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine
 CC BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective,
 CC neurotropic, antischismic, vulnerary, cytoskeletal, antiviral,
 CC anarthritic, antiinflammatory and immunosuppressive activities, and
 CC can be used as an apoptosis inducer or inhibitor. BAD polypeptides and
 CC polynucleotides can be used for screening candidate compounds and drugs
 CC for activity that promote cell survival or apoptosis. Other uses include
 CC inducing or inhibiting apoptosis in a cell. Candidate compounds
 CC identified and (mutant) BAD polypeptides are useful in treating
 CC immunodeficiency diseases, neurodegenerative diseases, ischemic cell
 CC death, reperfusion cell death, wound healing, cancer, viral infections,
 CC lymphoproliferative conditions, arthritis, infertility, inflammation and
 CC autoimmune diseases. The present sequence represents a specifically
 CC claimed longer murine BAD mutant amino acid sequence from the present
 CC invention.
 CC
 CC Sequence 204 AA;
 SO
 Query Match 100.0%; Score 138; DB 22; Length 204;
 Best Local Similarity 100.0%; Pred. No. 1.4e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NIMAARGRELRMSDEPGSFKGL 26
 DB 140 nlwaagrygrellrmadefegsfkgl 165
 ID AAU00220 standard; Protein; 567 AA.
 XX
 AC AAU00220;
 XX
 DT 31-MAY-2001 (first entry)
 XX
 DE Bad-DTRR apoptosis-modifying fusion protein.
 XX
 KM Mouse; Bad-DTRR: apoptosis; cancer; spinal muscular atrophy;
 KM diphtheria toxin receptor binding domain; DTR: neoplasm; tumour;
 KM hyperproliferation; Alzheimer's disease; neurodegenerative disorder;
 KM transient ischemic neuronal injury; stroke; spinal cord injury;
 KM Huntington's disease.
 XX
 OS Chimeric - Mus sp.

OS Chimeric - Corynebacterium diphtheriae.
 OS Synthetic.
 XX Key Location/Qualifiers
 XX Region 3..12 /note="10x histidine tag"
 XX WO200112661-A2.
 XX 22-FEB-2001.
 XX 15-AUG-2000; 2000WO-US22293.
 XX 16-AUG-1999; 99US-0149220.
 XX (HARD) HARVARD COLLEGE.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Youle RJ, Liu X, Collier RJ;
 PI WPI: 2001-218343/22.
 DR N-PSDB; NAS00248.
 XX
 PT Novel fusion protein for modifying apoptosis in target cell and
 PT inducing apoptosis after transient ischemic neuronal injury, has two
 PT domains which targets protein to a cell and modifies apoptotic response
 PT of cell -
 XX
 XX Claim 4: Page 59-61; 65pp: English.
 PS
 CC The sequence represents the amino acid sequence of Bad-DTRR apoptosis-
 CC modifying fusion protein comprising Bad gene sequence fused via a short
 CC linker to diphtheria toxin translocation domain (DTR). The
 CC functional apoptosis-modifying fusion protein is capable of binding a
 CC target cell and integrating into or being a cellular membrane of the
 CC target cell. The apoptosis-modifying fusion protein comprises at least
 CC two domains: the DTR domain which targets the fusion protein to the
 CC target cell and the Bcl-XL domain which modifies an apoptotic response
 CC (inhibiting or enhancing) apoptosis in a target cell, such as neuron,
 CC lymphocyte, cancer, neoplasm, macrophage, epithelial, smooth or
 CC hyper-proliferative cell or an adipocyte. It is also useful for inducing
 CC apoptosis in a subject after trans on ischemic neuronal injury, reducing
 CC especially spinal cord injury. The fusion protein may be used to treat
 CC various diseases and injury conditions through inhibition or enhancement
 CC of apoptotic cellular response, including neurodegenerative disorders
 CC such as Alzheimer's disease, Huntington's disease, spinal muscular
 CC atrophy, stroke episodes and unregulated cell growth as in tumours and
 CC various cancers. The apoptosis-modifying fusion proteins can be delivered
 CC effectively throughout the body and targeted to selective tissue and
 CC cells.
 CC
 CC Sequence 567 AA;
 SO
 Query Match 100.0%; Score 138; DB 22; Length 567;
 Best Local Similarity 100.0%; Pred. No. 4.3e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NIMAARGRELRMSDEPGSFKGL 26
 DB 161 nlwaagrygrellrmadefegsfkgl 186
 ID AAM32476 standard; Protein; 166 AA.
 XX
 AC AAM32476;
 XX
 DT 15-JAN-1998 (first entry)
 XX
 DE BBC6 protein for regulating cell death.
 XX
 OS

XX BRC6 gene; cell death; cell cycle; Bcl2; human.
 KM Homo sapiens.
 OS
 XX US5663316-A.
 PN
 XX 02-SEP-1997.
 PD
 XX 18-JUN-1996; 96US-0665617.
 PE
 XX 18-JUN-1996; 96US-0665617.
 PR
 XX (CLON-) CLONTECH LAB INC.
 PA
 XX Xudong Y;
 PI
 XX WPI: 1997-447980/41.
 DR N-PSDB; AAT91561.
 XX
 XX Isolated BRC6 gene - encodes a protein that regulates cell death
 PT through interaction with Bcl-2
 PS
 XX Claim 1: Column 11-12: 7pp; English.
 CC The present sequence represents a protein of 166 amino acids. The
 CC sequence is disclosed as being a protein called BRC6 which regulates
 CC cell death through interaction with Bcl-2. The DNA may be used for the
 CC production of the recombinant protein, which can be used in unspecified
 CC therapeutic or diagnostic procedures, as a molecular weight marker, and
 CC to raise antibodies that can be used in unspecified diagnostic or
 CC therapeutic applications and to reduce or eliminate the biological
 CC activity of the BRC6 protein in vivo.
 XX
 SQ Sequence 166 AA:

Query Match 82.6%; Score 114; DB 18; Length 166;
 Best Local Similarity 91.7%; Pred. NO. 6.1e-10;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 NMAAQRVGRRLRMSDEFGSFX 24
 Db 101 nlwaagrygrelrmsdefvdsfk 124

Search completed: September 20, 2002, 10:35:56
 Job time: 424 sec



Fri Sep 20 11:03:02 2002

us-09-544-664-1.ra1

Page 1

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 20, 2002, 10:30:33; Search time 75.64 Seconds

(without alignments)
6.336 Million cell updates/sec

Title: US-09-544-664-1

Reflected score: 138

Sequence: 1 MUMAQRGRLRMSDFGSPKGL 26

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents AA:*

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6: /cgn2_6/p/ptodata/2/1aa/PC/US.COMB.pdp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	138	100.0	204	1	US-08-333-565-2
2	138	100.0	204	2	US-08-661-479-2
3	138	100.0	204	2	US-08-733-505A-1
4	138	100.0	204	2	US-08-733-505A-12
5	138	100.0	204	2	US-08-733-505A-13
6	138	100.0	204	2	US-08-733-505A-14
7	135	97.8	204	2	US-08-717-123-3
8	114	82.6	166	1	US-08-665-617-2
9	114	82.6	166	3	US-08-717-123-2
10	114	82.6	166	3	US-08-985-335-1
11	114	82.6	166	3	US-08-985-335-7
12	114	82.6	166	4	US-09-410-372-1
13	114	82.6	166	4	US-09-410-372-7
14	113	81.9	23	1	US-08-333-565-10
15	113	81.9	23	2	US-08-661-479-10
16	102	73.9	59	2	US-08-733-505A-55
17	102	73.9	59	2	US-08-733-505A-56
18	102	73.9	59	2	US-08-733-505A-57
19	102	73.9	59	2	US-08-733-505A-58
20	86	62.3	16	1	US-08-333-565-26
21	86	62.3	16	2	US-08-661-479-26
22	61	44.2	11	2	US-08-733-505A-34
23	61	44.2	11	2	US-08-706-741B-69
24	51	37.0	11	2	US-08-924-655A-69
25	46	33.3	66	3	US-08-667-087B-40
26	46	33.3	946	3	US-09-074-579-3
27	46	33.3	946	4	US-09-388-774-3

28	44	31.9	263	4	US-09-651-656-27	Sequence 27, Appl
29	43	31.2	81	3	US-08-497-312-19	Sequence 19, Appl
30	43	31.2	213	3	US-08-718-738-18	Sequence 18, Appl
31	43	31.2	213	4	US-09-221-844-18	Sequence 18, Appl
32	43	31.2	380	1	US-08-153-848-40	Sequence 40, Appl
33	43	31.2	380	3	US-09-299-843A-40	Sequence 40, Appl
34	43	31.2	380	4	US-09-299-843A-40	Sequence 40, Appl
35	43	31.2	380	5	US-08-317B-40	Sequence 40, Appl
36	42	30.4	322	4	US-09-359-161-7	Sequence 7, Appl
37	42	30.4	322	4	US-08-997-080-170	Sequence 170, Appl
38	42	30.4	348	2	US-08-997-363-170	Sequence 170, Appl
39	42	30.4	348	2	US-09-095-855-170	Sequence 170, Appl
40	42	30.4	348	4	US-09-324-542-170	Sequence 170, Appl
41	42	30.4	393	2	US-08-947-080-94	Sequence 94, Appl
42	42	30.4	393	3	US-08-947-363-94	Sequence 94, Appl
43	42	30.4	393	3	US-08-873-970-94	Sequence 94, Appl
44	42	30.4	393	4	US-09-095-855-94	Sequence 94, Appl
45	42	30.4	393	4	US-09-324-542-94	Sequence 94, Appl

ALIGNMENTS

RESULT: 1
US-08-333-565-2
Sequence 2, Application US/08333565
Patent No. 5622852
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
NUMBER OF INVENTION: 59
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,565
FILING DATE: 31-Oct-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2422
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURES:
NAME/KEY: Protein
LOCATION: 1..204
OTHER INFORMATION: /note= "Deduced amino acid sequence of mouse BMD."
US-08-333-565-2
Query Match 100.0%, Score 138, DB 1, Length 204:
Best Local Similarity 100.0%, Pred. No. 4e-14, Indels 0, Gaps 0:
Matches 26, Conservative 0, Mismatches 0

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QY      1  NMAAORYGRELRRMSDEFGSPKGL 26
DB      140 NMAAORYGRELRRMSDEFGSPKGL 165

RESULT  2
US-08-661-479-2
; Sequence 2, Application US/08661479
; Patent No. 5834209
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourile and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/661,479
; FILING DATE: 11-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/333,565
; FILING DATE: 31-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000700
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: protein
; LOCATION: 1..204
; OTHER INFORMATION: /note= "Deduced amino acid sequence
; OTHER INFORMATION: of mouse BAD."
US-08-661-479-2

Query Match      100.0%; Score 138; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 4e-14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  NMAAORYGRELRRMSDEFGSPKGL 26
DB      140 NMAAORYGRELRRMSDEFGSPKGL 165

RESULT  3
US-08-733-505A-1
; Sequence 1, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourile and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733,505A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965458
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-733-505A-1

Query Match      100.0%; Score 138; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 4e-14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  NMAAORYGRELRRMSDEFGSPKGL 26
DB      140 NMAAORYGRELRRMSDEFGSPKGL 165

RESULT  4
US-08-733-505A-12
; Sequence 12, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733,505A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965458
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-733-505A-1
```


TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-733-505A-12

Query Match 100.0%; Score 138; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 4e-14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 NLMAORYGRELIRMSDEFGSFKGL 26
DB 140 NLMAORYGRELIRMSDEFGSFKGL 165

RESULT 5
US-08-733-505A-13
Sequence 13, Application US/08733505A
Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
NUMBER OF SEQUENCES: 60
BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-733-505A-13

Query Match 100.0%; Score 138; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 4e-14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 NLMAORYGRELIRMSDEFGSFKGL 26
DB 140 NLMAORYGRELIRMSDEFGSFKGL 165
RESULT 6

US-08-733-505A-14
Sequence 14, Application US/08733505A
Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
NUMBER OF SEQUENCES: 60
BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-733-505A-14

Query Match 100.0%; Score 138; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 4e-14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLMAORYGRELIRMSDEFGSFKGL 26
DB 140 NLMAORYGRELIRMSDEFGSFKGL 165

RESULT 7
US-08-717-123-3
Sequence 3, Application US/08717123
Patent No. 5965703
GENERAL INFORMATION:
APPLICANT: Horne, William A.
TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
Acids and Methods of Use
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/717.123
 FILING DATE: 20-SEP-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-ID 1929
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 204 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-717-123-3

Query Match 97.8%; Score 135; DB 2; Length 204;
 Best Local Similarity 96.2%; Pred. No. 1.2e-13;
 Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLMAAORYGRLRMSDEFGSKL 26
 DB 140 NLMAAORYGRLRMTDDEFGSKL 165

RESULT 8
 US-08-665-617-2
 Sequence 2, Application US/08665617
 Patent No. 5663316
 GENERAL INFORMATION:
 APPLICANT: Xudong, Yin
 TITLE OF INVENTION: Gene and Protein for Regulation of Cell Death
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Salliwanchik & Salliwanchik
 STREET: 2421 N.W. 41st Street, Suite A-1
 CITY: Gainesville
 STATE: Florida
 COUNTRY: USA
 ZIP: 32606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/665,617
 FILING DATE:
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Salliwanchik, David R.
 REGISTRATION NUMBER: 31,794
 REFERENCE/DOCKET NUMBER: CL-8
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (352) 375-8100
 TELEFAX: (352) 372-5800
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 166 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-665-617-2

Query Match 82.6%; Score 114; DB 1; Length 166;
 Best Local Similarity 91.7%; Pred. No. 1.8e-10;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 NLMAAORYGRLRMSDEFGSK 24

DB 101 NLMAAORYGRLRMSDEFGSK 124

RESULT 9
 US-08-717-123-2
 Sequence 2, Application US/08717123
 Patent No. 5965703
 GENERAL INFORMATION:
 APPLICANT: Horne, William A.
 TITLE OF INVENTION: Human BAD polypeptides, Encoding Nucleic
 TITLE OF INVENTION: Acids and Methods of Use
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Campbell and Flores
 STREET: 4370 La Jolla Village Drive, Suite 700
 CITY: San Diego
 STATE: California
 COUNTRY: United States
 ZIP: 92122
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/717,123
 FILING DATE: 20-SEP-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-ID 1929
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 168 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-717-123-2

Query Match 82.6%; Score 114; DB 2; Length 168;
 Best Local Similarity 91.7%; Pred. No. 1.8e-10;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 NLMAAORYGRLRMSDEFGSK 24
 DB 103 NLMAAORYGRLRMSDEFGSK 126

RESULT 10
 US-08-985-335-1
 Sequence 1, Application US/08985335
 Patent No. 6080847
 GENERAL INFORMATION:
 APPLICANT: Hillman, Jennifer L.
 APPLICANT: Yue, Henry
 APPLICANT: Lal, Preethi
 APPLICANT: Shah, Purvi
 TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
 PROLIFERATION
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Dr.
 CITY: Palo Alto
 STATE: CA

COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,335
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-845-4166
TELEFAX: 650-845-0555
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SYNORAB01
CLONE: 358673
US-08-985-335-1

Query Match 82.6%; Score 114; DB 3; Length 168;
Best Local Similarity 91.7%; Pred. No. 1.8e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 NMAAORYGRELRMSDEFGSFK 24
DB 103 NMAAORYGRELRMSDEFGSFK 126

RESULT 11
US-08-985-335-7
Sequence 7, Application US/08985335
Patent No. 6080847
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
PROLIFERATION
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,335
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-845-4166
TELEFAX: 650-845-0555
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1683637
US-08-985-335-7

Query Match 82.6%; Score 114; DB 3; Length 168;
Best Local Similarity 91.7%; Pred. No. 1.8e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 NMAAORYGRELRMSDEFGSFK 24
DB 103 NMAAORYGRELRMSDEFGSFK 126

RESULT 12
US-09-410-372-1
Sequence 1, Application US/09410372
Patent No. 6281334
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
PROLIFERATION
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/410,372
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985,335
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-845-4166
TELEFAX: 650-845-0555
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SYNORAB01

CLONE: 358673
US-09-410-372-1

Query Match 82.6%; Score 114; DB 4; Length 168;
Best Local Similarity 91.7%; Pred. No. 1.8e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NLMAORYGRELRLMSDEFGSFK 24
|||||
DB 103 NLMAORYGRELRLMSDEFGSFK 126

RESULT 13
US-09-410-372-7
Sequence 7, Application US/09410372
Patent No. 6281334

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Yue, Henry

APPLICANT: Lal, Preeti

APPLICANT: Shah, Purvi

APPLICANT: Corley, Neil C.

TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL

NUMBER OF INVENTION: 9

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Dr.

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTED for windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/410.372

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/985.335

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0421 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555

TELEFAX: 650-845-4166

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 168 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GenBank

CLONE: 1683637

US-09-410-372-7

Query Match 82.6%; Score 114; DB 4; Length 168;
Best Local Similarity 91.7%; Pred. No. 1.8e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NLMAORYGRELRLMSDEFGSFK 24
|||||
DB 103 NLMAORYGRELRLMSDEFGSFK 126

US-08-333-565-10

Sequence 10, Application US/08333565

Patent No. 5622852

GENERAL INFORMATION:

APPLICANT: KORSMEYER, Stanley J.

TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH

NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Kourile and Crew

STREET: 379 Lytton Avenue

CITY: Palo Alto

STATE: California

COUNTRY: US

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/333.565

FILING DATE: 31-OCT-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M.

REGISTRATION NUMBER: 30,723

REFERENCE/DOCKET NUMBER: 15726A-000700

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400

TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 23 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-333-565-10

Query Match 81.9%; Score 113; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLMAORYGRELRLMSDEFG 21
|||||
DB 3 NLMAORYGRELRLMSDEFG 23

RESULT 15

US-08-661-479-10

Sequence 10, Application US/08661479

Patent No. 5834209

GENERAL INFORMATION:

APPLICANT: KORSMEYER, Stanley J.

TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH

NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Kourile and Crew

STREET: 379 Lytton Avenue

CITY: Palo Alto

STATE: California

COUNTRY: US

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/661.479

FILED DATE: 11-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/333,565
FILING DATE: 31-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-661-479-10

Query Match 81.9%; Score 113; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLMAQRYGRELRRMSDEPEG 21
|||||
Db 3 NLMAQRYGRELRRMSDEPEG 23

Search completed: September 20, 2002, 10:37:18
Job time: 406 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 20, 2002, 10:31:08 ; Search time 95.59 Seconds
(without alignments)
26.136 Million cell updates/seq.

Title: US-09-544-664-1
138
Sequence: 1 NLMAGRYGRELRLMSDEFGSFKGL 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	138	100.0	204	2	bad protein - mouse
2	54	39.1	946	2	inter-alpha-trypsi
3	53	38.4	223	2	hypothetical prote
4	53	38.4	946	2	inter-alpha-inhibi
5	52	37.7	370	2	2-dehydro-3-deoxyp
6	51	37.0	232	2	floral homeotic pr
7	50	36.2	374	2	spermidine/putresc
8	50	36.2	516	2	probable threonine
9	49	35.5	453	2	conserved hypothet
10	48.5	35.1	134	2	Ig kappa chain - h
11	48.5	35.1	206	2	annexin p35 - maiz
12	48	34.8	214	2	transforming prote
13	48	34.8	206	2	oxido-reductase, so
14	48	34.8	220	2	threonine synthase
15	48	34.8	526	2	oxaloacetate decar
16	47	34.1	597	2	oxoglutarate dehyd
17	47	34.1	967	2	hypothetical prote
18	46.5	33.7	5138	2	hypothetical prote
19	46.5	33.7	314	2	anthropin p33 - maiz
20	46.5	33.7	435	2	anthropin p33 - maiz
21	46.5	33.7	1140	2	hypothetical prote
22	46	33.3	399	2	probable polyamine
23	46	33.3	946	1	inter-alpha-trypsi
24	46	33.3	1164	2	hypothetical prote
25	45.5	33.0	1378	2	DNA-directed RNA p
26	45.5	33.0	261	2	conserved hypothet
27	45.5	33.0	287	2	neuropeptide Pol-R
28	45.5	33.0	334	2	anthropin p33 - maiz
29	45.5	33.0	562	2	hypothetical prote
			905	2	NADH dehydrogenase

30	45	32.6	165	2	S59899	chlorocruorin chain
31	45	32.6	295	2	F83201	conserved hypothet
32	45	32.6	346	2	H95406	conserved hypothet
33	45	32.6	591	2	B44465	sodium ion pump ox
34	45	32.6	591	2	AB0509	oxaloacetate decar
35	45	32.6	591	2	AE0909	oxaloacetate decar
36	45	32.6	596	2	A28088	oxaloacetate decar
37	45	32.6	715	2	S52675	probable membrane
38	45	32.6	864	1	VCLRG4	env polyprotein -
39	45	32.6	1263	2	T19472	hypothetical prote
40	45	32.6	1557	2	T28811	hypothetical prote
41	45	32.6	2325	2	T13566	hypothetical prote
42	44.5	32.2	75	2	T01993	hypothetical prote
43	44.5	32.2	455	2	D83264	hypothetical prote
44	44.5	32.2	536	2	AG1482	hypothetical prote
45	44.5	32.2	910	2	G91024	NADH dehydrogenase

ALIGNMENTS

RESULT 1
A55671
Bad protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 05-Nov-1999
C:Accession: A55671
R:Yang, E.; Zha, J.; Jockel, J.; Boise, L.H.; Thompson, C.B.; Korsmeyer, S.J.
Cell 80, 285-291, 1995
A>Title: Bad, a heterodimeric partner for Bcl-xL and Bcl-2, displaces Bax and promot
A:Reference number: A55671; MUID:95136361
A:Accession: A55671
A:Molecule type: mRNA
A:Residues: 1-204 <YAN>
A:Cross-references: GB:L37296; NID:g639778; PIDN:AAA64465.1; PID:g639779
C:Keywords: heterodimer

Query Match 100.0%; Score 138; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 7.1e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NLMAGRYGRELRLMSDEFGSFKGL 26
DB 140 NLMAGRYGRELRLMSDEFGSFKGL 165
RESULT 2
JC5575
Inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster
C:Species: Mesocricetus auratus (golden hamster)
C:Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 20-Jun-2000
R:Nakatani, T.; Suzuki, Y.; Yamamoto, T.; Sinoheara, H.
J. Biochem. 122, 71-82, 1997
A>Title: Molecular cloning and sequencing of cDNAs encoding three heavy-chain precurs
sin inhibitor heavy chain family.
A:Reference number: JC5575; MUID:97420688
A:Accession: JC5575
A:Molecule type: mRNA
A:Residues: 1-946 <NAK>
A:Cross-references: DBJ:D89286; NID:g1694689; PIDN:BAAL3939.1; PID:g1694690
A:Experimental source: Liver
A:Accession: PC4485
A:Molecule type: protein
A:Residues: 55-64;140-146;151-156;424-447;500-528;577-605 <NA2>
C:Comment: in the plasma three inter-alpha-trypsin inhibitor heavy chains 1, 2 and 3
that the complexes play important role for pancreatic cancer.
C:Superfamily: Inter-alpha-trypsin inhibitor complex component II
F:261-264,717-916/Disulfide bonds: #status predicted

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
C:Accession: S38185; S46126; S46130; JN0322; B98651
R:Doignon, F.; Billeau, N.; Aigle, M.; Crouzet, M.
Yeast 9, 1131-1137, 1993
A:Title: The complete sequence of a 6794 bp segment located on the right arm of chrom
A:Reference number: S38185; MUID:34078675
A:Accession: S38185

A: Molecule type: DNA
A: Residues: 1-370 <DOI>
A: Cross-references: GB:J20296; NID:g311101; PIDN:AAA65607.1; PID:g311102
R: Ajljinovic, G.; Pohl, F.M.; Pohl, T.M.
submitted to the Protein Sequence Database, August 1994
A: Reference number: S45906
A: Accession: S46126
A: Molecule type: DNA
A: Residues: 1-370 <ALJ>
A: Cross-references: EMBL:Z26118; NID:g536664; PIDN:CAA85212.1; PID:g536665; MIPS:YBR2
R: Aigle, M.; Bachellet, M.C.; Barthe, C.; Biteau, N.; Crouzet, M.; Dolignon, F.
submitted to the Protein Sequence Database, August 1994
A: Reference number: S45940
A: Accession: S46130
A: Molecule type: DNA
A: Residues: 1-370 <AIG>
A: Cross-references: EMBL:Z26118; NID:g536664; PIDN:CAA85212.1; PID:g536665; MIPS:YBR2
R: Kuenstler, M.; Paravicini, G.; Egli, C.M.; Irniger, S.; Brous, G.H.
Gene 113, 67-74, 1992
A: Title: Cloning, primary structure and regulation of the ANO4 gene, encoding the tyr
A: Reference number: J03222; M01D:9.2225349
A: Accession: J03222

A:Accession: J204206.370 (A0065)
A:Cross-references: EMBL:X61107
R:Kuenzler, M.; Balmeill, T.; Egli, C.M.; Paravicini, G.; Braus, G.H.
J. Bacteriol. 175, 5548-5558, 1993
A:title: Cloning, primary structure, and regulation of the *HIS7* gene encoding a bifun
A:Reference number: A48651, MUID:93374850
A:Accession: B48651
A:Status: preliminary

A:Residues: 552-570 (R025)
 A:Cross-references: GB:X61107
 C:Comment: This enzyme catalyzes the condensation of phosphoenolpyruvate and D-erythr
 C:Genetic:
 A:Gene: SGD:ARO4
 A:Cross-references: SGD:S0000453; MIPS:YBR249c
 A:Map position: 2R
 C:Function:
 A:Description: aldehyde-lyase; carbon-carbon lyase
 A:Pathway: aromatic amino acid biosynthesis; shikimate pathway
 A:Note: first step in shikimate pathway
 C:Superfamily: phospho-2-dehydro-3-deoxyheptonate aldolase
 C:Keywords: aldehyde-lyase; aromatic amino acid biosynthesis; carbon-carbon lyase; cy

```

QY      1 NIMAAQRYGRELRRMSDEFEQ 21
      : | | | | : : : | | : |
Ddb     80 DLEAAQGYALRLKKLSDELKG 100

```

Cell 68, 683-697, 1992
C:Accession: M2095; S52653; T47593
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Alternate names: homeotic protein APETALA3; MADS-box regulatory protein AP3
C:Date: 04-Mar-1993 #sequence revision 18-Nov-1994 #text_change 21-Jul-2000
C:Author: R.Jack, T.; Brockman, L.L.; Meyerowitz, E.M.

C:Species: Homo sapiens (man)
 C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C:Accession: S40376
 R:Klein, R.; Jøenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A:Title: Expressed human immunoglobulin chl genes and their hypermutation.
 A:Reference number: S40376; MUID:94080891
 A:Accession: S40376
 A:Status: preliminary; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1134 <RLE>
 A:Cross-references: EMBL:722486; NID:9441440; PIDN:CAA51154.1; PID:9441441
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:34-113/Domain: Immunoglobulin homology <IMM>

Query Match 35.1% Score 48.5; DB 2; Length 134;
 Best Local Similarity 38.2% Pred. No. 7.8;
 Matches 13; Conservative 1; Mismatches 9; Indels 11; Gaps 1;

OY 3 WAAQYGRLELRN-----SDEFGSFKG 25
 DB 58 WFRQPCRPRLRYVSKSCVSDRSGSGSG 91

RESULT 11
 T02975
 A:Species: Zea mays (maize)
 C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
 C:Accession: T02975
 R:Barley, N.H.; James, N.C.; Greenland, A.J.
 Plant Physiol. 112, 1391-1396, 1996
 A:Title: cDNA isolation and gene expression of maize annexins P33 and P35.
 A:Reference number: Z14796; MUID:97092863
 A:Accession: T02975
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-314 <PAT>
 A:Cross-references: EMBL:X98245; NID:91370602; PIDN:CAA66901.1; PID:91370603
 A:Experimental source: cultivar cross: root tip
 C:Superfamily: annexin I; annexin repeat homology
 F:14-85/Domain: annexin repeat homology <ANN>

Query Match 35.1% Score 48.5; DB 2; Length 314;
 Best Local Similarity 47.6% Pred. No. 19;
 Matches 10; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

OY 5 AQRGRLRRMSDEFGSFK 24
 DB 54 AEAQKELRLALQDEIHGKFE 74

RESULT 12
 C36365
 A:Species: Rhizomucor racemosus
 C:Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 19-Jan-2001
 C:Accession: C36365
 R:Casale, W.L.; McConnell, D.G.; Wang, S.Y.; Lee, Y.J.; Linz, J.E.
 Mol. Cell. Biol. 10, 6654-6663, 1990
 A:Title: Expression of a gene family in the dimorphic fungus Mucor racemosus which exhibit
 A:Reference number: A36365; MUID:91061774
 A:Accession: C36365
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-206 <CAS>
 A:Cross-references: GB:M55177
 C:Superfamily: ras transforming protein; translation elongation factor Tu homology
 C:Keywords: GTP binding; nucleotide binding; P-loop
 F:11-126/Domain: translation elongation factor Tu homology <ETU>

F:17-24/Region: nucleotide-binding motif A (P-loop)
 F:133-126/Region: GTP-binding NKXD motif
 F:153-155/Region: GTP-binding SAK/L motif
 F:23,24,42,123,124,126,153/Binding site: Mg-GTP (Lys, Ser, Thr, Asn, Lys, Asp, Ser) #

Query Match 34.8% Score 48; DB 2; Length 206;
 Best Local Similarity 62.5% Pred. No. 14;
 Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 10 RELRMSDEFGSFKG 25
 DB 169 RLRRNKKKEGERSKG 184

RESULT 13
 F72289
 A:Species: Thermotoga maritima
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
 C:Accession: F72289
 R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hic
 Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
 C.M.; Nature 399, 323-329, 1999
 A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
 A:Reference number: A72200; MUID:99287316
 A:Accession: F72289
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-220 <ARN>
 A:Cross-references: GB:AE001772; GB:AE00512; NID:94981693; PIDN:AAD36230.1; PID:9498
 C:Experimental source: strain MSB8
 C:Genetics:
 A:Gene: TM1154
 C:Superfamily: yeast SOL3 protein

Query Match 34.8% Score 48; DB 2; Length 220;
 Best Local Similarity 34.8% Pred. No. 15;
 Matches 8; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

OY 4 AAQRYGRLRRMSDEFGSFKGL 26
 DB 111 ACERYERETRSATDQFDLALIGM 133

RESULT 14
 T08545
 A:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 07-Dec-1999
 C:Accession: T08545; S71362; S74307
 R:Bevan, M.; Zimmermann, A.; Gruenewald, R.; Bancroft, I.; Meyers, H.N.;
 submitted to the Protein Sequence Database, May 1999
 A:Reference number: Z16442
 A:Accession: T08545
 A:Molecule type: DNA
 A:Residues: 1-526 <BEV>
 A:Cross-references: EMBL:AL050352; GSPDB:GN00062; ATSP:F27B13.80
 A:Experimental source: cultivar Columbia; BAC clone F27B13
 R:Curran, G.; Dumas, R.; Ravanel, S.; Douce, R.
 FEBS Lett. 390, 85-90, 1996
 A:Title: Characterization of an Arabidopsis thaliana cDNA encoding an S-adenosylmethi
 A:Reference number: S71362; MUID:96314555
 A:Accession: S71362
 A:Molecule type: mRNA
 A:Residues: 11, 3-526 <CUR>
 A:Cross-references: EMBL:L141666; NID:91448916; PIDN:AAB04607.1; PID:91448917
 A:Accession: S74307
 A:Molecule type: protein
 A:Residues: 40-54 <CUR>

C;Genetics:
A;Gene: ATSP:F27B13.80

A;Map position: 4
A;Genome: nuclear

A; Genome: nuclear

C;Keywords: carbon-oxygen lyase; chloroplast
F;1-39/Domain: transit peptide (chloroplast) #status predicted <TNP>

F;40-526/Product: threonine synthase #status experimental <MAT>

Query Match	34.8%;	Score 48;	DB 2;	Length 526;
Best local similarity	35.3%;	Pred NO	37.	

Best local similarity	55.50	66.66	57.77
Matches	12	Conservative	6
		Mismatches	8
		Indels	8
		Gaps	1

QY	1	NLWAAQRYGRELRRMSD	-----	EFECSFKGL	26

Db 172 NLFWAERFGKQFLGMNDLWVKHCGISHTGSFKDL 205

RESULT 15
207209

002306
Oxalacetate decarboxylase, alpha chain W0550 [similarly] - *Vibrio cholerae* (strain N1)

C: Species: *Vibrio cholerae*
G: Data: 18-Aug-2000 #sequence 30-Aug-2000 #text change 02-Feb-2001

C/Date: 16-Aug-2000
C/Accession: G82308

1. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
K. Heideberg, J.E.; Eisen, J.A.; Nelson, W.C.; Clayton, R.H.; Oshima, M.D.; Dougan, R.C.;
Chadson, D.; Ermolaeva, M.D.; Yamatevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, F.

A/Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae* Nature 406, 477-483, 2000

A;Reference number:
A;Accession: G82308

A:Status: preliminary
A:Molecule type: DNA

A;Residues: 1-597 <HEI>
A;Cross-references: GB:

A; Experimental source: serogroup O1; strain M15961; biotype El Tor
C; Genetics:

A:Gene: VC0550
A:Map position: 1

C;superfamily:

Query Match

Best Local Similarity	47.48;	Pred. No. 60;			
Matches	9; Conservative	4; Mismatches	6; Indels	0; Gaps	0;

0Y 8 YGREL RMSD EFGSFKGL 26

272 YREVRKKYAKFEGOLKV 290

100

Search completed: September 20, 2011

Search completed: 20/ 2002/ 10:25:30
Job time: 474 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 20, 2002, 10:37:23 : Search time 44.99 Seconds
(without alignments) 22.376 Million cell updates/sec

Title: US-09-544-664-1

Perfect score: 138
Sequence: 1 N1MAA0RYGRELRLRNSEDPEGSFKGL 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : swissprot_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	138	100.0	204	1	BAD_MOUSE
2	138	100.0	205	1	BAD_RAT
3	138	100.0	158	1	BAD_HUMAN
4	138	100.0	158	1	BAD_MOUSE
5	138	100.0	158	1	BAD_MOUSE
6	138	100.0	158	1	BAD_MOUSE
7	138	100.0	158	1	BAD_MOUSE
8	138	100.0	158	1	BAD_MOUSE
9	138	100.0	158	1	BAD_MOUSE
10	138	100.0	158	1	BAD_MOUSE
11	138	100.0	158	1	BAD_MOUSE
12	138	100.0	158	1	BAD_MOUSE
13	138	100.0	158	1	BAD_MOUSE
14	138	100.0	158	1	BAD_MOUSE
15	138	100.0	158	1	BAD_MOUSE
16	138	100.0	158	1	BAD_MOUSE
17	138	100.0	158	1	BAD_MOUSE
18	138	100.0	158	1	BAD_MOUSE
19	138	100.0	158	1	BAD_MOUSE
20	138	100.0	158	1	BAD_MOUSE
21	138	100.0	158	1	BAD_MOUSE
22	138	100.0	158	1	BAD_MOUSE
23	138	100.0	158	1	BAD_MOUSE
24	138	100.0	158	1	BAD_MOUSE
25	138	100.0	158	1	BAD_MOUSE
26	138	100.0	158	1	BAD_MOUSE
27	138	100.0	158	1	BAD_MOUSE
28	138	100.0	158	1	BAD_MOUSE
29	138	100.0	158	1	BAD_MOUSE
30	138	100.0	158	1	BAD_MOUSE
31	138	100.0	158	1	BAD_MOUSE
32	138	100.0	158	1	BAD_MOUSE
33	138	100.0	158	1	BAD_MOUSE

34	43.5	31.5	1014	1	UVR1_STRCO	Q9507 streptomyc
35	43	31.2	377	1	AP1_MOUSE	Q9w08 mus musculu
36	43	31.2	380	1	AP1_HUMAN	P35414 homo sapien
37	43	31.2	380	1	AP1_MACMU	O97666 macaca mula
38	43	31.2	578	1	ACER_ECOLI	P11071 escherichia
39	43	31.2	583	1	ACER_SALTY	P51067 salmonella
40	43	31.2	695	1	MDL1_YEAS	P33310 saccharomyc
41	43	31.2	905	1	W03_MOUSE	Q9gxx7 mus musculu
42	42	30.4	207	1	TRTE_PYPAB	Q9uz65 pyrococcus
43	42	30.4	280	1	RPR1_YEAS	P55257 versinia en
44	42	30.4	322	1	SRF1_YEAS	P12904 saccharomyc
45	42	30.4	463	1	P030_MPVAC	P41434 autographa

ALIGNMENTS

RESULT	ID	BAD_MOUSE	STANDARD:	PRT:	204 AA.
AC	061337:				
DT	01-NOV-1997 (Rel. 35, Created)				
DT	01-NOV-1997 (Rel. 35, Last sequence update)				
DT	01-MAR-2002 (Rel. 41, Last annotation update)				
DE	Bcl-2-antagonist of cell death (BAD) (Bcl-2 binding component				
DE	6) (Bcl-XL/Bcl-2 associated death promoter).				
GN	BAD OR BCL6.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
OX	NCBI_Taxid=10090:				
RN	[1]				
RP	SEQUENCE FROM N. A.				
RP	TISSUE=Brain, and Thymus;				
RP	MDL=95136361; PubMed=7834748;				
RA	Yang E., Zhu J., Jockel J., Boise L.H., Thompson C.B., Korsmeyer S.J.;				
RT	"Bad, a heterodimeric partner for Bcl-XL and Bcl-2, displaces Bax and				
RT	promotes cell death."				
RL	Cell 80:285-291(1995).				
RL	[2]				
RP	PHOSPHORYLATION, AND MUTAGENESIS OF SER-112 AND SER-136.				
RP	MDL=9802283; PubMed=9381178;				
RA	Del Peso L., Gonzalez-Garcia M., Page C., Herrera R., Nunez G.;				
RT	"Interleukin-3-induced phosphorylation of BAD through the protein				
RT	kinase Akt."				
RL	Science 278:687-689(1997).				
RL	[3]				
RP	MUTAGENESIS OF SERINE RESIDUES.				
RP	MDL=20403502; PubMed=10945026;				
RA	Delella S.R., Katslov A., Hu L., Petros A., Pesik S.W., Yaffe M.B.;				
RA	Greenberg M.E.;				
RT	"14-3-3 proteins and survival kinases cooperate to inactivate BAD by				
RT	BH3 domain phosphorylation."				
RL	Cell 6:41-51(2000).				
CC	1-1 FUNCTION: Promotes cell death. Successfully competes for the				
CC	binding to Bcl-X(L), Bcl-2 and Bcl-w, thereby affecting the level				
CC	of heterodimerization of these proteins with BAX. Can reverse the				
CC	death repressor activity of Bcl-X(L), but not that of Bcl-2.				
CC	Appears to act as a link between growth factor receptor signaling				
CC	and the apoptotic pathways.				
CC	1-1 SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-				
CC	X(L), Bcl-2 and Bcl-w. Also binds protein s100A10 (by similarity).				
CC	The Ser-112/Ser-136 phosphorylated form binds 14-3-3 proteins.				
CC	1-1 SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon				
CC	phosphorylation, located to the cytoplasm.				
CC	1-1 DOMAIN: Inactive BH3 domain is required by BIK, BID, BAK, BAD AND				
CC	BAX for their pro-apoptotic activity and for their interaction				
CC	with anti-apoptotic members of the Bcl-2 family.				
CC	1-1 PTM: Phosphorylated on Ser-112 in response to survival stimuli.				
CC	Subsequent phosphorylation on Ser-136 promotes heterodimerization				
CC	with 14-3-3 proteins. This interaction then facilitates the				
CC	phosphorylation at Ser-135, a site within the BH3 domain, leading				
CC	to the release of Bcl-X(L) and the promotion of cell survival.				

Ser-136 is the major site of AKT/PKB phosphorylation. Ser-155 the major site of protein kinase A (CAPK) phosphorylation.

-1- SIMILARITY: CONTAINS A BCL-3 HOMOLOG DOMAIN 3 (BH3).

-1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

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EMBL: L37296; AAA64465.1; -

MGD: MGI:1096330; Bad.

InterPro: IPR000712; Bcl-2.

PROSITE: PS01259; BH3; FALSE_NEG.

Apoptosis: Phosphorylation.

DOMAIN 147 161

MOD_RES 112 112 PHOSPHORYLATION (BY CAPK AND PKB).

MOD_RES 136 136 PHOSPHORYLATION (BY CAPK AND PKB).

MOD_RES 135 135 PHOSPHORYLATION (BY CAPK AND PKB).

MUTAGEN 112 112 S->A: NO PHOSPHORYLATION.

MUTAGEN 136 136 S->A: NO PHOSPHORYLATION.

MUTAGEN 135 135 BCL-X(L).

SEQUENCE 204 AA; 22080 MW; 6C2BA910205053F7 CRC64;

Query Match 100.0%; Score 138; DB 1; Length 204;
Best Local Similarity 100.0%; Pred. No. 8, 6e-14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 NLMAAQRGRLRMSDEFGSKCL 26
140 NLMAAQRGRLRMSDEFGSKCL 165

RESULT 2
BAD_RAT
ID BAD_RAT STANDARD; PRT: 205 AA.
AC 035147; 070256; 09JHX1;
DT 16-OCT-2001 (Rel. 40; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 01-MAR-2002 (Rel. 41; Last annotation update)
DE Bcl-2 antagonist of cell death (BAD) (Bcl-2 binding component 6) (Bcl-xL/Bcl-2 associated death promoter).
DE Bcl-2 antagonist of cell death (BAD) (Bcl-2 binding component 6) (Bcl-xL/Bcl-2 associated death promoter).
GN BAD.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF SER-113 AND SER-137.
RC TISSUE-Ovary;
RX MEDLINE=98034386; PubMed=9369453;
RA Haw S.Y., Karpis A., Zhu L., Hsueh A.J.W.;
RT "Interference of BAD (Bcl-xL/Bcl-2 associated death promoter)-induced apoptosis in mammalian cells by 14-3-3 isoforms and P11.";
RL Moll. Endocrinol. 11:1858-1867(1997).
RM [2]
RN SEQUENCE FROM N.A.
RC TISSUE-Brain;
RX MEDLINE=98194755; PubMed=9535132;
RA D'Agata V., Magro G., Travali S., Musco S., Cavallaro S.;
RT "Cloning and expression of the programmed cell death regulator BAD in the rat brain.";
RL Neurosci. Lett. 243:137-140(1998).
RM [3]
RN SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RC TISSUE-Brain;
RX MEDLINE=21109372; PubMed=11161472;
RA Hammer S., Arumae U., Yu L.-Y., Sun Y.-F., Saez M., Lindholm D.;

Functional characterization of two splice variants of rat BAD and their interaction with Bcl-w in sympathetic neurons.;
Mol. Cell. Neurosci. 17:97-106(2001).
CC -1- FUNCTION: Promotes cell death. Successfully competes for the binding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level of heterodimerization of these proteins with BAX. Can reverse the death repressor activity of Bcl-x(L), but not that of Bcl-2 (By similarity). Appears to act as a link between growth factor receptor signaling and the apoptotic pathways.
CC -1- SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-x(L), Bcl-2 and Bcl-w. Also binds protein S100A10. The Ser-113/Ser-137 phosphorylated form binds 14-3-3 proteins.
CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon phosphorylation, localizes to the cytoplasm (By similarity).
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; alpha (shown here) and beta; are produced by alternative splicing. They differ only in their C-terminal regions.
CC -1- TISSUE SPECIFICITY: Expressed in all tissues tested, including brain, liver, spleen and heart. In the brain, restricted to epithelial cells of the choroid plexus. Isoform alpha is the more abundant form.
CC -1- DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND BAX for their pro-apoptotic activity and for their interaction with anti-apoptotic members of the Bcl-2 family.
CC -1- PTM: Phosphorylated on Ser-113 in response to survival stimuli. Subsequent phosphorylation on Ser-137 promotes heterodimerization with 14-3-3 proteins. This interaction then facilitates the phosphorylation at Ser-156, a site within the BH3 domain, leading to the release of Bcl-x(L) and the promotion of cell survival.
CC Ser-137 is the major site of AKT/PKB phosphorylation. Ser-156 the major site of protein kinase A (CAPK) phosphorylation (By similarity).
CC -1- SIMILARITY: CONTAINS A BCL-3 HOMOLOG DOMAIN 3 (BH3).
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
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EMBL: AF003523; M55337.1; -
EMBL: AF013227; M55100.1; -
EMBL: AF279810; M551427.1; -
EMBL: AF279811; M551428.1; -
DR InterPro: IPR000712; Bcl-2;
DR PROSITE: PS01259; BH3; FALSE_NEG.
KM Apoptosis: Phosphorylation; Alternative splicing.
FT DOMAIN 146 102
FT MOD_RES 113 113 BH3
FT MOD_RES 137 137 PHOSPHORYLATION (BY CAPK AND PKB) (BY SIMILARITY).
FT MOD_RES 156 156 PHOSPHORYLATION (BY CAPK AND PKB) (BY SIMILARITY).
FT MOD_RES 166 205 PHOSPHORYLATION (BY CAPK AND PKB) (BY SIMILARITY).
FT VANSPLIC 166 205 LPRKSGRATQROSATWMTIISWMDNRKGGSTPSSQ
-> EELTVSEELPRAIYMGWDLMSFGSPFLPTPP
EVAMFLRYTALRLC (IN ISOFORM BETA).
FT MUTAGEN 113 113 S->A: NO EFFECT ON HETERODIMERIZATION
WITH 14-3-3 PROTEINS.
FT MUTAGEN 137 137 S->A: NO HETERODIMERIZATION WITH 14-3-3
PROTEINS. NO EFFECT ON HETERODIMERIZATION
WITH BCL2 NOR WITH PROTEIN P11.
FT CONFLICT 29 34 WITH BCL2 NOR WITH PROTEIN P11.
SDAGGR -> ERRGRK (IN REF. 1).
SQ SEQUENCE 205 AA; 22228 MW; 7AFAT1DAE9CFA81 CRC64;

Query Match 100.0%; Score 138; DB 1; Length 205;
Best Local Similarity 100.0%; Pred. No. 8, 7e-14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	NTMAAQRGRLRRMSDFEGSPFGL	26
Db	141	NTMAAQRGRLRRMSDFEGSPFGL	166
RESULT	3		
BAD_HUMAN			
ID	BAD_HUMAN	STANDARD;	PRT; 168 AA.
AC	Q92934;	014803;	
DT	01-NOV-1997	(Rel. 35, Created)	
DT	16-OCT-2001	(Rel. 40, last sequence update)	
DT	01-MAR-2002	(Rel. 41, last annotation update)	
DE	Bcl-2, antagonist of cell death (BAD) (Bcl-2 binding component 6) (Bcl-xL/Bcl-2 associated death promoter).		
GN	BAD OR BBC OR BCL2L8.		
OS	Homo sapiens (human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.		
OX	NCBI_Taxid=9606;		
NP	SEQUENCE FROM N.A.		
RA	Xin D.X., Li Z., Huang B., Chen S., Zhou H.;		
RT	"A human protein that interacts with Bcl-2 and have homology to mouse		
RT	BAD."		
RL	Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
RP	SEQUENCE FROM N.A., AND PHOSPHORYLATION BY RAF-1.		
RX	MEDLINE=97083574; PubMed=8929532;		
RA	Mang H.-g., Rapp U.R., Reed J.C.;		
RT	"Bcl-2 targets the protein kinase Raf-1 to mitochondria."		
RL	Cell 87:629-638(1996).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RA	Takayama S., Reed J.C.;		
RL	Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.		
RN	[4]		
RP	SEQUENCE FROM N.A., AND DIMERIZATION.		
RC	TISSUE=bone marrow;		
RX	MEDLINE=86049554; PubMed=9388232;		
RA	Ottolillo S., Diaz J.-L., Horne W., Chang J., Wang Y., Wilson G.,		
RT	Chang S., Weeks S., Fritz L.C., Oltersdorf T.;		
RL	"Dimerization properties of human BAD."		
RN	J. Biol. Chem. 272:30866-30872(1997).		
RN	[5]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Lung;		
RA	Strausberg R.;		
RL	Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.		
RN	[6]		
RP	STRUCTURE BY NMR OF 103-127.		
RA	MEDLINE=21073561; PubMed=11206074;		
RA	Petross A.M., Nettesheim D.G., Wang Y., Olejniczak E.T., Meadows R.P.,		
RA	Mack J., Swift K., Matsuyoshi E.D., Zhang H., Thompson C.B.,		
RA	Fesk S.W.;		
RT	"Rationale for Bcl-xL/Bad peptide complex formation from structure,		
RT	mutagenesis, and biophysical studies."		
RL	Protein Sci. 9:2528-2534(2000).		
CC	-1- FUNCTION: Promotes cell death. Successfully competes for the		
CC	binding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level		
CC	of heterodimerization of these proteins with BAX. Can reverse the		
CC	death repressor activity of Bcl-x(L), but not that of Bcl-2 (By		
CC	similarity). Appears to act as a link between growth factor		
CC	receptor signaling and the apoptotic pathways.		
CC	-1- SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl		
CC	x(L), Bcl-2 and Bcl-w. Also binds protein 140kDa10 (By similarity)		
CC	The Ser-75/Ser-99 phosphorylated form binds 14-3-3 proteins (By		
CC	similarity).		
CC	-1- SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon		
CC	phosphorylation, localizes to the cytoplasm.		
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.		
CC	-1- DOMAIN: Interact BH3 domain is required by BIK, BID, BAK, BAD AND		
CC	BAX for their pro-apoptotic activity and for their interaction		
CC	with anti-apoptotic members of the Bcl-2 family.		

```

CC -i- PMM Phosphorylation on Ser-75 in response to survival stimuli.
CC Subsequent phosphorylation on Ser-99 promotes heterodimerization
CC with 14-3-3 proteins. This interaction then facilitates the
CC phosphorylation at Ser-118, a site within the BH3 domain, leading
CC to the release of Bcl-x(L) and the promotion of cell survival.
CC Ser-99 is the major site of AKT/PKB phosphorylation, Ser-118 the
CC major site of protein kinase A (CAK) phosphorylation (by
CC similarity).
CC -i- SIMILARITY: CONTAINS 1 BCL-3 HOMOLOGUE DOMAIN 3 (BH3).
CC -i- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL: U66879; AAB36516.1; -.
CC DR EMBL: AF021792; AAB72092.1; -.
CC DR EMBL: AF031523; AAB8124.1; -.
CC DR EMBL: BC001901; AAH01901.1; -.
CC DR PDB: 1G5J; 07-FEB-01.
CC DR MIM: 603167; -.
CC DR InterPro: IPR000712; Bcl-2.
CC DR PROSITE: PS01259; BH3; FALSE NEG.
CC KW Apoptosis; Phosphorylation; 3D-structure.
CC FT DOMAIN 110 124
CC FT MOD_RES 75 75 BH3.
CC FT MOD_RES 99 99 PHOSPHORYLATION (BY CAK AND PKB) (BY
CC FT MOD_RES 99 99 SIMILARITY).
CC FT MOD_RES 118 118 PHOSPHORYLATION (BY CAK AND PKB) (BY
CC FT MOD_RES 118 118 SIMILARITY).
CC FT CONFLICT 64 91 AGAVEIRSRHSYSYAGTGDGSGMEEPS -> RMGCGPPES
CC FT POLYPGDCGGRROGGNO (IN REF. 1).
CC FT SEQUENCE 168 AA; 18392 MW; 659PDB27DDEE3241 CAC64;
CC -----
CC Query Match 82.6%; Score 114; DB 1; length 168;
CC Best Local Similarity 91.7%; Pred. No. 3e-10;
CC Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
CC -----
CC QY 1 NLMAAORYGRLRMSDPEEGSFK 24
CC Db 103 NLMAAORYGRLRMSDPEVDSFK 126
CC -----
CC RESULT 4
CC ID ITH2_MESAU STANDARD; PRT; 946 AA.
CC AC P97279;
CC DT 15-JUL-1998 (Rel. 36, Created)
CC DT 15-JUL-1998 (Rel. 36, Last sequence update)
CC DT 01-MAR-2002 (Rel. 41, Last annotation update)
CC DE Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITI heavy
CC DE chain H2) (HC2).
CC GN ITH2.
CC GN Mesocricetus auratus (Golden hamster).
CC OS Euxaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
CC OC Mesocricetus.
CC OC NCBI_Taxid=10036;
CC RX NCBI_Taxid=10036;
CC RN (1)
CC RP SEQUENCE FROM N.A.
CC RC TISSUE=Liver;
CC RX MEDLINE=97420688; PubMed=9276673;
CC RA Nakatani T., Suzuki Y., Yamamoto T., Sinochara H.;
CC RT "Molecular cloning and sequencing of cDNAs encoding three heavy-chain
CC RT precursors of the inter-alpha-trypsin inhibitor in Syrian hamster:
CC RT implications for the evolution of the inter-alpha-trypsin inhibitor
CC RT heavy chain family";

```

RL J. Blochem. 122:71-82(1997).
 RP SEQUENCE OF 55-64; 140-146; 151-156; 424-447; 500-528 AND 577-605,
 AND SUBUNITS.
 RC TISSUE-Plasma;
 RX MEDLINE-97018241; PubMed-8864857;
 RA Yamamoto T., Yamamoto K., Sinochata H.;
 RT "Inter-alpha-tryptin inhibitor and its related proteins in Syrian
 hamster urine and plasma."
 RL J. Blochem. 120:145-152(1996).
 -1- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A
 BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,
 INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE
 LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE
 ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
 SIMILARITY).
 CC -1- SUBUNIT: I-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM
 ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,
 BIKUNIN, INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2
 AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND
 BIKUNIN, AND PRE-ALPHA-LIKE INHIBITOR (P-ALPHA-I) OF H3 AND
 CC -1- P.TM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN
 4-SULFATE BRIDGE TO THEIR C-TERMINAL ASPARTATE (BY
 SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE ITIH FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 VMFA DOMAIN.

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 DR EMBL: D89286; BAA13939.1;
 DR InterPro: IPR002035; VMFA.
 DR Pfam: PF00092; vma; 1.
 DR SMART: SM00327; VMA; 1.
 DR PROSITE: PS00234; VMFA; 1.
 DR Serine protease inhibitor; Repeat; Signal; Multigene family;
 KW Glycoprotein.
 FT SIGNAL 1 18
 FT PROPEP 19 54
 FT CHAIN 55 702
 FT PROPEP 703 946
 FT DOMAIN 308 468
 FT CARBOHYD 118 118
 FT CARBOHYD 263 263
 FT CARBOHYD 445 445
 FT CARBOHYD 578 578
 FT BINDING 702 702
 FT CONFLICT 510 510
 FT CONFLICT 595 595
 FT SEQUENCE 946 AA; 106580 MW; CA8BF565458F7B2E CRC64;
 OY 1 NLMAAQRVGRRLRMSDEFGSPKGL 26
 DB 212 NWVIVELQGRFLHVPDTFEGHGOV 237
 Query Match 39.1%; Score 54; DB 1; Length 946;
 Best Local Similarity 34.6%; Pred. No. 2.6; Mismatches 12; Indels 0; Gaps 0;
 Matches 9; Conservative 5;
 RESULT 5
 ID ITIH2_MOUSE STANDARD; PRT; 946 AA.
 AC 061703;
 DT 15-JUL-1998 (rel. 36, Created)

DT 15-JUL-1998 (rel. 36, Last sequence update)
 DT 15-JUL-1999 (rel. 38, Last annotation update)
 DE Inter-alpha-tryptin inhibitor heavy chain H2 precursor (ITI heavy
 DE chain H2).
 GN ITIH2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6N; TISSUE-Liver;
 RX MEDLINE-95194326; PubMed-7534067;
 RA Chan P., Ristler J.-L., Ragueau G., Saller J.-P.;
 RT "The three heavy-chain precursors for the inter-alpha-inhibitor
 RT family in mouse: new members of the multicopper oxidase protein group
 RT with differential transcription in liver and brain."
 RL Blochem. J. 306:505-512(1995).
 -1- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A
 BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,
 INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE
 LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE
 ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
 SIMILARITY).
 CC -1- SUBUNIT: I-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM
 ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,
 BIKUNIN, INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2
 AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND
 BIKUNIN, AND PRE-ALPHA-LIKE INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN BOTH LIVER AND BRAIN.
 CC -1- P.TM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN
 4-SULFATE BRIDGE TO THEIR C-TERMINAL ASPARTATE (BY
 SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE ITIH FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 VMFA DOMAIN.

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 DR EMBL: X70392; CAA49842.1;
 DR MGI: 96619; ITIH2.
 DR InterPro: IPR002035; VMFA.
 DR Pfam: PF00092; vma; 1.
 DR SMART: SM00327; VMA; 1.
 DR PROSITE: PS00234; VMFA; 1.
 DR Serine protease inhibitor; Repeat; Signal; Multigene family;
 KW Glycoprotein.
 FT SIGNAL 1 18
 FT PROPEP 19 54
 FT CHAIN 55 702
 FT PROPEP 703 946
 FT DOMAIN 308 468
 FT CARBOHYD 118 118
 FT CARBOHYD 263 263
 FT CARBOHYD 445 445
 FT BINDING 702 702
 FT CONFLICT 510 510
 FT CONFLICT 595 595
 FT SEQUENCE 946 AA; 105927 MW; 40DB6716433BD9DC CRC64;
 OY 1 NLMAAQRVGRRLRMSDEFGSPKGL 26
 DB 212 NWVIVELQGRFLHVPDTFEGHGOV 237
 Query Match 38.4%; Score 53; DB 1; Length 946;
 Best Local Similarity 34.6%; Pred. No. 3.7; Mismatches 12; Indels 0; Gaps 0;
 Matches 9; Conservative 5;

RA Rooney T., Rizzo M., Walts A., Uterback T., Fujii C.Y., Shea T.P.,
 RA Cressy T.H., Haas B., Walts R., Wu D., Peterson J., Van Aken S.,
 RA Pal G., Miltscher J., Sellers P., Gill J.E., Feldblum T.V.,
 RA Preuss D., Lin X., Nieman W.C., Salzberg S.L., White O., Venter J.C.,
 RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asaiizu E.,
 RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
 RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakayama S., Nakazaki N., Shino S., Takeuchi C., Wada T.,
 RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
 RT "Sequence and analysis of chromosome 3 of the plant *Arabidopsis*
 RT *thaliana*.";
 RL Nature 408:820-822(2000).
 CC -1- FUNCTION: TRANSCRIPTION FACTOR INVOLVED IN THE GENETIC CONTROL OF
 CC FLOWER DEVELOPMENT.
 CC -1- SUBUNIT: FORMS AN HETERODIMER WITH PISTILLATA.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN PETALS AND STAMENS.
 CC -1- MISCELLANEOUS: MUTATIONS IN AP3 CAUSE TRANSFORMATION OF PETALS
 CC INTO SEPALs AND STAMIN INTO CARPels.
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
 CC FACTORS.
 CC -1- SIMILARITY: CONTAINS A PROBABLE DIMERIZATION DOMAIN FOUND IN
 CC SRF-TYPE TRANSCRIPTION FACTORS (K-BOX).
 CC -----
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 CC -----
 DR EMBL: M66357; AAA32740.1;
 DR EMBL: D21125; BAA04665.1;
 DR EMBL: AF115799; AAD51888.1;
 DR EMBL: AF115800; AAD51889.1;
 DR EMBL: AF115803; AAD51891.1;
 DR EMBL: AF115804; AAD51893.1;
 DR EMBL: AF115811; AAD51900.1;
 DR EMBL: AF115814; AAD51903.1;
 DR EMBL: AL132971; CAB81799.1;
 DR PIR: A42095; A42095.
 DR HSSP: P11746; IMNM.
 DR TRASNAPC: TP01776;
 DR InterPro: IPR002487; K-box.
 DR InterPro: IPR002100; MADS-box.
 DR Pfam: PF01486; K-box; 1.
 DR Pfam: PF00319; SRF-TE; 1.
 DR PRINTS: PR00404; MADSDOMAIN.
 DR SMART: SM00432; MADS; 1.
 DR PROSITE: PS00350; MADS_BOX_1; 1.
 DR PROSITE: PS50066; MADS_BOX_2; 1.
 DR Transcription regulation; DNA-binding; Activator; Nuclear protein;
 KW Developmental protein;
 KW DOMAIN 3
 FT DOMAIN 3
 FT CONFLICT 199 165 A->R (IN REF. 2).
 FT CONFLICT 199 165 A->R (IN REF. 2).
 SQ SEQUENCE 232 AA; 27341 MW; 669070319F9857C3 CRC64;

Query Match 37.0%; Score 51; DB 1; Length 232;
 Best Local Similarity 44.4%; Pred. No. 1.5;
 Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;
 Oy 6 GRVY-----RELRRSDEPGSFK 24
 Db 107 QRLGECLELDIOELRRLEDEMENTFK 133

RESULT 8
 RMUC_PSEAE STANDARD: PRT: 453 AA.
 ID RMUC_PSEAE
 AC Q914U3;

DT 01-MAR-2002 (rel. 41, Created)
 DT 01-MAR-2002 (rel. 41, Last sequence update)
 DE 01-MAR-2002 (rel. 41, Last annotation update)
 GN DNA recombination protein rmuc homolog.
 GN RMUC OR PA1031.
 OS Pseudomonas aeruginosa.
 OC Bacteria: Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 NCBI_TaxID=287;
 OX NCBI_TaxID=4841;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.L., Hutnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garner R.L., Collier L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Lardig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Mond G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of *Pseudomonas aeruginosa* PA01, an
 RT opportunistic pathogen.";
 RL Nature 406:959-964(2000).
 CC -1- FUNCTION: Involved in DNA recombination (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE RMUC FAMILY.
 CC -----
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 CC -----
 DR EMBL: AE004535; AAC04420.1;
 DR InterPro: IPR003798; DUF195.
 DR Pfam: PF02646; DUF195; 1.
 KW DNA recombination; coiled coil; Complete proteome.
 KW DOMAIN 16
 FT DOMAIN 16
 SQ SEQUENCE 453 AA; 51539 MW; 1E7EA97EB2EC5E4B CRC64;

Query Match 35.5%; Score 49; DB 1; Length 453;
 Best Local Similarity 55.6%; Pred. No. 6.5;
 Matches 10; Conservative 4; Mismatches 2; Indels 2; Gaps 1;
 Oy 3 WAAQRYGR--ELRRMSDE 18
 Db 65 WASERQGREELRLASE 82

RESULT 9
 RAS3_RHRA STANDARD: PRT: 205 AA.
 ID RAS3_RHRA
 AC P22280;
 DT 01-AUG-1991 (rel. 19, Created)
 DT 01-AUG-1991 (rel. 19, Last sequence update)
 DT 30-MAY-2000 (rel. 39, Last annotation update)
 DE Ras-like protein 3.
 GN RAS3.
 OS Rhizomucor racemosus (Mucor circinelloides f. lusitanicus).
 OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;
 OC Mucor.
 NCBI_TaxID=4841;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 1215B;
 RX MEDLINE=91061774; PubMed=1701021;
 RA Casale W.L., McConnell D.G., Wang S.-Y., Lee Y.-J., Linz J.E.;
 RT "Expression of a gene family in the dimorphic fungus *Mucor racemosus*
 RT which exhibits striking similarity to human ras genes.";
 RL Mol. Cell. Biol. 10:6654-6663(1990).
 CC -1- ENZYME REGULATION: ALTERNATE BETWEEN AN INACTIVE FORM BOUND TO GDP
 CC AND AN ACTIVE FORM BOUND TO GTP. ACTIVATED BY A GUANINE

Query Match 34.8%; Score 48; DB 1; Length 519;
 Best Local Similarity 35.3%; Pred. No. 11;
 Matches 12; Conservative 6; Mismatches 8; Indels 8; Gaps 1;
 QY 1 NUNAAQRYGRELRLMSD-----EFGSFGKL 26
 Db 165 NLFMAERFGKQFLGMDLWVKHCGISHTGSEFMDL 198

RESULT 12
 THRC-ARATH STANDARD; PRT: 526 AA.
 ID THRC-ARATH Q957B5; Q93144;
 AC 01-MAR-2002 (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Threonine synthase, chloroplast precursor (EC 4.2.99.2) (TS).
 GN ARA229840 OR F27813.80.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=CV. Wassilewskij;
 RA MEDLINE=99418329; PubMed=10490396;
 RA Bartlem D., Tamaki Y., Naito S.;
 RT "Genomic nucleotide sequence of the Arabidopsis threonine synthase
 gene.";
 RT (In) Plant Gene Register PCR99-108.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. Columbia;
 RA MEDLINE=20083488; PubMed=10617198;
 RA Mayer K.F.X., Schueller C., Wandt R., Murphy G., Volckaert G.,
 RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,
 RA Harits B., Ansoorge W., Brandt P., Grivell L.A., Rieger M.,
 RA Welzenegger T., de Simone V., Obermaler B., Meche R., Mueller M.,
 RA Kreis M., Delsen M., Pildomenech P., Watson M., Schmidheini T.,
 RA Rehbert B., Portelle D., Perez-Alonso M., Bouty M., Baneroff I.,
 RA Vos P., Hohnel J., Zimmermann W., Wedler H., Ridley P.,
 RA Langham S.A., McCullagh B., Billam L., Roben J.,
 RA Van der Schueren F., Grymoprez B., Chuang Y.-J., Vandenbussche F.,
 RA Braeken M., Willems I., Voet M., Bastiaens I., Aert R., DeLoof E.,
 RA Welzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
 RA Holzer E., Brandt A., Peters S., van Staveren M., Dikse W.,
 RA Moeljan P., Klein Lankhorst R., Rose M., Hauf J., Koelter P.,
 RA Berner S., Hempel S., Feldmann M., Lamberth S., Van der Daele H.,
 RA De Keyser A., Buysbaert C., Gielen J., Villarroel R., De Clercq R.,
 RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
 RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McIlroy K., Hayes R.,
 RA Patek A., Rajandream M.-A., Lyne M., Benes V., Rechmann S.,
 RA Borova D., Bloembergen H., Scharf M., Grimm M., Loehner T.-H.,
 RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fartmann B., Grandjean R., Dunner D., Herl A.,
 RA Neumann S., Agitoni A., Vitale D., Liguori R., Piravandi E.,
 RA Massenet O., Guigley F., Clabaud G., Mendlein A., Felder R.,
 RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aboung S.,
 RA Chedof F., Cooke R., Berger C., Monfort A., Casacuberta E.,
 RA Gibbons T., Weber N., Vandenbol M., Barges M., Terol J., Torres A.,
 RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
 RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Belke C.,
 RA Frishman D., Haase D., Lemcke K., Meyers H.-W., Stocker S.,
 RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Haeremans K.,
 RA Parnell L., Dedha N., Gao J., Schutz K., Huang E., Spiegel L.,
 RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
 RA Stoecklin T., Kalicki J., Graves T., Harmon G., Edwards J.,
 RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
 RA Mux P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
 RA Krumer J., Fulton L., Mordis E., Dante M., Pepin K., Hillier L.,

RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
 RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,
 RA Antoniou B., Zidan M., Strong C., Sun H., Lamar B., Jordan C.,
 RA Ma P., Zhong J., Preston R., Vill D., Shekhar M., Matero A., Shah R.,
 RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Tili S.,
 RA Grant S., Shohdy N., Hasegawa A., Hamed A., Lodi M., Johnson A.,
 RA Chen E., Marra M., Martensen R., McCombie W.R.;
 RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
 thaliana.";
 RT Nature 402:769-777(1999).
 RN [3]
 RP SEQUENCE OF 2-526 FROM N.A., AND CHARACTERIZATION.
 RC STRAIN=CV. Columbia;
 RX PubMed=8706836;
 RA Currien G., Dumas R., Ravanal S., Douce R.;
 RT "Characterization of an Arabidopsis thaliana cDNA encoding an
 RT S-adenosylmethionine-sensitive threonine synthase. Threonine synthase
 RT from higher plants.";
 RL FEBS Lett. 390:85-90(1996).
 RN [4]
 RP CHARACTERIZATION.
 RX PubMed=9748328;
 RA Currien G., Job D., Douce R., Dumas R.;
 RT "Allosteric activation of Arabidopsis threonine synthase by
 RT S-adenosylmethionine.";
 RL Biochemistry 37:13212-13221(1998).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 41-526.
 RX PubMed=11344332;
 RA Thomazeau K., Currien G., Dumas R., Blou V.;
 RT "Crystal structure of threonine synthase from Arabidopsis thaliana";
 RL Protein Sci. 10:638-648(2001).
 CC -1- CATALYTIC ACTIVITY: O-phospho-L-homoserine + H(2)O = L-threonine +
 CC phosphate.
 CC -1- COFACTOR: Pyridoxal phosphate.
 CC -1- ENZYME REGULATION: Allosterically activated up to 20-fold by S-
 CC adenosyl-methionine (SAM).
 CC -1- SUBUNIT: Threonine biosynthesis; last step.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
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 CC -----
 CC EMBL: AB027151; BAA77707.1; -
 CC EMBL: AL050352; CAB43659.1; -
 CC EMBL: AL461575; CAB7942.1; -
 CC EMBL: LA1666; AAB04607.1; -
 CC PDB: 1ESX; 02-AUG-01.
 CC INTERPRO: IPR001926; PALP.
 CC Pfam: PF00291; PALP; 1.
 DR PROSITE: PS00165; DEHYDRATASE_SER_THR; 1.
 KW Threonine biosynthesis; lyase; Pyridoxal phosphate; Allosteric enzyme;
 KW Chloroplast; Transit peptide; 3D structure.
 FT TRANSIT 1 40
 FT CHLOROPLAST.
 FT CHAIN 41 526
 FT BINDING 203 203
 FT PYRIDOXAL PHOSPHATE.
 FT CONFLICT 2 2
 FT A -> L (IN REF. 3).
 SQ SEQUENCE 526 AA; 57776 MW; B27787A57B882AD0 CRC64;

Query Match 34.8%; Score 48; DB 1; Length 526;
 Best Local Similarity 35.3%; Pred. No. 11;
 Matches 12; Conservative 6; Mismatches 8; Indels 8; Gaps 1;
 QY 1 NUNAAQRYGRELRLMSD-----EFGSFGKL 26
 Db 165 NLFMAERFGKQFLGMDLWVKHCGISHTGSEFMDL 198

Db 172 NLFNAERFQKOPFLNMDLWKHCIGHSITGSPFDL 205

RESULT 13

ID B1M_HUMAN STANDARD: PRT; 198 AA.

AC 043521; 043522; 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DE Bcl-2-like protein 11 (Bcl2 interacting mediator of cell death).

GN BCL2L1L OR B1M.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxId=9606;

RN [1]

RP SEQUENCE FROM N.A., FUNCTION, AND ALTERNATIVE SPLICING.

RC TISSUE=peripheral blood, and spleen;

RX MEDLINE=98094360; PubMed=9430630;

RA O'Connor L., Strasser A., O'Reilly L.A., Hausmann G., Adams J.M., Cory S., Huang D.C.S., Bcl-2 family that promotes apoptosis.;

RT Bcl-2 family that promotes apoptosis.;

RU EMBL J. 17384-395(1998).

CC -1- FUNCTION: INDUCES APOPTOSIS. ISOFORM B1M IS MORE POTENT THAN ISOFORM B1MEL.

CC -1- SUBUNIT: FORMS HETERODIMERS WITH A NUMBER OF ANTIAPOPTOTIC BCL-2 PROTEINS INCLUDING MCL-1, BCL-2, BCL-XL, BFL-1, AND BHRF-1. DOES NOT HETERODIMERIZE WITH PROAPOPTOTIC PROTEINS SUCH AS BAD, BOK, BAX OR BAK (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: ASSOCIATED WITH INTRACYTOSOLIC MEMBRANES (BY SIMILARITY).

CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: B1MEL (SHOWN HERE) AND B1M. ARE PRODUCED BY ALTERNATIVE SPLICING.

CC -1- DOMAIN: THE B1M DOMAIN IS REQUIRED FOR BCL-2 BINDING AND CYTOTOXICITY.

CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 3 (BH3).

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CC EMBL: AF032457; AAC39593.1; -

DR EMBL: AF032458; AAC39594.1; -

DR MIM: 603827; -

DR InterPro: IPR000712; BCL-2.

DR PROSITE: PS01259; BH3; FALSE_NEG.

DR Apoptosis: Alternative splicing; Membrane.

FT DOMAIN 148 162 BH3.

FT VASPEPIC 42 101 MISSING (IN ISOFORM B1MEL).

FT SEQUENCE 198 AA; 22171 MW; D75735469CA997 CRC64;

SO SEQUENCE

Query Match 34.18; Score 47; DB 1; Length 198;

Best Local Similarity 45.58; Pred. No. 5.1;

Matches 10; Conservative 3; Mismatches 5; Indels 4; Gaps 1;

Oy 2 LMAAQRGRLRMSDEFGSP 23

Db 146 IMAQ-----ELRIIDDEFNAVY 163

RESULT 14

ID FMR2_ANTEL STANDARD: PRT; 429 AA.

AC Q16994; 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Antho-RFamide neuropeptides type 2 precursor.

OS Eukaryota; Metazoa; Chordata; Anthozoa; Zoantharia; Actinoptera;

OC Nymphaeae; Actinidae; Anthopleura.

OX NCBI_TaxId=6110;

RN [1]

RP SEQUENCE FROM N.A.

RA Schmützler C., Darmer D., Diekhoff D., Grimelikhuisen C.J.P.;

RT *Identification of a novel type of processing sites in the precursor from Anthopleura elegantissima.*;

RU J. Biol. Chem. 267:22534-22541(1992).

CC -1- FUNCTION: NOT KNOWN BUT IT COULD ACT AS A TRANSMITTER AT NEURONAL SYNAPSES.

CC -1- SUBCELLULAR LOCATION: Secreted.

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CC EMBL: M99170; AAA27739.1; -

DR Neuropeptide; Amidation; Repeat; Signal.

KW SIGNAL 1 22

FT PEPTIDE 234 237 ANTHO-RFAMIDE.

FT PEPTIDE 242 245 ANTHO-RFAMIDE.

FT PEPTIDE 250 253 ANTHO-RFAMIDE.

FT PEPTIDE 258 261 ANTHO-RFAMIDE.

FT PEPTIDE 266 269 ANTHO-RFAMIDE.

FT PEPTIDE 274 277 ANTHO-RFAMIDE.

FT PEPTIDE 290 293 ANTHO-RFAMIDE.

FT PEPTIDE 298 301 ANTHO-RFAMIDE.

FT PEPTIDE 306 309 ANTHO-RFAMIDE.

FT PEPTIDE 322 325 ANTHO-RFAMIDE.

FT PEPTIDE 330 333 ANTHO-RFAMIDE.

FT PEPTIDE 343 346 ANTHO-RFAMIDE.

FT PEPTIDE 356 359 ANTHO-RFAMIDE.

FT PEPTIDE 369 372 ANTHO-RFAMIDE.

FT MOD_RES 237 245 AMIDATION (G-238 PROVIDE AMIDE GROUP).

FT MOD_RES 245 245 AMIDATION (G-254 PROVIDE AMIDE GROUP).

FT MOD_RES 245 253 AMIDATION (G-254 PROVIDE AMIDE GROUP).

FT MOD_RES 261 261 AMIDATION (G-262 PROVIDE AMIDE GROUP).

FT MOD_RES 269 269 AMIDATION (G-270 PROVIDE AMIDE GROUP).

FT MOD_RES 277 277 AMIDATION (G-278 PROVIDE AMIDE GROUP).

FT MOD_RES 293 293 AMIDATION (G-294 PROVIDE AMIDE GROUP).

FT MOD_RES 301 301 AMIDATION (G-302 PROVIDE AMIDE GROUP).

FT MOD_RES 309 309 AMIDATION (G-310 PROVIDE AMIDE GROUP).

FT MOD_RES 325 325 AMIDATION (G-326 PROVIDE AMIDE GROUP).

FT MOD_RES 333 333 AMIDATION (G-334 PROVIDE AMIDE GROUP).

FT MOD_RES 346 346 AMIDATION (G-347 PROVIDE AMIDE GROUP).

FT MOD_RES 359 359 AMIDATION (G-360 PROVIDE AMIDE GROUP).

FT MOD_RES 372 372 AMIDATION (G-372 PROVIDE AMIDE GROUP).

SO SEQUENCE 429 AA; 50564 MW; 7C54F5C60D537F4 CRC64;

Query Match 33.78; Score 46.5; DB 1; Length 429;

Best Local Similarity 52.48; Pred. No. 15;

Matches 11; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

Oy 4 AAQRYGRLR-RMSDEFGSP 23

Db 209 AAGRGRLGGRGFRGFRGFR 229

RESULT 15

ID FMR1_ANTEL STANDARD: PRT; 435 AA.

AC P10419; 01-MAR-1989 (Rel. 10, Created)

DT 01-OCT-1993 (rel. 27, Last sequence update)
 DT 16-OCT-2001 (rel. 40, Last annotation update)
 DE Antho-Ramide neuropeptides type 1 precursor.
 OS Anthopleura elegantissima (Sea anemone).
 CC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actinaria;
 OK Nemathe: Actinidae; Anthopleura.
 NC NCBI_TaxID=6110;
 RM (1)
 RM SEQUENCE FROM N.A.
 RA MEDLINE=93054550; PubMed=1429603;
 RA Schmutzler C., Darter D., Diekhoff D., Grimmelikhuijzen C.J.P.;
 RT "Identification of a novel type of processing sites in the precursor
 RT for the sea anemone neuropeptide Antho-Ramide (<Glu-Gly-Arg-Phe-NH2)
 RT from Anthopleura elegantissima.";
 RL J. Biol. Chem. 267:22534-22541(1992).
 RN (2)
 RN SEQUENCE OF MATURE PEPTIDE.
 RX MEDLINE=87092339; PubMed=2879288;
 RA Grimmelikhuijzen C.J.P., Graff D.;
 RT "Isolation of pyroGlu-Gly-Arg-Phe-NH2 (Antho-Ramide), a neuropeptide
 RT from sea anemones.";
 RL Proc Natl Acad Sci U S A. 83:9817-9821(1986).
 CC -1- FUNCTION: NOT KNOWN BUT IT COULD ACT AS A TRANSMITTER AT
 CC NEUROMUSCULAR SYNAPSES.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC
 DR EMBL: M98269; AAA27738.1;
 DR PIR: A26666; ECXAA.
 DR PIR: A44308; A44308.
 DR InterPro: IPR002544; FARP.
 DR Pfam: PF01581; FARP; 13.
 KW Neuropeptide; Amidation; Repeat; Signal.
 FT SIGNAL 1 22
 FT PEPTIDE 194 197 ANTHO-REAME.
 FT PEPTIDE 202 205 ANTHO-REAME.
 FT PEPTIDE 210 213 ANTHO-REAME.
 FT PEPTIDE 218 221 ANTHO-REAME.
 FT PEPTIDE 226 229 ANTHO-REAME.
 FT PEPTIDE 234 237 ANTHO-REAME.
 FT PEPTIDE 242 245 ANTHO-REAME.
 FT PEPTIDE 250 253 ANTHO-REAME.
 FT PEPTIDE 258 261 ANTHO-REAME.
 FT PEPTIDE 266 269 ANTHO-REAME.
 FT PEPTIDE 274 277 ANTHO-REAME.
 FT PEPTIDE 282 285 ANTHO-REAME.
 FT PEPTIDE 290 293 ANTHO-REAME.
 FT PEPTIDE 298 301 ANTHO-REAME.
 FT PEPTIDE 306 309 ANTHO-REAME.
 FT PEPTIDE 314 317 ANTHO-REAME.
 FT PEPTIDE 322 325 ANTHO-REAME.
 FT PEPTIDE 330 333 ANTHO-REAME.
 FT PEPTIDE 343 346 ANTHO-REAME.
 FT PEPTIDE 355 359 ANTHO-REAME.
 FT PEPTIDE 369 372 ANTHO-REAME.
 FT DOMAIN 376 386 POLY-ALA.
 FT MOD_RES 194 194 PYROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 197 197 AMIDATION (G-198 PROVIDE AMIDE GROUP).
 FT MOD_RES 205 205 AMIDATION (G-206 PROVIDE AMIDE GROUP).
 FT MOD_RES 213 213 AMIDATION (G-214 PROVIDE AMIDE GROUP).
 FT MOD_RES 221 221 AMIDATION (G-222 PROVIDE AMIDE GROUP).
 FT MOD_RES 229 229 AMIDATION (G-230 PROVIDE AMIDE GROUP).
 FT MOD_RES 237 237 AMIDATION (G-238 PROVIDE AMIDE GROUP).
 FT MOD_RES 245 245 AMIDATION (G-246 PROVIDE AMIDE GROUP).
 FT MOD_RES 253 253 AMIDATION (G-254 PROVIDE AMIDE GROUP).
 FT MOD_RES 261 261 AMIDATION (G-262 PROVIDE AMIDE GROUP).

FT MOD_RES 269 269 AMIDATION (G-270 PROVIDE AMIDE GROUP).
 FT MOD_RES 277 277 AMIDATION (G-278 PROVIDE AMIDE GROUP).
 FT MOD_RES 285 285 AMIDATION (G-286 PROVIDE AMIDE GROUP).
 FT MOD_RES 293 293 AMIDATION (G-294 PROVIDE AMIDE GROUP).
 FT MOD_RES 301 301 AMIDATION (G-302 PROVIDE AMIDE GROUP).
 FT MOD_RES 309 309 AMIDATION (G-310 PROVIDE AMIDE GROUP).
 FT MOD_RES 317 317 AMIDATION (G-318 PROVIDE AMIDE GROUP).
 FT MOD_RES 325 325 AMIDATION (G-326 PROVIDE AMIDE GROUP).
 FT MOD_RES 333 333 AMIDATION (G-334 PROVIDE AMIDE GROUP).
 FT MOD_RES 346 346 AMIDATION (G-347 PROVIDE AMIDE GROUP).
 FT MOD_RES 359 359 AMIDATION (G-360 PROVIDE AMIDE GROUP).
 FT MOD_RES 372 372 AMIDATION (G-373 PROVIDE AMIDE GROUP).
 SQ SEQUENCE 435 AA; 50940 MW; B0C44020CD5B061 CRC64;

Query Match 33.7%; Score 46.5; DB 1; Length 435;
 Best Local Similarity 52.4%; Pred. No. 15;
 Matches 11; Conservative 3; Mismatches 6; Indels 1; Gaps 1;
 QY 4 AAQRYGREL-RMSDEPGSF 23
 1:|||||: 1 11:1 1
 DB 209 AAGRGRELQGRGRGRGRF 229

Search completed: September 20, 2002, 11:04:28
 Job time: 1625 sec

[Faint, illegible text and a horizontal line]

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 20, 2002, 10:36:03 ; Search time 172.19 Seconds
(without alignments)
26.122 Million cell updates/sec

Title: US-09-544-664-1
Perfect score: 138
Sequence: 1 LMAAQRGRRLRMSDFEGSPKGL 26

Scoring table: BL0SDM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 17294929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP_archaea:*
2: SP_bacteria:*
3: SP_fungi:*
4: SP_human:*
5: SP_invertebrate:*
6: SP_mammal:*
7: SP_mmc:*
8: SP_orignale:*
9: SP_plague:*
10: SP_plant:*
11: SP_rodent:*
12: SP_virus:*
13: SP_vertebrate:*
14: SP_unclassified:*
15: SP_virus:*
16: SP_bacteriaph:*
17: SP_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	ID	Description
1	87	63.0	146	13 Q919N2	Q919N2 brachydanio
2	53	38.4	223	16 Q10843	Q10843 mycobacteri
3	51	37.0	231	10 Q9SE60	Q9SE60 arabidopsis
4	51	37.0	232	10 Q9S703	Q9S703 arabidopsis
5	51	37.0	232	10 Q9S022	Q9S022 arabidopsis
6	51	37.0	232	10 Q9S021	Q9S021 arabidopsis
7	51	37.0	232	10 Q9S020	Q9S020 arabidopsis
8	51	37.0	232	10 Q9S019	Q9S019 arabidopsis
9	51	37.0	232	10 Q9S018	Q9S018 arabidopsis
10	51	37.0	232	10 Q9S017	Q9S017 arabidopsis
11	51	37.0	232	10 Q9S016	Q9S016 arabidopsis
12	51	37.0	232	10 Q9S015	Q9S015 arabidopsis
13	50.5	36.6	904	2 Q9KGM3	Q9KGM3 pseudomonas
14	50	36.2	374	15 Q9HNM9	Q9HNM9 chimpanzee
15	50	36.2	374	17 Q9HNM9	Q9HNM9 halobacteri
16	50	36.2	516	10 Q9SPS5	Q9SPS5 arabidopsis

17	49.5	35.9	153	5 Q9UB33	Q9UB33 anopheles g
18	48.5	35.9	401	5 Q97A07	Q97A07 anopheles g
19	48.5	35.9	503	8 Q47148	Q47148 menziesia c
20	48.5	35.9	506	8 Q63950	Q63950 rhododendro
21	48.5	35.9	506	8 Q62972	Q62972 rhododendro
22	48.5	35.9	506	8 Q62973	Q62973 rhododendro
23	48.5	35.9	506	8 Q62974	Q62974 rhododendro
24	48.5	35.9	506	8 Q62975	Q62975 rhododendro
25	48.5	35.9	506	8 Q62976	Q62976 rhododendro
26	48.5	35.9	506	8 Q62977	Q62977 rhododendro
27	48.5	35.9	506	8 Q62978	Q62978 rhododendro
28	48.5	35.9	506	8 Q62981	Q62981 rhododendro
29	48.5	35.9	506	8 Q62982	Q62982 rhododendro
30	48.5	35.9	506	8 Q62983	Q62983 rhododendro
31	48.5	35.9	506	8 Q62984	Q62984 rhododendro
32	48.5	35.9	506	8 Q62988	Q62988 rhododendro
33	48.5	35.9	506	8 Q62989	Q62989 rhododendro
34	48.5	35.9	506	8 Q62990	Q62990 rhododendro
35	48.5	35.9	506	8 Q62991	Q62991 rhododendro
36	48.5	35.9	506	8 Q62992	Q62992 ledum palus
37	48.5	35.9	506	8 Q62993	Q62993 menziesia m
38	48.5	35.9	506	8 Q47149	Q47149 rhododendro
39	48.5	35.9	506	8 Q47152	Q47152 rhododendro
40	48.5	35.9	506	8 Q47155	Q47155 rhododendro
41	48.5	35.9	506	8 Q47168	Q47168 menziesia p
42	48.5	35.9	506	8 Q47170	Q47170 rhododendro
43	48.5	35.9	506	8 Q47171	Q47171 rhododendro
44	48.5	35.9	506	8 Q47173	Q47173 rhododendro
45	48.5	35.9	506	8 Q47174	Q47174 tsusitophy11

ALIGNMENTS

RESULT 1
ID Q919N2 PRELIMINARY: PRT: 146 AA.
AC Q919N2
DE 01-DEC-2000 (TRENBLER, 15, Created)
DI 01-DEC-2001 (TRENBLER, 15, Last sequence update)
DI 01-DEC-2001 (TRENBLER, 15, Last annotation update)
DE BAD.
GN Brachydanio rerio (Zebrafish) (Zebrafish danio).
OS Brachydanio rerio (Zebrafish) (Zebrafish danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=20373792; PubMed=10917738;
RA Inohara N., Nunez G.;
RT "Genes with homology to mammalian apoptosis regulators identified in
RT zebrafish."
RL Cell Death Differ. 7:509-510(2000).
DR EMBL; AF231017; AAF66962.2;
SO SEQUENCE 146 AA; 16546 MW; 28A5650BB5107ECB CRC64;

Query Match 63.0%; Score 87; DB 13; length 146;
Best Local Similarity 65.2%; Pred. No. 2.8e-05;
Matches 15; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 2 LMAAQRGRRLRMSDFEGSPK 24
DB 89 LMAAQRGRRLRMSDFEGSPK 111
RESULT 2
ID Q10843 PRELIMINARY: PRT: 223 AA.
AC Q10843
DI 01-NOV-1998 (TRENBLER, 08, Created)

DT 01-NOV-1998 (TRENBLURE, 08, last sequence update)
DT 01-DEC-2001 (TRENBLURE, 19, last annotation update)
DE HYPOHETHELICAL 24.1 KDA PROTEIN C193.03C.
GN RV2014 OR MTCY39.03C.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxId=1773;
RN [1]
RP
RP SEQUENCE FROM N.A.
RC
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekaia F.,
RA Davidson K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feldwell T., Gentles S., Hamlin N., Holroyd S.,
RA Oliver S., Osborne J., O'Krogh A., McLean J., Moule S., Murphy L.,
RA Rulter S., Seeger K., Skellern S., Skellern M.A., Rogers J.,
RA Snelson J.E., Taylor K., Whitehead S., Barrett B.G.;
RT Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence. " "
LT Nature 393:537-544(1998).
CC -1 SIMILARITY: TO M.PARATUBERCULOSIS IS900.
DR EMBL: Z74025; CAAG8415.1; -
DR Tuberculosis; RV2014; -
DR InterPro: IPR003346; Transposase_20.
DR Pfam: PF02371; Transposase_20; 1.
KW Hypochemical protein; Complete proteome.
KW SEQUENCE 223 AA: 24132 MW: 70456750017FEF37 CRC64;

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Query Match Similarity      38.4%; Score 53; DB 16; Length 223;
Best Local Similarity      58.8%; Pred. No. 5.4;
Matches    10; Conservative   1; Mismatches     6; Indels       0; Gaps       0;

QY          1 NLMAADRGRELRMSD 17
              ||||| |} }-|-|
DB         165 NLMADRYNRRIARGHD 181

RESULT      3
Q9SECO      PRELIMINARY; PRT: 231 AA.
AC           Q9SECO;
DT           01-MAY-2000 (TREMBLrel. 13, Created)
DT           01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT           01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE           APTAL3 (FRAGMENT).
OS           Arabidopsis lyrata.
OC           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC           Spermatophytes; Magnoliopsida; eudicotyledons; core eudicots; Rosidae;
OC           eurosids II; Brassicales; Brassicaceae; Arabidopsidae.
OX           NCBI_TaxID=59689;
RN           [1]
RX           SEQUENCE FROM N.A. MEDLINE=99404148; PubMed=10474900;
RA           Lawton-Rauh A.L., Buckler E.S. IV, Purugganan M.D.;
RT           Patterns of molecular evolution among paralogous floral homeotic
RL           genes.*;
RU           MOL. BIOL. EVOL. 16:1037-1045(1999).
DR           EMBL: AF143380; AAC25590.1; -.
DR           HSSP: P13745; IJNMW.
DR           InterPro: IPR002487; K-box.
DR           InterPro: IPR002100; MADS-box.
DR           Pfam: PF01486; K-box; 1.
DR           Pfam: PF00319; SR-TF; 1.
DR           PRINTS: PR00404; MADSDOMAIN.
DR           SMART: SM00432; MADS_1.
DR           PROSITE: PS50066; MADS_BOX_2; 1.
FT           NON_TER      231
SQ           SEQUENCE 231 AA: 27176 MW; A67CAEIEBDBDF7AA CRC64;
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Query Match 37.0%; Score 51; DB 10; Length 231;
Best Local Similarity 44.4%; Pled. No. 11;
Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1.
QY 6 QRYG-----RLRMSDPFGSGFK 24
      111111111111111111111111
Db 107 QRAGCCDLDDIQLRLKLEDEMTK 133

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RESULT	4			
ID	093703	PRELIMINARY:	PT:	232 AA.
AC	093703;			
DT	01-MAY-2000 (Tremblere, 13, Created)			
DT	01-MAY-2000 (Tremblere, 13, Last sequence update)			
DT	01-JUN-2001 (Tremblere, 17, Last annotation update)			
DE	FLORAL HOMEOTIC PROTEIN AP3.			
GN	APETALA3.			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons: core eudicots; Rosidae			
OC	eucosids II; Brassicales; Brassicaceae; Arabidopsis.			
NC	NCBI_TaxID=3702;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CV, GR-3, AND CV, CHI-1;			
RC	MEDLINE=99126449; PubMed=99247474;			
RA	Purugganan M.D., Sudduth J.I.;			
RT	Molecular Population genetics of floral homeotic loci. Departures			
RT	from the equilibrium-neutral model at the APETALA3 and PISTILLATA			
RL	genes of Arabidopsis thaliana.";			
RL	Genetics 151:839-848(1999).			
CC	-1- SUCCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).			
CC	-1- SIMILARITY: TO THE MAGD2-1.			
CC	EMBL, AF115803; AAD51892.1; -			
CC	EMBL, AF115798; AAD51887.1; -			
DR	HSSP, P11746; INM.			
DR	InterPro, IPR002487; K-box.			
DR	InterPro, IPR002100; MADS-box.			
DR	Pfam, PF01486; K-box; 1.			
DR	Pfam, PF00319; SRP-TF; 1.			
DR	PRINTS, PR00404; MADSOMAIN.			
DR	SMART, SM00432; MADS; 1.			
DR	PROSITE, PS00350; MADS_BOX_1; 1.			
DR	PROSITE, PS50066; MADS_BOX_2; 1.			
DR	DNA-binding; Nuclear protein; Transcription regulation.			
QO	SEQUENCE 232 AA: 27340 MW: 66907039p99CPD63 CRC64;			

Query MatchScore	37.0%	Score 51	DB 10	Length 232
Best Local Similarity	44.4%	Pred. No. 11		
Matches 12	Conservative	3	Mismatches	4
			Indels	8
			Gaps	1
Oy	6	ORV-----RELMSPEFESGFK	24	
		: :	:	
Db	107	ORLGECDKDKIDQLRLLEDENMFK	133	
RESULT	5			
08SQ22				
ID	09SQ22	PRELIMINARY	PRT	232 AA.
AC	09SQ22			
DT	01-MAY-2000	(TREMBLrel. 13, Created)		
DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)		
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)		
DE	FLORAL HOMEOTIC PROTEIN AP3.			
GN	APETALA3.			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	eucosids II; Brassicales; Brassicaceae; Arabidopsis.			
NCBI_TaxID=3702:				

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RN 11] SEQUENCE FROM N.A.
RP STRAIN-CV, LI-8;
RC MEDLINE-99126449; PubMed-9927474;
RA Purganan M.D., Suddith J.I.;
RT "Molecular population genetics of floral homeotic loci. Departures
RT from the equilibrium-neutral model at the APETALA3 and PISTILLATA
RT genes of Arabidopsis thaliana."
RL Genetics 151:839-848(1999).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR EMBL, AF115801; MADS1890.1;
DR HSSP, P11746; IMNM.
DR InterPro: IPR002487; K-box.
DR InterPro: IPR002100; MADS-box.
DR Pfam: PF01486; K-box; 1.
DR Pfam: PF00319; SRP-TF; 1.
DR PRINTS: PR00404; MADSDOMAIN.
DR SMART: SM00432; MADS_BOX_1; 1.
DR PROSITE: PS00350; MADS_BOX_1; 1.
DR PROSITE: PS0066; MADS_BOX_2; 1.
DR DNA-binding: Nuclear protein; Transcription regulation.
SQ SEQUENCE 232 AA; 27267 MW; 42A852D657E22A65 CRC64;

Query Match 37.0%; Score 51; DB 10; Length 232;
Best Local Similarity 44.4%; Pred. No. 11;
Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;

QY 6 ORG-----RELRLMSDFEGSFK 24
DB 107 ORGECLELDIDGELRLDEMDENMFK 133

RESULT 6
Q9SO21 PRELIMINARY; PRT; 232 AA.
AC Q9SO21.
DT 01-MAY-2000 (TREMBL) 13, Created)
DT 01-MAY-2000 (TREMBL) 13, Last sequence update)
DT 01-DEC-2001 (TREMBL) 19, Last annotation update)
DE FLORAL HOMEOTIC PROTEIN AP3.
GN APETALA3.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Eudicotyledons; Core eudicots; Rosidae;
OC Eucosids II; Brassicales; Brassicaceae; Arabidops.
OX NCBI_TaxID=3702;
RN 11] SEQUENCE FROM N.A.
RP STRAIN-CV, KENT;
RC MEDLINE-99126449; PubMed-9927474;
RA Purganan M.D., Suddith J.I.;
RT "Molecular population genetics of floral homeotic loci. Departures
RT from the equilibrium-neutral model at the APETALA3 and PISTILLATA
RT genes of Arabidopsis thaliana."
RL Genetics 151:839-848(1999).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR EMBL, AF115805; MADS1894.1;
DR HSSP, P11746; IMNM.
DR InterPro: IPR002487; K-box.
DR InterPro: IPR002100; MADS-box.
DR Pfam: PF01486; K-box; 1.
DR Pfam: PF00319; SRP-TF; 1.
DR PRINTS: PR00404; MADSDOMAIN.
DR SMART: SM00432; MADS_BOX_1; 1.
DR PROSITE: PS00350; MADS_BOX_1; 1.
DR PROSITE: PS0066; MADS_BOX_2; 1.
DR DNA-binding: Nuclear protein; Transcription regulation.
SQ SEQUENCE 232 AA; 27286 MW; 66976305B88B63E3 CRC64;

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Query Match 37.0%; Score 51; DB 10; Length 232;
Best Local Similarity 44.4%; Pred. No. 11;
Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;

QY 6 ORG-----RELRLMSDFEGSFK 24
DB 107 ORGECLELDIDGELRLDEMDENMFK 133

RESULT 7
Q9SO20 PRELIMINARY; PRT; 232 AA.
AC Q9SO20.
DT 01-MAY-2000 (TREMBL) 13, Created)
DT 01-MAY-2000 (TREMBL) 13, Last sequence update)
DT 01-DEC-2001 (TREMBL) 19, Last annotation update)
DE FLORAL HOMEOTIC PROTEIN AP3.
GN APETALA3.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Eudicotyledons; Core eudicots; Rosidae;
OC Eucosids II; Brassicales; Brassicaceae; Arabidops.
OX NCBI_TaxID=3702;
RN 11] SEQUENCE FROM N.A.
RP STRAIN-CV, CORSCALLA;
RC MEDLINE-99126449; PubMed-9927474;
RA Purganan M.D., Suddith J.I.;
RT "Molecular population genetics of floral homeotic loci. Departures
RT from the equilibrium-neutral model at the APETALA3 and PISTILLATA
RT genes of Arabidopsis thaliana."
RL Genetics 151:839-848(1999).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR EMBL, AF115806; MADS1895.1;
DR HSSP, P11746; IMNM.
DR InterPro: IPR002487; K-box.
DR InterPro: IPR002100; MADS-box.
DR Pfam: PF01486; K-box; 1.
DR Pfam: PF00319; SRP-TF; 1.
DR PRINTS: PR00404; MADSDOMAIN.
DR SMART: SM00432; MADS_BOX_1; 1.
DR PROSITE: PS00350; MADS_BOX_1; 1.
DR PROSITE: PS0066; MADS_BOX_2; 1.
DR DNA-binding: Nuclear protein; Transcription regulation.
SQ SEQUENCE 232 AA; 27342 MW; BPFDCB5B73FA601 CRC64;

Query Match 37.0%; Score 51; DB 10; Length 232;
Best Local Similarity 44.4%; Pred. No. 11;
Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;

QY 6 ORG-----RELRLMSDFEGSFK 24
DB 107 ORGECLELDIDGELRLDEMDENMFK 133

RESULT 8
Q9SO19 PRELIMINARY; PRT; 232 AA.
AC Q9SO19.
DT 01-MAY-2000 (TREMBL) 13, Created)
DT 01-MAY-2000 (TREMBL) 13, Last sequence update)
DT 01-JUN-2001 (TREMBL) 17, Last annotation update)
DE FLORAL HOMEOTIC PROTEIN AP3.
GN APETALA3.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Eudicotyledons; Core eudicots; Rosidae;
OC Eucosids II; Brassicales; Brassicaceae; Arabidops.
OX NCBI_TaxID=3702;
RN 11] SEQUENCE FROM N.A.

```

RC STRAIN-CV. BRETAGNY;
 RX MEDLINE-99126449; PubMed-9927474;
 RA Purganan M.D.; Suddith J.I.;
 RT "Molecular population genetics of floral homeotic loci. Departures
 from the equilibrium-neutral model at the APETALA3 and PISTILLATA
 genes of Arabidopsis thaliana.";
 RL Genetics 151:839-848(1999).
 DE FLORAL HOMEOTIC PROTEIN AP3.
 GN APETALA3.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
 NCBI_TaxID-3702;
 RX HSSP; P11746; 1MM.
 DR InterPro: IPR002487; K-box.
 DR InterPro: IPR002100; MADS-box.
 DR Pfam: PF01486; K-box; 1.
 DR Pfam: PF00319; SRF-TE; 1.
 DR PRINTS: PR00404; MADSDOMAIN.
 DR SMART: SM00432; MADS_1.
 DR PROSITE: PS50066; MADS_BOX_2; 1.
 SQ SEQUENCE 232 AA; 27311 MW; 71AE593FBA67EC3 CRC64;

Query Match 37.0%; Score 51; DB 10; Length 232;
 Best Local Similarity 44.4%; Pred. No. 11;
 Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;

OY 6 QRYG-----RELRRMSDEFGSGFK 24
 DB 107 ORLGCELDLDIOLRLRLEDEMENTFK 133

RESULT 9
 ID O9S018 PRELIMINARY; PRT; 232 AA.
 AC O9S018;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE FLORAL HOMEOTIC PROTEIN AP3.
 GN APETALA3.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
 NCBI_TaxID-3702;
 RX HSSP; P11746; 1MM.
 DR InterPro: IPR002487; K-box.
 DR InterPro: IPR002100; MADS-box.
 DR Pfam: PF01486; K-box; 1.
 DR Pfam: PF00319; SRF-TE; 1.
 DR PRINTS: PR00404; MADSDOMAIN.
 DR SMART: SM00432; MADS_1.
 DR PROSITE: PS50066; MADS_BOX_2; 1.
 SQ SEQUENCE 232 AA; 27369 MW; 742A15F107D2320E CRC64;

Query Match 37.0%; Score 51; DB 10; Length 232;
 Best Local Similarity 44.4%; Pred. No. 11;
 Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;

OY 6 QRYG-----RELRRMSDEFGSGFK 24
 DB 107 ORLGCELDLDIOLRLRLEDEMENTFK 133

RESULT 10

O9S017
 ID O9S017 PRELIMINARY; PRT; 232 AA.
 AC O9S017;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE FLORAL HOMEOTIC PROTEIN AP3.
 GN APETALA3.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
 NCBI_TaxID-3702;
 RX HSSP; P11746; 1MM.
 DR InterPro: IPR002487; K-box.
 DR InterPro: IPR002100; MADS-box.
 DR Pfam: PF01486; K-box; 1.
 DR Pfam: PF00319; SRF-TE; 1.
 DR PRINTS: PR00404; MADSDOMAIN.
 DR SMART: SM00432; MADS_1.
 DR PROSITE: PS50066; MADS_BOX_2; 1.
 DR PROSITE: PS50066; MADS_BOX_2; 1.
 KW DNA-binding; Nuclear Protein; Transcription regulation.
 SQ SEQUENCE 232 AA; 27284 MW; 04FCFC5B73C7729 CRC64;

Query Match 37.0%; Score 51; DB 10; Length 232;
 Best Local Similarity 44.4%; Pred. No. 11;
 Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;

OY 6 QRYG-----RELRRMSDEFGSGFK 24
 DB 107 ORLGCELDLDIOLRLRLEDEMENTFK 133

RESULT 11
 ID O9S016 PRELIMINARY; PRT; 232 AA.
 AC O9S016;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE FLORAL HOMEOTIC PROTEIN AP3.
 GN APETALA3.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
 NCBI_TaxID-3702;
 RX HSSP; P11746; 1MM.
 DR InterPro: IPR002487; K-box.
 DR InterPro: IPR002100; MADS-box.
 DR Pfam: PF01486; K-box; 1.
 DR Pfam: PF00319; SRF-TE; 1.
 DR PRINTS: PR00404; MADSDOMAIN.
 DR SMART: SM00432; MADS_1.
 DR PROSITE: PS50066; MADS_BOX_2; 1.
 DR PROSITE: PS50066; MADS_BOX_2; 1.
 KW DNA-binding; Nuclear Protein; Transcription regulation.
 SQ SEQUENCE 232 AA; 27284 MW; 04FCFC5B73C7729 CRC64;

Query Match 37.0%; Score 51; DB 10; Length 232;
 Best Local Similarity 44.4%; Pred. No. 11;
 Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;

OY 6 QRYG-----RELRRMSDEFGSGFK 24
 DB 107 ORLGCELDLDIOLRLRLEDEMENTFK 133

DR HSP; P11746; 1MM.
DR InterPro: IPR002487; K-box.
DR InterPro: IPR002100; MADS-box.
DR Pfam: PF01486; K-box; 1.
DR Pfam: PF00319; SRP-TF; 1.
DR PRINTS: PR00404; MADSOMAIN.
DR SMART: SM00432; MADS; 1.
DR PROSITE: PS00350; MADS_BOX_1; 1.
DR PROSITE: PS50066; MADS_BOX_2; 1.
DR DNA-binding; Nuclear protein; Transcription regulation.
KW SEQUENCE 232 AA; 27314 MW; DB8CA1FC835557D6 CRC64;

Query Match 37.0%; Score 51; DB 10; Length 232;
Best Local Similarity 44.4%; Pred. No. 11;
Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;

QY 6 QRYG-----RELRRMSDEFGSK 24
||| :|||: |||: |||
Db 107 QRYGCELDLDIQLRLDEDMENYFK 133

RESULT 12
Q9SQ15 PRELIMINARY; PRT; 232 AA.
ID Q9SQ15;
AC Q9SQ15;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE FLORAL HOMEOTIC PROTEIN AP3.
GN APTAL3.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. KAS-1;
RX MEDLINE-99126449; PubMed-9927474;
RA Purganan M.D., Sudhith J.I.;
RT "Molecular population genetics of floral homeotic loci. Departures
RT from the equilibrium-neutral model at the APTAL3 and PISTILLATA
RT genes of Arabidopsis thaliana.";
RU Genetics 151:839-848(1999).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR EMBL: AF115812; AAD51901.1; -
DR HSP; P11746; 1MM.
DR InterPro: IPR002487; K-box.
DR InterPro: IPR002100; MADS-box.
DR Pfam: PF01486; K-box; 1.
DR Pfam: PF00319; SRP-TF; 1.
DR PRINTS: PR00404; MADSOMAIN.
DR SMART: SM00432; MADS; 1.
DR PROSITE: PS00350; MADS_BOX_1; 1.
DR PROSITE: PS50066; MADS_BOX_2; 1.
DR DNA-binding; Nuclear protein; Transcription regulation.
KW SEQUENCE 232 AA; 27300 MW; 5CA05FD4F824DF0 CRC64;

Query Match 37.0%; Score 51; DB 10; Length 232;
Best Local Similarity 44.4%; Pred. No. 11;
Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;

QY 6 QRYG-----RELRRMSDEFGSK 24
||| :|||: |||: |||
Db 107 QRYGCELDLDIQLRLDEDMENYFK 133

RESULT 13
Q9KGM3 PRELIMINARY; PRT; 904 AA.

AC Q9KGM3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NADH DEHYDROGENASE I SUBUNIT G.
GN NUDG.
OS Pseudomonas fluorescens.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=294;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WCS365;
RA Camacho Carvajal M.M., Lugtenberg B.J.J., Bloemberg G.V.;
RT "Characterization of NADH dehydrogenases of Pseudomonas fluorescens
RT WCS365 and their role in competitive root colonisation.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF281148; AAF97803.1; -
DR InterPro: IPR000283; Complex1_75K.
DR PROSITE: PS00641; COMPLEX1_75K_1; 1.
DR PROSITE: PS00642; COMPLEX1_75K_2; 1.
DR PROSITE: PS00643; COMPLEX1_75K_3; 1.
KW SEQUENCE 904 AA; 98157 MW; C25E86C6D4DFA57 CRC64;

Query Match 36.6%; Score 50.5; DB 2; Length 904;
Best Local Similarity 50.0%; Pred. No. 63;
Matches 11; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

QY 1 NMAAORYGRELRRMSDEFGS 22
||| :|||: |||: |||
Db 236 NISGERYG-ELRRLENRFNGS 256

RESULT 14
Q37056 PRELIMINARY; PRT; 283 AA.
ID Q37056;
AC Q37056;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
GN CHV.
OS Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
OC Viruses; Retroviruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11723;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SIVAGMIPR185;
RX MEDLINE-98343740; PubMed-9680146;
RA van Rensburg E.J., Engelbrecht S., Mwenda J., Laten J.D., Robson B.A.,
RA Standen J., Chege G.K.;
RT "Simian immunodeficiency viruses (SIVs) from eastern and southern
RT Africa: detection of a SIVagm variant from a chacma baboon.";
RL J. Gen. Virol. 79:1809-1814(1998).
DR EMBL: AF015909; AAC59621.1; -
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR AIDS; Coat protein; Glycoprotein.
FT NON_TER 1
FT TER 283
KW AIDS; Coat protein; Glycoprotein.
KW SEQUENCE 283 AA; 32477 MW; 49ED5450188A2871 CRC64;

Query Match 36.2%; Score 50; DB 15; Length 283;
Best Local Similarity 42.9%; Pred. No. 20;
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 5 AORYGRELRRMSDEFGSK 25
||| :|||: |||: |||
Db 74 SOKYNLRQAQSCHFQGMWG 94

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RESULT 15
O9HNZ9 PRELIMINARY: PRT: 374 AA.
AC O9HNZ9.
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT 01-OCT-2001 (TREMblrel. 18, Last annotation update)
DE SPERMIDINE/PUTRESCINE ABC TRANSPORTER.
GN POTAZ OR VNG1871G.
OS Halobacterium sp. (Strain NRC-1).
OC Archaea: Euryarchaeota: Halobacteriales: Halobacteriaceae:
OC Halobacterium
CX NCBI_TaxID=64091;
RN {1}
RP SEQUENCE FROM N.A.
RX MEDLINE=20504483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Bergquist B., Pan M.,
RA Shukla H.D., Laskey S.R., Baliga N.S., Thorson V., Shrogha J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Weir R., Goo Y.A.,
RA Leithauer B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudis J.L., Jung K.-H.,
RA Alam M., Freltas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ebnhardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassa S.,
RT "Genome sequence of Halobacterium species NRC-1."
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
CC -1- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
  (ABC TRANSPORTERS).
DR EMBL: AE005086; ANG2071.1; -.
DR InterPro: IPR003593; AAA.
DR InterPro: IPR003439; ABC_transport.
DR InterPro: IPR001687; ATP_GTP_A.
DR Pfam: PF00005; ABC_tran; 1.
DR SMART: SM00382; AAA; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
KM ATP-binding, Complete proteome: Transport.
SO SEQUENCE 374 AA; 39190 MW; 1442EF7823037E16 CRC64;

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Query Match 36.2%; Score 50; DB 17; Length 374;
Best Local Similarity 76.9%; Pred. No. 27;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 11 ELRRMSDEFEGSF 23
DB 197 ELRRLSDAVESGF 209

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Search completed: September 20, 2002, 11:03:36
 Job time: 1653 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 20, 2002, 10:35:57 : Search time 228.86 Seconds
(without alignments)
13.104 Million cell updates/sec

Title: US-09-544-664-14

Sequence: 1 QEDIRNRIARHLAQVDSMDRSPPL 27

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

1: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT:*
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22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	137	100.0	27	21	AA1980.DAT
2	137	100.0	135	21	AA1981.DAT
3	137	100.0	140	21	AA1982.DAT
4	137	100.0	194	22	AA1983.DAT
5	137	100.0	195	19	AA1984.DAT
6	137	100.0	195	20	AA1985.DAT
7	137	100.0	195	20	AA1986.DAT
8	137	100.0	195	21	AA1987.DAT
9	137	100.0	200	19	AA1988.DAT
10	137	100.0	26	21	AA1989.DAT
11	121	88.3	26	22	AA1990.DAT

12	113	82.5	29	19	AA1980.DAT
13	99	72.3	27	21	AA1981.DAT
14	99	72.3	32	21	AA1982.DAT
15	99	72.3	33	19	AA1983.DAT
16	99	72.3	44	19	AA1984.DAT
17	99	72.3	55	19	AA1985.DAT
18	99	72.3	122	21	AA1986.DAT
19	99	72.3	136	21	AA1987.DAT
20	99	72.3	195	21	AA1988.DAT
21	99	72.3	195	21	AA1989.DAT
22	99	72.3	195	22	AA1990.DAT
23	98	71.5	195	22	AA1991.DAT
24	81	59.1	16	20	AA1992.DAT
25	81	59.1	16	21	AA1993.DAT
26	77	56.2	20	19	AA1994.DAT
27	77	56.2	20	19	AA1995.DAT
28	77	56.2	20	19	AA1996.DAT
29	74	54.0	15	22	AA1997.DAT
30	66	48.2	15	22	AA1998.DAT
31	66	48.2	15	22	AA1999.DAT
32	66	48.2	15	20	AA2000.DAT
33	66	48.2	16	21	AA2001.DAT
34	66	48.2	16	21	AA2002.DAT
35	66	48.2	16	21	AA2003.DAT
36	57	41.6	13	22	AA2004.DAT
37	57	41.6	20	22	AA2005.DAT
38	51	37.2	251	22	AA2006.DAT
39	50	36.5	359	22	AA2007.DAT
40	49	35.8	939	22	AA2008.DAT
41	48	35.0	617	22	AA2009.DAT
42	47	34.3	416	21	AA2010.DAT
43	47	34.3	416	21	AA2011.DAT
44	47	34.3	416	21	AA2012.DAT
45	47	34.3	429	21	AA2013.DAT

ALIGNMENTS

RESULT 1

AA1980.DAT standard: peptide: 27 AA.

AA1981.DAT:

28-FEB-2001 (first entry)

Bcl2 polypeptide BH3 domain peptide #14.

Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;
cardiac; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;
apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;
colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;
melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
stroke; myocardial infarction.

Homo sapiens.

WO200059526-A1.

12-OCT-2000.

06-APR-2000; 2000MO-US09352.

07-APR-1999; 99US-0128202.

(UYJE-) UNIV JEFFERSON THOMAS.

Huang Z, Wang J, Zhang Z, Shan S, Lu Z;

WPI: 2000-679325/66.

New peptide conjugates for modulating apoptosis or for inhibiting B

BH3 interacting do
Bcl2 polypeptide B
Mouse BID BH3 doma
Mouse BID truncate
Tat-BH3 fusion pro
Mouse BID truncate
Mouse BID truncate
Amino acid sequenc
Mouse BH3 interact
Human bcl-2-like p
Human BID BH3 doma
Bcl2 polypeptide B
Mouse BID BH3 doma
Tat-BID fusion pro
BH3 domain of Bid
Mouse BID BH3 doma
Mouse BID BH3 doma
Bcl2 polypeptide B
Peptide SEQ ID NO:
Human Bcl-2-like p
Mouse Bcl-2-like p
Drosophila melanog
Drosophila melanog
Novel human diagno
Arabidopsis thaliana
Arabidopsis thaliana
Arabidopsis thaliana

PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for
 PT treating neurodegenerative disorders, stroke, or cancer
 PS Claim 18: Page 18: 74pp: English.
 XX
 CC The invention relates to a peptide conjugate having the formula:
 CC (R-X)-peptide where n = 1-10; X = C=O, when the R-X group is attached
 CC to the N-terminus of the peptide, or a side chain of the peptide where
 CC the functional group of the side chain is NH₂ or OH; or X = O or NH,
 CC when the R-X group is attached to the C-terminus of the peptide, or a
 CC side chain of the peptide, where the side chain functional group is COOH
 CC or CONH₂; and R = 2-18C alkyl or alkoxy, 2-14C alkenyl optionally
 CC or two double bonds, cyclohexyl, cyclopentyl, cyclohexyl optionally
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain
 CC alkyl group, or benzyl. The peptides AAB37001-837058 represent examples
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of
 CC the Bcl-2 domain of the cell death agonist Bcl-2. The peptide conjugate is
 CC useful for modulating apoptosis in the cells of a subject, or for
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockade of
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2
 CC function. In particular, the peptide conjugate is useful for treating a
 CC subject afflicted with a cancer characterized by cancer cells that
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric,
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
 CC conjugate is also useful for treating disorders characterized by
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
 XX
 SQ Sequence 27 AA:
 Query Match 100.0%; Score 137; DB 21; Length 27;
 Best Local Similarity 100.0%; Pred. No. 9, 5e-15;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QEDIRNIRARHQAQVDSMDRSIPPL 27
 DB 1 qedirnarhraqvdsmdrsippl 27
 RESULT 2
 AAY84017 standard; protein: 135 AA.
 XX
 AC AAY84017;
 XX
 DT 03-JUL-2000 (first entry)
 XX
 DE Amino acid sequence of human p15 BID polypeptide.
 XX
 KW p15 BID: cell death agonist; tumour necrosis factor; FAS signalling;
 KW cytochrome C.
 XX
 OS Homo sapiens.
 XX
 PN W0200011162-A1.
 XX
 PD 02-MAR-2000.
 XX
 PF 28-JUL-1999; 99WO-US16966.
 XX
 PR 19-AUG-1998; 98US-0136879.
 PR 20-AUG-1998; 98US-0137038.
 XX
 PA (UNIW) UNIV WASHINGTON.
 XX
 PI Gross A, Korsmeyer SJ;
 XX
 DR WPI: 2000-224697/19.
 XX

PT Human and murine p15 BID polypeptides with cell death agonist activity
 PT are produced by caspase cleavage of BID in cells undergoing FAS or
 PT tumour necrosis mediated cell death, useful as modulators of target cell
 PT death -
 XX
 PS Claim 27: Fig 2A; 55pp: English.
 XX
 CC The present sequence represents a human p15 BID polypeptide. p15 BID
 CC polypeptides have cell death agonist activity. Cell death mediated by
 CC tumour necrosis factor (TNF) and FAS signalling pathways includes the
 CC generation of p15 BID, which is translocated to the mitochondria where
 CC it exerts cell death agonist activity, probably by inducing release of
 CC cytochrome C. The p15 BID polypeptides are useful in methods for
 CC modulating death of a target cell. Mutants of p15 BID, comprising an
 CC inactivating mutation in the BH3 domain, are used in methods for
 CC inhibiting death of a target cell. Agents that specifically inhibit
 CC caspase cleavage of p22 BID at the p15 cleavage site are also useful
 CC for inhibiting death of a target cell.
 XX
 SQ Sequence 135 AA:
 Query Match 100.0%; Score 137; DB 21; Length 135;
 Best Local Similarity 100.0%; Pred. No. 5, 9e-14;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QEDIRNIRARHQAQVDSMDRSIPPL 27
 DB 19 qedirnarhraqvdsmdrsippl 45
 RESULT 3
 AAY84018 standard; protein: 140 AA.
 XX
 AC AAY84018;
 XX
 DT 03-JUL-2000 (first entry)
 XX
 DE Amino acid sequence of human variant of p15 BID polypeptide.
 XX
 KW p15 BID: cell death agonist; tumour necrosis factor; FAS signalling;
 KW cytochrome C.
 XX
 OS Homo sapiens.
 XX
 PN W0200011162-A1.
 XX
 PD 02-MAR-2000.
 XX
 PF 28-JUL-1999; 99WO-US16966.
 XX
 PR 19-AUG-1998; 98US-0136879.
 PR 20-AUG-1998; 98US-0137038.
 XX
 PA (UNIW) UNIV WASHINGTON.
 XX
 PI Gross A, Korsmeyer SJ;
 XX
 DR WPI: 2000-224697/19.
 XX
 PF Human and murine p15 BID polypeptides with cell death agonist activity
 PT are produced by caspase cleavage of BID in cells undergoing FAS or
 PT tumour necrosis mediated cell death, useful as modulators of target cell
 PT death -
 XX
 PS Claim 27: Fig 2B; 55pp: English.
 XX
 CC The present sequence represents a variant of p15 BID polypeptide. p15 BID
 CC polypeptides have cell death agonist activity. Cell death mediated by
 CC tumour necrosis factor (TNF) and FAS signalling pathways includes the
 CC generation of p15 BID, which is translocated to the mitochondria where
 CC it exerts cell death agonist activity, probably by inducing release of
 CC cytochrome C. The p15 BID polypeptides are useful in methods for
 CC modulating death of a target cell. Mutants of p15 BID, comprising an
 CC inactivating mutation in the BH3 domain, are used in methods for
 CC inhibiting death of a target cell. Agents that specifically inhibit
 CC caspase cleavage of p22 BID at the p15 cleavage site are also useful
 CC for inhibiting death of a target cell.

CC cytochrome C. The p15 BID polypeptides are useful in methods for
 CC modulating death of a target cell. Mutants of p15 BID, comprising an
 CC inactivating mutation in the BH3 domain, are used in methods for
 CC inhibiting death of a target cell. Agents that specifically inhibit
 CC caspase cleavage of p22 BID at the p15 cleavage site are also useful
 CC for inhibiting death of a target cell.

XX Sequence 140 AA:

Query Match 100.0%; Score 137; DB 21; Length 140;
 Best Local Similarity 100.0%; Pred. No. 6, 1e-14;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QEDIRNIRARHLAQQVDSMDRSIPGL 27
 DB 19 qedirnarhlraqvdsmdrsippgl 45

RESULT 4
 ID AAE09570 standard; Protein: 194 AA.

XX AAE09570:
 XX 19-NOV-2001 (first entry)

DE Human pro-BID sequence.

XX Negative selection: cytotoxic agent; cytostatic agent; cancer:
 KW human; pro-BID; BH3 Interacting Domain Death Agonist;
 KW HT29; colon cancer cell.

OS Homo sapiens.

XX Key Location/Qualifiers
 FT 55..56 /note= "Caspase 8 cleavage site"

FT 33..194 /label= BID_clone_#1
 FT /note= "This fragment serves as a cytotoxic agent
 and is specifically claimed in claim 55"

FT 76..194 /label= BID_clone_#2
 FT /note= "This fragment serves as a cytotoxic agent
 and is specifically claimed in claim 56"

FT 89..97 /label= BH3-domain
 FT /note= "Bcl-2 homology domain"

XX Domain

XX WO200161346-A2.

XX 23-AUG-2001.

XX 14-FEB-2001; 2001WO-US04750.

XX 15-FEB-2000; 2000US-0504132.

XX (ARCA-) ARCARIS INC.

XX Kamb CA, Caponigro GM;

XX WPI; 2001-541660/60.

XX Negative selection of cells for the identification of cytostatic or
 XX cytotoxic agents -

XX Claim 55; Fig 9A; 75pp; English.

XX The invention relates to a method for negative selection assay that
 CC comprises introducing a genetic library encoding putative cytotoxic
 CC agent into a population of target cells, plating the cells on
 CC a surface, collecting a subpopulation of the cells that disattach from

CC the surface for a period of time and recovering a first pool of genetic
 CC material from the subpopulation. The method is useful to identify
 CC cytostatic or cytotoxic agents that cause a lethal phenotype. The method
 CC is also useful to identify conditional cytotoxicity and cell specific
 CC cytotoxicity. The cytostatic or cytotoxic agents are useful in the
 CC treatment of cancer and other diseases involving abnormal cell
 CC proliferation. The present sequence is human pro-BID (BH3 interacting
 CC domain Death Agonist) protein. Peptide fragments of BID referred as
 CC clones #1 and #2 are identified as cytotoxic agents by negative
 CC selection of HT29 colon cancer cells.

XX Sequence 194 AA:

Query Match 100.0%; Score 137; DB 22; Length 194;
 Best Local Similarity 100.0%; Pred. No. 6, 8e-14;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QEDIRNIRARHLAQQVDSMDRSIPGL 27
 DB 78 qedirnarhlraqvdsmdrsippgl 104

RESULT 5
 ID AAW50254 standard; Protein: 195 AA.

XX AAW50254:
 XX 20-JUL-1998 (first entry)

DE Human BH3 interacting domain death agonist protein.

XX Human; BH3 interacting domain death agonist; BID; Bcl-2 family;
 KW apoptosis; regulation; cell death; inflammation; cancer; arthritis;
 KW autoimmune disease; viral infection; lymphoproliferative.

OS Homo sapiens.

XX Key Location/Qualifiers
 FT 166 /note= "encoded by TTGC"

FT 175 /note= "encoded by GT"

XX W09809980-A1.

XX 12-MAR-1998.

XX 09-SEP-1997; 97WO-US15872.

XX 09-SEP-1996; 96US-0706741.

XX (UNITW) UNIV WASHINGTON.

XX Korsmeyer SJ;

XX WPI; 1998-193546/17.

XX N-PSDB; AAV22145.

XX BH3 interacting domain death agonist polypeptide - used for treating
 XX decreased apoptotic conditions resulting from inflammation etc.

XX Claim 3; Page 68-69; 118pp; English.

XX The present sequence represents a BH3 interacting domain death agonist
 CC (BID) protein given in the present invention. The protein, the DNA
 CC encoding it or antisense sequences can be used for preventing or treating
 CC a decreased apoptotic state of a cell. The decreased apoptotic state that
 CC is treated results from a disease such as cancer, viral infections,
 CC lymphoproliferative conditions, arthritis, inflammation and autoimmune
 CC diseases. Antibodies against the BID protein can be used for detecting a
 CC BID polypeptide in a cell or population of cell. The nucleic acid

sequence and the BID protein can also be used for treating immunodeficiency diseases (including AIDS), senescence, neurodegenerative disease, ischemic and reperfusion cell death, infertility and the BID wound-healing. Primers derived from the nucleic acid encoding the BID protein can be used for detecting/quantitating the protein and for detecting alterations in the nucleic acid encoding the BID protein.

Sequence 195 AA:

Query Match 100.0%: Score 137; DB 19; Length 195;
Best Local Similarity 100.0%: Pred. No. 8, 9e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QEDIRRIARHLAOGVDSMDRSIPGL 27
DB 79 qedirriarhlavqgdmsdrisipgl 105

RESULT 6
ID AAY05417 standard; peptide: 195 AA.
XX
XX AAY05417;

DT 02-JUL-1999 (first entry)
XX
XX HIV-1 Tat 1 protein.

DE BH3 domain; cell death agonist; bcl homology domain; BCL-2 family;
XX apoptosis promoter; cancer cell; virus infected cell; inflammation;
KW autoantibody producing cell; cancer; lymphoproliferative condition;
KW arthritis; autoimmune disease; therapy;
XX
XX

OS Human immunodeficiency virus type 1.
XX
XX

PN MO9916787-A1.
XX
XX

PD 08-APR-1999.
XX
XX

PF 22-SEP-1998; 98MO-US19765.
XX
XX

PR 07-OCT-1997; 97US-0946039.
XX
XX 26-SEP-1997; 97US-0060133.

PA (UNIM) UNIV WASHINGTON.
XX
XX

PI Korsemyer SJ;
XX
XX

DR WPI: 1999-255058/21.
XX
XX

PT Bcl homology domain 3 polypeptide
XX
XX

PS Example 10; Page 62; 104pp; English.
XX
XX

CC This sequence represents the HIV-1 Tat 1 protein.
CC The invention relates to a bcl homology domain 3 (BH3 domain),
CC derived from a proapoptotic member of the Bcl-2 family. The
CC BH3 polypeptide can be used in a method for promoting apoptosis in a
CC target cell, especially where the cell is a cancer cell, a virus infected
CC cell or an autoantibody producing cell. The BH3 polypeptide can be used
CC in therapeutic compositions for treating disease including cancer, other
CC lymphoproliferative conditions, arthritis, inflammation, and autoimmune
CC diseases, which may result from the down regulation of cell death
CC regulation.
XX
XX

Sequence 195 AA:

Query Match 100.0%: Score 137; DB 20; Length 195;
Best Local Similarity 100.0%: Pred. No. 8, 9e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QEDIRRIARHLAOGVDSMDRSIPGL 27
DB 79 qedirriarhlavqgdmsdrisipgl 105

RESULT 7

ID AAM67837 standard; Protein: 195 AA.
XX
XX AAM67837;

DT 25-MAR-1999 (first entry)
XX
XX

DE Human secreted protein encoded by gene 31 clone H17BX31.
XX
XX

KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
XX

OS Homo sapiens.
XX
XX

PN MO9842738-A1.
XX
XX

PD 01-OCT-1998.
XX
XX

PF 19-MAR-1998; 98MO-US05311.
XX
XX

PR 30-MAY-1997; 97US-0050937.
XX
XX 21-MAR-1997; 97US-0041276.

PR 21-MAR-1997; 97US-0041277.
XX
XX 21-MAR-1997; 97US-0041281.

PR 21-MAR-1997; 97US-0042344.
XX
XX 30-MAY-1997; 97US-0048069.

PR 30-MAY-1997; 97US-0048094.
XX
XX 30-MAY-1997; 97US-0048096.

PR 30-MAY-1997; 97US-0048096.
XX
XX 30-MAY-1997; 97US-0048131.

PR 30-MAY-1997; 97US-0048135.
XX
XX 30-MAY-1997; 97US-0048124.

PR 30-MAY-1997; 97US-0048160.
XX
XX 30-MAY-1997; 97US-0048186.

PR 30-MAY-1997; 97US-0048187.
XX
XX 30-MAY-1997; 97US-0048188.

PR 30-MAY-1997; 97US-0048350.
XX
XX 30-MAY-1997; 97US-0048351.

PR 30-MAY-1997; 97US-0048352.
XX
XX 30-MAY-1997; 97US-0048355.

PR 05-AUG-1997; 97US-0054804.
XX
XX

PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX

PI Brener LA, Duan R, Epler R, Ferrle AM, Florence KA;
XX
XX Greene JA, Hu JS, Lafleur DM, Moore PA, Nl J, Olsen HS;

PI Rosen CA, Ruben SM, Shi Y, Young P;
XX
XX

DR WPI: 1999-070066/06.
XX
XX

DR N-PSDB; AAX00641.
XX
XX

PT New isolated human genes and the secreted polypeptides they encode
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders
XX
XX

PS Claim 11; Page 288-289; 385pp; English.
XX
XX This sequence represents a secreted human protein encoded by the gene
XX clone detailed in the descriptor line. The gene can be used to generate
XX fusion proteins by linking to the gene to a human immunoglobulin Fc

CC protein can be used for detecting/quantitating the protein and for
 CC detecting alterations in the nucleic acid encoding the BID protein.
 XX
 SQ Sequence 200 AA;

Query Match 100.0%; Score 137; DB 19; Length 200;
 Best Local Similarity 100.0%; Pred. No. 9.1e-14;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QEDIRNARHLAOGVDSMDRSIPGL 27
 Db 79 qedlrnarhlavqgdmsdrslppgl 105

RESULT 10
 AAY96325 standard; Peptide: 26 AA.
 XX
 AC AAY96325;
 XX
 DT 17-AUG-2000 (first entry)
 XX
 DE Mammalian Bcl-2 homology domain 3 domain.
 XX
 KW Mammal; apoptosis; cell death; BRC3; apoptosis promotion; Bid;
 KW apoptosis inhibition; malignant cell; autoimmune disease.
 XX
 OS Mammalia.
 XX
 PN WO200026228-A1.
 XX
 PD 11-MAY-2000.
 XX
 PF 28-OCT-1999; 99WO-US25285.
 XX
 PR 02-NOV-1998; 98US-0184168.
 XX
 PA (CLON-) CLONTECH LAB INC.
 XX
 PI Zhu L, Yin X, Chittenden T;
 XX
 DR WPI: 2000-365560/31.
 XX
 PT Novel polynucleotide encoding a BRC3 protein which is useful for
 PT modulating apoptosis, especially in the treatment of cancer and
 PT autoimmune diseases.
 XX
 PS Disclosure: Fig 4; 47pp; English.
 XX
 CC The present sequence is the mammalian Bid Bcl-2 homology domain 3
 CC (BH3) domain, which was used in a sequence alignment with the same
 CC domain of a putative version of the mammalian apoptosis
 CC regulator BRC3, which was designated BRC3-ORF2. The BRC3 protein,
 CC nucleic acids and antibodies are suitable for use in promoting cell
 CC death or for preventing apoptosis in malignant cells and those causing
 CC autoimmune diseases.
 XX
 SQ Sequence 26 AA;

Query Match 88.3%; Score 121; DB 21; Length 26;
 Best Local Similarity 100.0%; Pred. No. 3.2e-12;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 IIRNARHLAOGVDSMDRSIPGL 27
 Db 1 ilrnlarhlavqgdmsdrslppgl 24

RESULT 11
 AAB70375 standard; Peptide: 26 AA.
 ID AAB70375

XX
 AC AAB70375;
 XX
 DT 02-MAY-2001 (first entry)
 XX
 DE BID BH3 consensus peptide sequence SEQ ID NO:8.
 KW Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;
 KW immunostimulant; neuroprotective; neurotropic; antischismic; vulnery;
 KW cytosolic; antiviral; antitumor; antineoplastic; wound healing;
 KW immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;
 KW immunodeficiency disease; neurodegenerative disease; viral infection;
 KW ischaemic cell death; reperfusion cell death; arthritis; infertility;
 KW lymphoproliferative condition; inflammation; autoimmune disease.
 XX
 OS Unidentified.
 XX
 PN WO200110888-A1.
 XX
 PD 15-FEB-2001.
 XX
 PE 30-MAY-2000; 2000WO-US11864.
 XX
 PF 28-MAY-1999; 99US-0136783.
 XX
 PR (APOP-) APOPTOSIS TECHNOLOGY INC.
 XX
 PA Zhou X;
 XX
 PI WPI: 2001-138734/14.
 XX
 DR New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,
 PT useful for screening for candidate compounds which induce or inhibit
 PT apoptosis, comprises amino acid substitutions at Ser118, Ser135 or
 PT Ser113.
 XX
 PS Example 2; Fig 3a; 157pp; English.
 XX
 CC The present invention describes an isolated or synthetic polypeptide
 CC (1) comprising a less than full length amino acid sequence of a mutant
 CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its
 CC fragment, which contains amino acid substitutions at Ser118 of a human
 CC BAD, Ser135 of a murine BAD (longer murine BAD) or Ser113 of a murine
 CC BAD (shorter murine BAD). (1) has immunostimulant, neuroprotective,
 CC neurotropic, antischismic, vulnery, antineoplastic, antitumor, and
 CC antitumor, antitumor, antitumor, antitumor, antitumor, antitumor,
 CC can be used as an apoptosis inducer or inhibitor. BAD polypeptides and
 CC polynucleotides can be used for screening candidate compounds and drugs
 CC for activity that promote cell survival of apoptosis. Other uses include
 CC inducing or inhibiting apoptosis in a cell. Candidate compounds
 CC identified and (mutant) BAD polypeptides are useful in treating
 CC immunodeficiency diseases, neurodegenerative diseases, ischaemic cell
 CC death, reperfusion cell death, wound healing, cancer, viral infections,
 CC lymphoproliferative conditions, arthritis, infertility, inflammation and
 CC autoimmune diseases. The present sequence represents a Bcl-family member
 CC BH3 domain consensus sequence which is used in an example from the
 CC present invention.
 XX
 SQ Sequence 26 AA;

Query Match 88.3%; Score 121; DB 22; Length 26;
 Best Local Similarity 100.0%; Pred. No. 3.2e-12;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 IIRNARHLAOGVDSMDRSIPGL 27
 Db 1 ilrnlarhlavqgdmsdrslppgl 24

RESULT 12
 AAM50273 standard; Peptide: 29 AA.
 ID AAM50273

XX AC AAM50273;
 XX XX 20-JUL-1998 (first entry)
 XX XX
 DE BH3 interacting domain death agonist epitope 33.
 XX XX
 KW Human: BH3 interacting domain death agonist; BID; Bcl-2 family;
 KW apoptosis; regulation; cell death; inflammation; cancer; arthritis;
 KW autoimmune disease; viral infection; lymphoproliferative.
 XX XX
 OS Homo sapiens.
 XX PN M098090980-A1.
 XX PD 12-MAR-1998.
 XX PF 09-SEP-1997; 97MO-US15872.
 XX PR 09-SEP-1996; 96US-0706741.
 XX PA (UNIV) UNIV WASHINGTON.
 XX PI Korsmeyer SJ;
 XX DR WPI: 1998-193546/17.
 XX PT BH3 interacting domain death agonist polypeptide - used for treating
 XX PT decreased apoptotic conditions resulting from inflammation etc.
 XX PS Disclosure: Page 24; 118pp; English.
 XX XX
 CC The present sequence represents a BH3 interacting domain death
 CC agonist (BID) polypeptide that is useful for treating conditions
 CC associated with apoptosis, such as cancer, viral infections, and
 CC protein, the DNA encoding it, or antisense sequences can be used for
 CC preventing or treating a decreased apoptotic state of a cell. The
 CC decreased apoptotic state that is treated results from a disease such as
 CC cancer, viral infections, lymphoproliferative conditions, arthritis,
 CC inflammation and autoimmune diseases. Antibodies against the BID protein
 CC can be used for detecting a BID polypeptide in a cell or population of
 CC cells. The nucleic acid sequence and the BID protein can also be used for
 CC treating immunodeficiency disease (including AIDS), senescence,
 CC neurodegenerative disease, ischemic and reperfusion cell death,
 CC infertility and wound-healing. Primers derived from the nucleic acid
 CC encoding the BID protein can be used for detecting/quantitating the
 CC protein and for detecting alterations in the nucleic acid encoding the
 CC BID protein.
 CC XX
 SQ Sequence 29 AA:
 Query Match 82.5%; Score 113; DB 19; Length 29;
 Best Local Similarity 100.0%; Pred. No. 6; 3e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 RNIAHRLAAGVDSMDRSPGL 27
 DB 1 IRIARHRLAQVDSMDRSPGL 22
 RESULT 13
 AAB37015
 ID AAB37015 standard; peptide: 27 AA.
 XX AAB37015;
 AC AAB37015;
 XX XX
 DE 28-FEB-2001 (first entry)
 XX XX
 DE Bcl2 polypeptide BH3 domain peptide #15.
 XX XX
 KW Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;
 KW cardiac; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;
 KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;
 KW KM

KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;
 KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
 KW stroke; myocardial infarction.
 XX XX
 OS Homo sapiens.
 XX PN M0200059526-A1.
 XX PD 12-OCT-2000.
 XX PF 06-APR-2000; 2000MO-US09352.
 XX PR 07-APR-1999; 99US-0128202.
 XX PA (UNIV) UNIV JEFFERSON THOMAS.
 XX XX
 DE Huang Z, Wang J, Zhang Z, Shan S, Lu Z;
 XX XX
 XX WPI: 2000-679325/66.
 XX PT New peptide conjugates for modulating apoptosis or for inhibiting B
 XX PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for
 XX PT treating neurodegenerative disorders, stroke, or cancer -
 XX PS Claim 18; Page 18; 74pp; English.
 XX XX
 CC The invention relates to a peptide conjugate having the formula:
 CC (R-X)n-peptide where n = 1-10; X = C=O, when the R-X group is attached
 CC to the N-terminus of the peptide, or a side chain of the peptide where
 CC the functional group of the side chain is NH2 or OH; or X = O or NH,
 CC when the R-X group is attached to the C-terminus of the peptide, or a
 CC side chain of the peptide, where the side chain functional group is COOH
 CC or CONH2; and R = a C-2-18C alkyl or alkoxy; 2-10C aryl; or a C-2-10C
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain
 CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent analogues
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of
 CC the BH3 domain of the cell death agonist Bad. The peptide conjugate is
 CC useful for modulating apoptosis in the cells of a subject, or for
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2
 CC function. In particular, the peptide conjugate is useful for treating a
 CC subject afflicted with a cancer characterized by cancer cells that
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric,
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
 CC conjugate is also useful for treating disorders characterized by
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
 CC XX
 SQ Sequence 27 AA:
 Query Match 72.3%; Score 99; DB 21; Length 27;
 Best Local Similarity 70.4%; Pred. No. 1; 1e-08;
 Matches 19; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 QY 1 QEDIIIRHRLAAGVDSMDRSPGL 27
 DB 1 QEEIIIRHRLAQVDSMDRSPGL 27
 RESULT 14
 AAM50264
 ID AAM50264 standard; peptide: 32 AA.
 XX AAM50264;
 AC AAM50264;
 XX XX
 DE 20-JUL-1998 (first entry)
 XX XX
 DE Mouse BID BH3 domain peptide A.

Fri Sep 20 11:03:04 2002

us-09-544-664-14.rat

age 1

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OM protein - protein search, using sw model

Run on: September 20, 2002, 10:37:19 ; Search time 75.64 seconds
(without alignments)
8,719 Million cell updates/sec

Title: US-09-544-664-14
Perfect score: 137
Sequence: 1 QEDIRNIAHRLAQVDSMDRSIPGL 27

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	137	100.0	135	4	US-09-136-879-3
2	137	100.0	140	4	US-09-136-879-4
3	137	100.0	195	2	US-08-706-741B-4
4	137	100.0	195	2	US-08-924-695A-4
5	137	100.0	195	4	US-09-136-879-5
6	137	100.0	200	2	US-08-924-695A-5
7	137	100.0	200	2	US-08-706-741B-5
8	113	82.5	29	2	US-08-706-741B-13
9	113	82.5	29	2	US-08-924-695A-13
10	99	72.3	32	2	US-08-706-741B-55
11	99	72.3	32	2	US-08-924-695A-55
12	99	72.3	33	2	US-08-706-741B-55
13	99	72.3	33	2	US-08-924-695A-53
14	99	72.3	44	2	US-08-706-741B-56
15	99	72.3	44	2	US-08-924-695A-56
16	99	72.3	55	2	US-08-706-741B-52
17	99	72.3	55	2	US-08-924-695A-52
18	99	72.3	122	2	US-08-706-741B-51
19	99	72.3	122	2	US-08-924-695A-51
20	99	72.3	136	4	US-09-136-879-5
21	99	72.3	136	4	US-08-706-741B-6
22	99	72.3	195	2	US-08-924-695A-6
23	99	72.3	195	4	US-09-136-879-2
24	99	72.3	20	2	US-08-706-741B-85
25	99	72.3	20	2	US-08-924-695A-85
26	99	72.3	32	2	US-08-706-741B-85
27	99	72.3	32	2	US-08-924-695A-87

28	66	48.2	15	2	US-08-706-741B-86	Sequence 86, Appl
29	66	48.2	15	2	US-08-924-695A-86	Sequence 86, Appl
30	66	48.2	27	2	US-08-706-741B-88	Sequence 88, Appl
31	66	48.2	27	2	US-08-924-695A-88	Sequence 88, Appl
32	53	38.7	13	2	US-08-706-741B-45	Sequence 45, Appl
33	53	38.7	13	2	US-08-924-695A-45	Sequence 45, Appl
34	45	32.1	9	2	US-09-081-320-11	Sequence 11, Appl
35	44	32.1	9	2	US-08-706-741B-8	Sequence 8, Appl
36	44	32.1	9	2	US-08-924-695A-8	Sequence 8, Appl
37	43.5	31.8	367	3	US-08-803-286B-2	Sequence 2, Appl
38	43.5	31.8	901	2	US-08-804-281-5	Sequence 2, Appl
39	43.5	31.8	901	3	US-09-420-002-7	Sequence 7, Appl
40	43.5	31.8	968	4	US-09-418-540-7	Sequence 7, Appl
41	43.5	31.8	210	3	US-09-081-320-22	Sequence 22, Appl
42	43	31.4	416	3	US-09-100-664A-9	Sequence 9, Appl
43	42.5	31.0	1462	3	US-07-792-600-32	Sequence 31, Appl
44	41.5	30.3	1462	3	US-09-157-021-31	Sequence 31, Appl
45	41.5	30.3	1462	3	US-09-157-021-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1
US-09-136-879-3
; Sequence 3, Application US/09136879B
; Patent No. 6326354
; GENERAL INFORMATION:
; APPLICANT: Gross, Alan
; APPLICANT: Kormeyer, Stanley J.
; TITLE OF INVENTION: MODULATION OF APOPTOSIS WITH BID
; FILE REFERENCE: 60296285Replacement
; CURRENT APPLICATION NUMBER: US/09/136, 879B
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-136-879-3

Query Match 100.0%; Score 137; DB 4; Length 135;
Best local similarity 100.0%; Pred. No. 1.6e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QEDIRNIAHRLAQVDSMDRSIPGL 27
DB 19 QEDIRNIAHRLAQVDSMDRSIPGL 45

RESULT 2
US-09-136-879-4
; Sequence 4, Application US/09136879B
; Patent No. 6326354
; GENERAL INFORMATION:
; APPLICANT: Gross, Alan
; APPLICANT: Kormeyer, Stanley J.
; TITLE OF INVENTION: MODULATION OF APOPTOSIS WITH BID
; FILE REFERENCE: 60296285Replacement
; CURRENT APPLICATION NUMBER: US/09/136, 879B
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 140
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-136-879-4

Query Match 100.0%; Score 137; DB 4; Length 140;

Best Local Similarity 100.0%; Pred. No. 1.7e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QEDIRNIAHRLA0VGDSDMSRIPGL 27
DB 19 QEDIRNIAHRLA0VGDSDMSRIPGL 45

RESULT 3
US-08-706-741B-4
Sequence 4, Application US/08706741B
Patent No. 5955593
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESSES:
ADDRESS: HOMELL & HAFERKAMP, L.C.
STREET: 7733 FORSTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63146

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/706,741B
FILING DATE: 09-SEP-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 195 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
US-08-706-741B-4

Query Match 100.0%; Score 137; DB 2; Length 195;
Best Local Similarity 100.0%; Pred. No. 2.5e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QEDIRNIAHRLA0VGDSDMSRIPGL 27
DB 79 QEDIRNIAHRLA0VGDSDMSRIPGL 105

RESULT 4
US-08-924-695A-4
Sequence 4, Application US/08924695A
Patent No. 5998583
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESSES:
ADDRESS: HOMELL & HAFERKAMP, L.C.
STREET: 7733 FORSTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/924,695A
FILING DATE: 09-SEP-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 971798
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 195 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
US-08-924-695A-4

Query Match 100.0%; Score 137; DB 2; Length 195;
Best Local Similarity 100.0%; Pred. No. 2.5e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QEDIRNIAHRLA0VGDSDMSRIPGL 27
DB 79 QEDIRNIAHRLA0VGDSDMSRIPGL 105

RESULT 5
US-09-136-879-1
Sequence 1, Application US/09136879B
Patent No. 6326354
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: MODULATION OF APOPTOSIS WITH BID
FILE REFERENCE: 60296283Replacement
CURRENT APPLICATION NUMBER: US/09/136,879B
FILING DATE: 1998-08-19
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patent Ver. 2.0
SEQ ID NO: 1
LENGTH: 195
TYPE: PRT
ORGANISM: Homo sapiens
US-09-136-879-1

Query Match 100.0%; Score 137; DB 4; Length 195;
Best Local Similarity 100.0%; Pred. No. 2.5e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QEDIRNIAHRLA0VGDSDMSRIPGL 27
DB 79 QEDIRNIAHRLA0VGDSDMSRIPGL 105

RESULT 6
US-08-706-741B-5
Sequence 5, Application US/08706741B
Patent No. 5955593
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESSES:

```

ADDRESS: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63146

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/706,741B
FILING DATE: 09-SEP-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 200 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-706-741B-5

Query Match      100.0%; Score 137; DB 2; Length 200;
Best Local Similarity 100.0%; Pred. No. 2.6e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 79 QEDIRNRIARLAOVGDSMDRISIPGL 105
QY 1 QEDIRNRIARLAOVGDSMDRISIPGL 27
|||||
|||||

RESULT 7
US-08-924-695A-5
Sequence 5, Application US/08924695A
Patent No. 5998583
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESS: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/924,695A
FILING DATE: 09-SEP-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-706-741B-33

Query Match      100.0%; Score 137; DB 2; Length 200;
Best Local Similarity 100.0%; Pred. No. 2.6e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 79 QEDIRNRIARLAOVGDSMDRISIPGL 105
QY 1 QEDIRNRIARLAOVGDSMDRISIPGL 27
|||||
|||||

RESULT 9
US-08-924-695A-33
Sequence 33, Application US/08924695A
Patent No. 5998583
GENERAL INFORMATION:

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SEQUENCE CHARACTERISTICS:
LENGTH: 200 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-924-695A-5

Query Match      100.0%; Score 137; DB 2; Length 200;
Best Local Similarity 100.0%; Pred. No. 2.6e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 79 QEDIRNRIARLAOVGDSMDRISIPGL 105
QY 1 QEDIRNRIARLAOVGDSMDRISIPGL 27
|||||
|||||

RESULT 8
US-08-706-741B-33
Sequence 33, Application US/08706741B
Patent No. 5955593
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESS: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63146
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/706,741B
FILING DATE: 09-SEP-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-706-741B-33

Query Match      82.5%; Score 113; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 6 RNIRARLAOVGDSMDRISIPGL 27
QY 1 RNIRARLAOVGDSMDRISIPGL 22
|||||
|||||

RESULT 9
US-08-924-695A-33
Sequence 33, Application US/08924695A
Patent No. 5998583
GENERAL INFORMATION:

```

APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/924,695A
FILING DATE: 09-SEP-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 971798
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-924-695A-33

Query Match 82.5%; Score 113; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 RNIAHRLAOGDSMDRSLPPGL 27
|||||
DB 1 RNIAHRLAOGDSMDRSLPPGL 22

RESULT 10
US-08-706-741B-55
Sequence 55; Application US/08706741B
Patent No. 5955593
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/706,741B
FILING DATE: 09-SEP-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965017

TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-706-741B-55

Query Match 72.3%; Score 99; DB 2; Length 32;
Best Local Similarity 70.4%; Pred. No. 3.3e-09;
Matches 19; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 QEDIIHRIARHLAOGDSMDRSLPPGL 27
||:|:| |||||:|:| ||:|:|
DB 5 QEDIIHRIARHLAOGDSMDRSLPPGL 31

RESULT 11
US-08-924-695A-55
Sequence 55; Application US/08924695A
Patent No. 5998583
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/924,695A
FILING DATE: 09-SEP-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 971798
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-924-695A-55

Query Match 72.3%; Score 99; DB 2; Length 32;
Best Local Similarity 70.4%; Pred. No. 3.3e-09;
Matches 19; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 QEDIIHRIARHLAOGDSMDRSLPPGL 27
||:|:| |||||:|:| ||:|:|
DB 5 QEDIIHRIARHLAOGDSMDRSLPPGL 31

RESULT 12

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US-08-706-741B-53
Sequence 53, Application US/08706741B
Patent No. 5955593
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63146
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/706,741B
FILING DATE: 09-SEP-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-706-741B-53

Query Match          72.3%; Score 99; DB 2; Length 33;
Best Local Similarity 70.4%; Pred. No. 3.4e-09;
Matches 19; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY      1 QEDIRNIAHLAQVGDSDMRISIPGL 27
        ||::||||||||::|||::|||
Db       6 QEETIHNIARHLAQIGDEMDHNIQPTL 32

RESULT 13
US-08-924-695A-53
Sequence 53, Application US/08924695A
Patent No. 5998583
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/924,695A
FILING DATE: 09-SEP-1997
CLASSIFICATION: 514

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[illegible]

Db 17 QEEIINHIAHLAQIGDEMDHNIQPTL 43

RESULT 15

US-08-924-695A-56
Sequence 56, Application US/08924695A

Patent No. 5998583

GENERAL INFORMATION:

APPLICANT: KORSMEYER, STANLEY J.

TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST

NUMBER OF SEQUENCES: 88

CORRESPONDENCE ADDRESS:

ADDRESSEE: HOWELL & HAERKAMP, L.C.

STREET: 7733 FORSYTH BLVD., SUITE 1400

CITY: ST. LOUIS

STATE: MISSOURI

COUNTRY: USA

ZIP: 63105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/924,695A

FILING DATE: 09-SEP-1997

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: HOLLAND, DONALD R.

REGISTRATION NUMBER: 35,197

REFERENCE/DOCKET NUMBER: 971798

TELECOMMUNICATION INFORMATION:

TELEPHONE: (314) 727-5188

TELEFAX: (314) 727-6092

INFORMATION FOR SEQ ID NO: 56:

SEQUENCE CHARACTERISTICS:

LENGTH: 44 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-924-695A-56

Query Match 72.3%; Score 99; DB 2; Length 44;

Best Local Similarity 70.4%; Pred. No. 4.7e-09;

Matches 19; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 QEDITRNIAHLAOGDSMDRSIPGL 27

Db 17 QEEIINHIAHLAQIGDEMDHNIQPTL 43

Search completed: September 20, 2002, 10:37:20
Job time: 408 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 20, 2002, 10:39:04 ; Search time 95.59 Seconds
(without alignments)
27.141 Million cell updates/sec

Title: US-09-544-664-14

Sequence: 137
1 DBDITRNIRHIAQVSDMSRIPQL 27

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 28338 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 28338

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Database :
1: PIR-71:*
2: PIR1:*
3: PIR2:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	41.6	457	2	F64095
2	51	37.2	183	2	T25102
3	48	35.0	401	2	T16661
4	48	35.0	849	2	D83285
5	47	34.3	273	2	C83182
6	47	34.3	416	2	C96725
7	46	33.3	1129	2	J00354
8	46	33.3	420	2	A82856
9	46	33.3	159	2	S75802
10	46	33.3	268	2	G75293
11	46	33.3	329	2	AF2445
12	46	33.3	365	2	S18954
13	46	33.3	693	2	B68112
14	45.5	33.2	335	2	A59765
15	45.5	33.2	1237	2	S18925
16	45	32.8	182	2	B87385
17	45	32.8	248	2	H83548
18	45	32.8	299	2	E83161
19	45	32.8	309	2	AB3021
20	45	32.8	331	2	G98263
21	45	32.8	374	2	G86267
22	45	32.8	472	2	C70853
23	45	32.8	812	2	P96744
24	45	32.8	855	2	T05981
25	45	32.8	1067	2	D82436
26	45	32.8	1164	2	S46769
27	45	32.8	1232	2	T05322
28	45	32.8	1417	2	P96613
29	45	32.8	1502	2	T48309

30	45	32.8	1513	2	T28158	probable DNA-dir
31	45	32.8	1740	2	T43215	fibronectin-like red
32	44.5	32.5	419	2	T33986	hypothetical prote
33	44	32.1	148	2	S26450	hypothetical prote
34	44	32.1	281	2	A62252	permease protein o
35	44	32.1	303	2	T50199	conserved hypothet
36	44	32.1	339	2	D87225	conserved membrane
37	44	32.1	397	2	AG0490	gamma-glutamyl pro
38	44	32.1	415	2	C69682	gamma-glutamyl pho
39	44	32.1	484	2	D82735	coenzyme a synthet
40	44	32.1	512	2	T41164	opha protein (limp
41	44	32.1	563	2	C98307	hypothetical prote
42	44	32.1	563	2	AH2975	probable insectici
43	44	32.1	833	2	AB0448	DNA polymerase I l
44	44	32.1	870	2	A86567	DNA polymerase I c
45	44	32.1	870	2	F72058	

ALIGNMENTS

RESULT 1
F64095
argininosuccinate lyase (EC 4.3.2.1) - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 16-Jul-1999
R:Accession: F64095
R:Releaschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodex, A.; Kelley, J.M.; Weidman
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fritchman, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630
A:Accession: F64095
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-457 <RTGR>
A:Cross-References: GB:U32763; GB:U42023; NID:91573817; PIDN:AMC22470.1; PID:91573823
C:Superfamily: argininosuccinate lyase
C:Keywords: amidase-lyase; carbon-nitrogen lyase

Query Match 41.6% Score 57; DN 2; Length 457;
Best local Similarity 32.0% Pred. No. 1;
Matches 8; Conservative 9; Mismatches 8; Indels 0; Gaps 0;
QY 2 EDITRNIRHIAQVSDMSRIPG 26
DB 129 QESVRNLRHIVGTAEFTQDAVMPG 153

RESULT 2
T25102
hypothetical protein T22C1.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
R:McMurry, A.
Submitted to the EMBL Data Library, June 1996
A:Reference number: Z19982
A:Accession: T25102
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-183 <WLL>
A:Cross-References: EMBL:Z75550; PIDN:CAA9921.1; GSPDB:GN00019; CESP:T22C1.2
C:Genetics:
A:Gene: CESP:T22C1.2
A:Map position: 1
A:Introns: 31/3; 88/1; 119/3; 164/1

Db 141 DLMRD--KHLAFIDGSMARN 158

RESULT 7

J00354

DNA-directed RNA polymerase (EC 2.7.7.6) I second largest chain - fruit fly (*Drosophila*

C:Species: *Drosophila melanogaster*

C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 21-Jul-2000

C:Accession: J00354; S07025

R:Kontermann, R.; Stizler, S.; Seifarth, W.; Petersen, G.; Bautz, E.K.F.

Mol. Gen. Genet. 219, 373-380, 1989

A:Title: Primary structure and functional aspects of the gene coding for the second-larg

A:Reference number: J00354; MUID:90158499

C:Accession: J00354

A:Molecule type: DNA

A:Residues: 1-1129 <KON>

A:Cross-References: EMBL:X17298; NID:98473; PIDN:CA35185.1; PID:98474

A:Note: the authors translated the codon CAG for residue 202 as Glu, TCG for residue 369

C:Genetics:

A:Gene: DmRP135

A:Cross-References: FlyBase:FBgn0003278

A:Insertions: 30/3; 530/3

C:Superfamily: DNA-directed RNA polymerase 132K polypeptide

C:Keywords: DNA binding; nucleotidyltransferase; nucleus; transcription; zinc finger

Query Match

Best Local Similarity 34.3%; Score 47; DB 2; Length 1129;

Matches 11; Conservative 6; Mismatches 9; Indels 4; Gaps 1;

2 EDITRNIAHRLAQC-----DSMDRSIPGL 27

Db 22 KQIPKLSRHLANLGGPHVDSFDEMLTVGL 51

RESULT 8

A82856

conserved hypothetical protein XF0042 [Imported] - *Xylella fastidiosa* (strain 9a5c)

C:Species: *Xylella fastidiosa*

C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C:Accession: A82856

R:anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequen

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.

A:Reference number: A82515; MUID:20365717

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: A82856

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-420 <SIM>

A:Cross-References: GB:AE003858; GB:AE003849; NID:99104799; PIDN:AAF82855.1; GSPDB:GN001

A:Experimental source: strain 9a5c

R:Simpon, A.J.G.; Relnach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

Brienes, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Carraro, D.M.; Carrer, H

as-Neto, E.; Docena, C.; El-Dorry, H.; Fachinani, A.P.; Ferreira, A.J.S.

submitted to Genbank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; From

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, U.P.; Krieger, J.E.; Krumme, E.E.; Laig

Chado, M.A.; Madella, A.M.B.N.; Madella, H.M.F.; Marinho, C.L.; Marques, M.V.; Martins, B

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir

M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A:Reference number: A59328

C:Contents: annotation

A:Gene: XF0042

Query Match

Best Local Similarity 33.9%; Score 46.5; DB 2; Length 420;

Matches 8; Conservative 7; Mismatches 6; Indels 1; Gaps 1;

QY 4 IIRNIAHRLAQC--GDSMDRSIP 24

Db 225 LIRNIAHRLAQC--GDSMDRSIP 246

RESULT 9

S75802

kdtb protein - *Synechocystis* sp. (strain PCC 6803)

N:Alternate names: protein slr0847

C:Species: *Synechocystis* sp.

A:Variety: PCC 6803

C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000

C:Accession: S75802

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima,

Y.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Matsubae, N.; Yamada, M.; Yas

DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocys*

s.

A:Reference number: S74322; MUID:97061201

A:Accession: S75802

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-159 <KAN>

A:Cross-References: EMBL:D64003; GB:AB001339; NID:q1001200; PIDN:BA10537.1; PID:9167

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C:Genetics:

A:Gene: kdtb

A:Start codon: GTG

C:Superfamily: 11polysaccharide core biosynthesis protein kdtb

Query Match

Best Local Similarity 33.6%; Score 46; DB 2; Length 159;

Matches 7; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

7 NIARHLAQCSDMSDRSIPGL 27

Db 128 STKEIAKFGSGVDLTPPSI 148

RESULT 10

G75293

probable manganese ABC transporter, permease protein - *Deinococcus radiodurans* (strai

C:Species: *Deinococcus radiodurans*

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000

C:Accession: G75293

R:White, O.; Eisen, J.A.; Heideberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J

, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Ulterback, T.; Zalewski, C.

S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.

A:Reference number: A75250; MUID:20036896

A:Accession: G75293

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-268 <NHT>

A:Cross-References: GB:AE002060; GB:AE000513; NID:96460082; PIDN:AA11829.1; PID:9646

A:Experimental source: strain R1

C:Genetics:

A:Gene: Dn283

A:Map position: 1

C:Superfamily: conserved hypothetical protein H10360

Query Match

Best Local Similarity 33.6%; Score 46; DB 2; Length 268;

Matches 7; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 8 IARHLAQCSDMSDRSIPGL 27

Db 35 VLKGLSYIDAMSHAVLPGL 54

RESULT 11

AF2445
hypothetical protein al15118 [imported] - Anabaena sp. (strain PCC 7120)

A:Species: Anabaena sp.

A:Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002

C:Accession: AF2445

R:Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kunitz, T.; Sasamoto, S.; Watanabe, A.; Iriyuchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anz

A:Reference number: AB1807, MUID:21595285; PMID:11759840

A:Accession: AF2445

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-329 <KOR>

A:Cross-references: GB:BA000019; PIDN:BA076817.1; PID:917134256; GSPDB:GN00179

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: al15118

C:Superfamily: stress response protein csb

Query Match 33.6%; Score 46; DB 2; Length 329;
Best Local Similarity 39.1%; Pred. No. 35;
Matches 9; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Oy 1 CEDIRNIAHRLAOGDSMDRST 23
Db 14 EEETITMYRISVOMDMDGVS 36

RESULT 12

S18954

fix23-2 protein - Rhizobium meliloti

C:Species: Rhizobium meliloti

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 08-Oct-1999

C:Accession: S18954

R:Petronovs, G.; Punok, P.; Kondrost, A.

submitted to the EMBL Data Library, January 1992

A:Description: A fatty acid synthase like gene cluster of Rhizobium meliloti is involved

A:Reference number: S18953

A:Accession: S18954

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-395 <PEP>

A:Cross-references: EMBL:X64131; NID:91235585; PIDN:CA445484.1; PID:946272

C:Superfamily: [acyl-carrier-protein] S-malonyltransferase homology <AMT>

F:44-327/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT>

Query Match 33.6%; Score 46; DB 2; Length 395;
Best Local Similarity 50.0%; Pred. No. 43;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Oy 2 EDITRNIAHRLAOGDSM 19
Db 13 EDIVRAINHLERKGSDI 30

RESULT 13

B85112

hypothetical protein AT4910730 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001

C:Accession: B85112

R:Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring

Nature 402, 769-777, 1999

A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.

A:Reference number: AB5001; MUID:20083488

A:Accession: B85112

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-693 <STO>

A:Cross-references: GB:NC_001268; NID:97267771; PIDN:CA81174.1; GSPDB:GN00140

C:Genetics:

A:Gene: AT4910730

A:Map position: 4

Query Match 33.6%; Score 46; DB 2; Length 693;
Best Local Similarity 34.5%; Pred. No. 84;
Matches 10; Conservative 6; Mismatches 9; Indels 4; Gaps 1;

Oy 1 CEDIRNIAHRLAOGDSMDRS---IPP 25
Db 584 QODLIMLVNTLQDAETTDGSONGKLPP 612

RESULT 14

S18015

protein-tyrosine kinase (EC 2.7.1.112) dtk7 - fruit fly (Drosophila melanogaster) (fr

C:Species: Drosophila melanogaster

C:Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 18-Feb-2000

C:Accession: S18015

R:Shishido, F.; Emori, Y.; Saigo, K.

FEBS Lett. 289, 235-238, 1991

A:Title: Identification of seven novel protein-tyrosine kinase genes of Drosophila by

A:Reference number: S17552; MUID:92008631

A:Accession: S18015

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-55 <SHI>

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom

C:Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase

F:1-55/Domain: protein kinase homology (fragment) <KIN>

Query Match 33.2%; Score 45.5; DB 2; Length 55;
Best Local Similarity 52.6%; Pred. No. 5.2;
Matches 10; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

Oy 9 ARHLAOGD-SMDRSIPG 26
Db 6 ARHOAKISDFGMSRLPG 24

RESULT 15

A56764

band 3-related protein, ileum - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 08-Sep-1995 #sequence_revision 08-Sep-1995 #text_change 20-Aug-1999

C:Accession: A56764

R:Chow, A.; Dobbins, J.W.; Aronson, P.S.; Igarashi, P.

Am. J. Physiol. 263, G345-G352, 1992

A:Title: cDNA cloning and localization of a band 3-related protein from ileum.

A:Reference number: A56764; MUID:93035730

A:Accession: A56764

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1237 <CHO>

A:Cross-references: GB:S45791; NID:9256659; PIDN:AAB23488.1; PID:9256660

A:Experimental source: New Zealand White rabbit, ileal epithelial cells

A:Note: sequence extracted from NCBI Backbone (NCBIN:115180, NCBI:P:115181)

C:Superfamily: band 3 anion transport protein

Query Match 33.2%; Score 45.5; DB 2; Length 1237;
Best Local Similarity 31.0%; Pred. No. 2e+02;
Matches 9; Conservative 9; Mismatches 8; Indels 3; Gaps 1;

Oy 2 EDITRNIA--RHLAGDSMDRSIPGL 27
Db 616 EELIRSVARHROQLMKKREGRLPLPG 644

Fri Sep 20 11:03:05 2002

us-09-544-664-14.rpt

Page 5

Search completed: September 20, 2002, 10:39:07
Job time: 479 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OW protein - protein search, using sw model

Run on: September 20, 2002, 11:04:30 : Search time 44.99 Seconds*
(without alignments)
23.237 Million cell updates/sec

Title: US-09-544-664-14

Perfect score: 137

Sequence: 1 GEDIRNARHIAQVGDSDRSTPGL 27

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	137	100.0	195	1	BID_HUMAN
2	99	72.3	195	1	BID_MOUSE
3	57	41.6	457	1	ARLY_HAETIN
4	47	34.3	397	1	AZAB_TALPU
5	47	34.3	1129	1	RP22_DROME
6	46	33.6	159	1	CON2_SYNY3
7	46	33.6	248	1	PCN2_SULOH
8	45.5	33.2	1237	1	B3A2_RABIT
9	45	32.8	472	1	YU87_MYCU
10	45	32.8	1164	1	KEU1_YEAST
11	45	32.8	1513	1	DPOA_OXYTR
12	44.5	32.5	511	1	G6PD_EMENT
13	44	32.1	148	1	YFX_METTF
14	44	32.1	415	1	PROA_BACSU
15	44	32.1	415	1	PROA_XLPA
16	44	32.1	530	1	PDP2_RAT
17	44	32.1	794	1	ST5A_BOVIN
18	43.5	31.8	298	1	YMA2_MYCHO
19	43.5	31.8	350	1	SUB1_SYNP7
20	43.5	31.8	689	1	YVAL_BACSU
21	43.5	31.8	901	1	OCRL_HUMAN
22	43	31.4	227	1	PMGY_HAETIN
23	43	31.4	279	1	RKI_PORPU
24	43	31.4	317	1	YK88_CAEPU
25	43	31.4	323	1	REC4_YEAST
26	43	31.4	324	1	VP35_VACCV
27	43	31.4	324	1	VP35_VACCV
28	43	31.4	324	1	VP35_VACCV
29	43	31.4	324	1	VP35_VACCV
30	43	31.4	324	1	VP35_VACCV
31	43	31.4	324	1	VP35_VACCV
32	43	31.4	324	1	VP35_VACCV
33	43	31.4	324	1	VP35_VACCV

RESULT	1	ALIGNMENTS
BID_HUMAN	STANDARD:	PRT; 195 AA.
AC	P55957:	
DT	01-NOV-1997 (Rel. 35, Created)	
DT	01-NOV-1997 (Rel. 35, Last sequence update)	
DT	16-OCT-2001 (Rel. 40, Last annotation update)	
DE	BH3 interacting domain death agonist (BID).	
GN	BID.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	
OX	NCBI_Taxid=9606;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	MEDLINE=97078762; PubMed=8918887;	
RA	Wang K., Yin X.-M., Chao D.T., Millman G.L., Korsmeyer S.J.;	
RT	*BID, a novel BH3 domain-only death agonist.*;	
RT	Genes Dev. 10:2859-2869(1996).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RA	MEDLINE=98389636; PubMed=9721221;	
RA	Footz T.K., Birtten B., Minoshima S., Asakawa S., Shimizu N.,	
RT	Riazl M.A., McDermid H.E.;	
RT	*The gene for death agonist BID maps to the region of human 22q11.2	
RT	6.*;	
RT	Genomics 51:472-475(1998).	
RN	[3]	
RP	SEQUENCE FROM N.A.	
RA	Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M.,	
RA	Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,	
RA	Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F.,	
RA	Trevaskis E., Waterston R., Williamson A., Wohlmann P., Wilson R.;	
RT	Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.	
RN	[4]	
RP	SEQUENCE OF 1-110 FROM N.A.	
RA	Fujisawa T., Hirano H., Hishigaki H., Horie M., Kawai A., Kuga Y.,	
RA	Kyushiki H., Nagata M., Okuno S., Ozaki K., Shimizu F.,	
RA	Shimada Y., Shinomiya H., Suzuki M., Takaiichi A., Takada S.,	
RA	Matsumoto T., Maekawa H., Nakamura Y., Takahashi E.;	
RT	Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.	
RN	[5]	
RP	SEQUENCE OF 1-74.	
RA	MEDLINE=96159527; PubMed=8593609;	
RA	Trofatter J.A., Long K.R., Murrell J.R., Stotler C.J.,	
RA	Gusella J.F., Buckler A.J.;	
RT	*An expression-independent catalog of genes from human chromosome	
RT	22.*;	
RT	Genome Res. 5:214-224(1995).	
RN	[6]	
RP	STRUCTURE BY NMR.	
RA	MEDLINE=99189747; PubMed=10069877;	
RA	Chou J.-J., Li H., Salvanes G.S., Yuan J., Wagner G.;	
RT	*Solution structure of BID, an intracellular amplifier of apoptotic	
RT	signaling.*;	

```

RL Cell 96:615-624(1999).
CC -1- FUNCTION: INDUCES ICE-LIKE PROTEASES AND APOPTOSIS. COUNTERS THE
CC PROTECTIVE EFFECT OF BCL-2 (BY SIMILARITY).
CC -1- SUBUNIT: FORMS HETERODIMERS EITHER WITH THE PRO-APOPTOTIC PROTEIN
CC BAX OR THE ANTI-APOPTOTIC PROTEIN BCL-2 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: PREDOMINANTLY CYTOPLASMIC (BY SIMILARITY).
CC -1- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND
CC BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF042083; AAC34365.1; -
DR EMBL: H23042; -; NOT_ANNOTATED_CDS.
DR EMBL: R09650; -; NOT_ANNOTATED_CDS.
DR EMBL: R09537; -; NOT_ANNOTATED_CDS.
DR EMBL: C12508; -; NOT_ANNOTATED_CDS.
DR EMBL: H55493; -; NOT_ANNOTATED_CDS.
DR PDB: 2BID; 27-JAN-00.
DR MTM: 601997; -
DR InterPro: IPR000712; Bcl_2.
DR PROSITE: PS01259; BH3; 1.
KW Apoptosis; 3D-structure.
FT DOMAIN 86 100 BH3.
SQ SEQUENCE 195 AA; 21994 MM; B17A07334CIAFBEF CRC64:

Query Match 100.0%; Score 137; DB 1; Length 195;
Best Local Similarity 100.0%; Pred. No. 1; Be-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QEDIIIRNIARHLAQVSDMSRISPGI 27
DB 79 QEDIIIRNIARHLAQVSDMSRISPGI 105

RESULT 2
BID_MOUSE STANDARD: PRT: 195 AA.
AC P70444;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE BH3 interacting domain death agonist (BID).
GN BID.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euteheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1}
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF BH3 DOMAIN.
RC TISSUE=T-cell;
RA MEDLINE=97078762; PubMed=8918887;
RA Wang K., Yin X.-M., Chao D.T., Millman C.L., Korsmeyer S.J.;
RT "BID: a novel BH3 domain-only death agonist.";
RL Genes Dev. 10:2859-2869(1996).
RN [2]
RP STRUCTURE BY NMR.
RA MEDLINE=99189748; PubMed=10089876;
RA McDowell J.M., Fushman D., Millman C.L., Korsmeyer S.J., Cowburn D.;
RT "Solution structure of the proapoptotic molecule BID: a structural
RT basis for apoptotic agonists and antagonists.";
RL Cell 96:625-634(1999).
CC -1- FUNCTION: INDUCES CASPASES AND APOPTOSIS. COUNTERS THE PROTECTIVE
CC EFFECT OF BCL-2.

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CC -1- SUBUNIT: FORMS HETERODIMERS EITHER WITH THE PRO-APOPTOTIC PROTEIN
CC BAX OR THE ANTI-APOPTOTIC PROTEIN BCL-2.
CC -1- SUBCELLULAR LOCATION: PREDOMINANTLY CYTOPLASMIC.
CC -1- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND
CC BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC -----
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CC -----
DR EMBL: U75506; AAC71064.1; -
DR PDB: 1DDb; 30-AUG-99.
DR MGD: MGI:108093; Bid.
DR InterPro: IPR000712; Bcl_2.
DR PROSITE: PS01259; BH3; 1.
KW Apoptosis; 3D-structure.
FT DOMAIN 86 100 BH3.
SQ SEQUENCE 195 AA; 21950 MM; BA023C7141BCCT7 CRC64:

Query Match 72.3%; Score 99; DB 1; Length 195;
Best Local Similarity 70.4%; Pred. No. 9; Se-08;
Matches 19; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 QEDIIIRNIARHLAQVSDMSRISPGI 27
DB 79 QEDIIIRNIARHLAQVSDMSRISPGI 105

RESULT 3
ARLY_HAEN STANDARD: PRT: 457 AA.
AC P44314;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Argininosuccinate lyase (EC 4.3.2.1) (Argininosuccinase) (ASAL).
GN ARGH OR H10811.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN 11}
RP SEQUENCE FROM N.A.
RC STRAIN=RD / RW20 / ATCC 51907;
RA MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spiggs T., Hedblom E., Cotton M.D.,
RA Ullrich T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Frickman J.L., Fuhrman J.L., Geophagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus
RT influenzae Rd.";
RL Science 269:496-512(1995).
RN [1]
RP CATALYTIC ACTIVITY: N-(L-arginino)succinate = fumarate + L-
RP arginine.
CC -1- PATHWAY: THE LAST STEP IN ARGININE BIOSYNTHESIS.
CC -1- SIMILARITY: BELONGS TO THE LYASE 1 FAMILY. ARGININOSUCCINATE LYASE
CC SUBFAMILY.
CC -----
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CC EMBL: U32763; NC02470.1; .
DR HSSD: P04424; IAO5.
DR TIGR: H10811; .
DR Interpro: IPR000362; Fumarate-lyase.
DR Pfam: P00206; Lyase_1.1.
DR PRINTS: PR00149; FUMARATE_LYASE.
DR PROSITE: PS00163; FUMARATE_LYASES; 1.
DR Arginine biosynthesis; 1.
KW Arginine biosynthesis; Complete proteome.
KW SEQUENCE 5157 AA: 51217 MW: 517220516MC1FE08 CRC64;

Query Match	41.6%;	Score 57;	DB 1;	Length 457;
Best Local Similarity	32.0%;	Pred. No. 0.49;		
Matches	8;	Conservative	9;	Mismatches 8; Indels 0; Gaps 0;

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QY      2 EDIIRNIARHLAQVGDSDMDRISPPC 26
          ::::| | | |:::| |
Db     129 QESVRNLQRHLVQTAENTQQAAMPG 153

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RESULT 4

1	A2AB_TALEU	STANDARD;	PRT;	397	AA
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DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alpha-2b adrenergic receptor (Alpha-2b adrenoceptor) (Fragment).
 ID AF082258
 AC European (European mole).
 CC Eutheria; Metazoa; Chordata; Gnathostomata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Insectivora; Talpidae; Talpa.
 CC NCBI_TaxID=9375;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP MEDLINE=97357151; PubMed=9214502;
 RA Springer M.S., Clevon G.C., Madsen O.J., de Jong W.W., Maddell V.G.,
 RA Amrine H.W., Stanhope M.J.;
 RA "Endemic African mammals shake the phylogenetic tree."

CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE
CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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DR EMBL; Y12520; CAA73120.1; -

DR InterPro; IPR000276; GPCR_Rhodpsn

DR PROSITE: PS00237; G_PROTEIN_RECEP
DR PROSITE: G_PROTEIN_RECEP

KM G-protein coupled receptor; Transmembrane; Multigene family;
KW Phosphorylation; Lipoprotein; Palmitate.

FT	TRANSMEM	<1	45	1 (POTENTIAL).
FT	DOMAIN	26	36	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	37	62	2 (POTENTIAL).
FT	DOMAIN	63	72	EXTRACELLULAR (POTENTIAL)

FT	TRANSMEM	73	95	3 (POTENTIAL).
FT	DOMAIN	96	117	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	118	140	4 (POTENTIAL).
FT	DOMAIN	141	156	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	157	180	5 (POTENTIAL).
FT	DOMAIN	181	361	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	362	385	6 (POTENTIAL).
FT	DOMAIN	386	394	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	395	>397	7 (POTENTIAL).
FT	TRANSMEM	72	151	BY SIMILARITY.
FT	DISULFID	282	300	ASP/Glu-RICH (ACIDIC).
FT	DOMAIN	79	79	IMPLICATED IN LIPID BINDING (BY SIMILARITY).
FT	SITE	163	163	IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
FT	SITE	167	167	IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
FT	SITE	397	397	IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
FT	NON_TER	397	397	
SO	SEQUENCE	397 AA:	43620 MW:	9C3812515ADC3BE4 CRC64:

Query Match	34.3%	Score 47	DB 1	Length 397
Best Local Similarity	40.9%	Pred. NO. 14		
Matches	9	Conservative	4	Mismatches 9
				Indels 0
				Gaps 0

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QY      5  IRNIARHLAÖVGDSMDRSIPPG  26
          : : | | | : : | | |
DB     221 VPNIARHLVAAGETNGRSKPTG  242

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RESULT 5

ID	RPA2_DROME	STANDARD;	PRT;	1129 AA
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DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1999 (Rel. 38, Last annotation update)
DE DNA-directed RNA polymerase I 135 kDa polypeptide (EC 2.7.7.6)
DE Rpl135
DE Rpl135 polymerase I subunit 2)
CN
ON
OS *Drosophila melanogaster* (Fruit fly).
OC Eukaryota; Metazoa; Anthropoda; Tracheata; Hexapoda; Insecta;
OC Eukaryota; Neoptera; Endopterygota; Diptera; Brachycastra; Muscomorpha,
OC Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
OX

RE SEQUENCE FROM R.A., PubMed-2482932.
 RX MEDLINE-50136493; PubMed-2482932.
 RA Kohnemann R., Sildler G., Seifrich W., Petersen G., Bantz E. K. F.:
 RA Primarily structure and not serinal aspects of the gene coding for the
 RA tRNA synthetase of *Escherichia coli*.
 RI Mol. Gen. Genet. 219:377-380(1995).
 CC -I: FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
 CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
 CC SUBSTRATES. RNA POLYMERASE I IS ESSENTIALLY USED TO TRANSCRIBE
 CC RIBOSOMAL DNA UNITS.
 CC -I: CATALYTIC ACTIVITY: N nucleoside triphosphatib + N diphosphate +

CC [RNA] (N).
CC -1 SUBUNIT: EACH CLASS OF RNA POLYMERASE IS ASSEMBLED FROM 9 TO 14
CC -1 SUBUNIT. THE FIRST SUBUNIT IS THE SECOND LARGEST
CC COMPONENT OF RNA POLYMERASE
CC SUBCELLULAR LOCATION: Nucleolus.
CC -1 MISCELLANEOUS: THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES ARE
CC FOUND IN BACTERIAL CELLULERS. THE FIRST POLYMERASE, RNA POLYMERASE
CC FOR 5S AND TRNA GENES, IS THE MINN PRECURSOR, AND POLYMERASE
CC -1 SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.

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 CC -----
 DR EMBL: J07298; CAJ5185.1; .
 DR PIR: J00334; J00334.
 DR Flybase: FB0002728; RP0135.
 DR PIR: J00334; J00334.
 DR Pfam: PF00562; RNA_POL_B.
 DR PROSITE: PS01166; RNA_POL_BETA.1
 DR Transferrase: DNA-directed RNA polymerase; transcription; zinc.
 KW Zinc-finger; Nuclear protein. C4-type (POTENTIAL).
 FT ZN-FING 1061 1093
 SQ SEQUENCE 1129 AA; 128414 MW; E0A15F1BCF1BD7 CRC64;

Query Match 34.38; Score 47; DB 1; Length 1129;
 Best Local Similarity 36.78; Pred. No. 42;
 Matches 11; Conservative 6; Mismatches 9; Indels 4; Gaps 1;
 Oy 2 EDIIRIRHAAVG---DSMDRSPICL 27
 Db 22 KQIPKSRHANTGSPHVSFDEMKTGCL 51

RESULT 6
 ID CONO_SYNY3 STANDARD; PRT: 159 AA.
 AC Q54435;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Phosphatidylcholine acetyltransferase (PCAT) (dephospho-CoA
 phosphate acetyltransferase) (PCAT) (dephospho-CoA
 COAD OR KOPR OR STR0847
 GN Synecocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synecocystis.
 OX NCBI_TaxID:1148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:96127529; PubMed:8590279;
 RA Kaneo T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
 RA Sugita M., Tanaka S.;
 RT Synecocystis sp. strain PCC 6803. Sequence features in the 1 kb
 RT genome map positions 648 to 924 of the genome.
 RU DNA Ref. 2:153-166(1995)
 CC -1- FUNCTION: REVERSIBLY TRANSFERS AN ADENYLYL GROUP FROM ATP TO 4'-
 PHOSPHOPANTHETHEINE, YIELDING DEPHOSPHO-COA (DPCOA) AND
 CC -1- CATALYTIC ACTIVITY: ATP + pantetheine 4'-phosphate + diphosphate +
 CC dephospho-CoA.
 CC -1- PATHWAY: COENZYME A (COA) BIOSYNTHESIS: FOURTH STEP.
 CC -1- SUBUNIT: HOMOHexamer (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE CONO FAMILY.
 CC -----
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 CC -----
 DR EMBL: D64003; BAA10537.1; .
 DR HSRP: P23875; 186T.
 DR InterPro: IPR001994; Cytidylyltransf.
 DR Pfam: PF01467; Cytidylyltransf. 1.
 DR PRINTS: PR01020; LPSBIOSTRANS.
 DR TRANS: P01020; LPSBIOSTRANS.
 KW Transf. Nucleosidyltransferase; Coenzyme A biosynthesis;
 KW Complete Proteome.

SQ SEQUENCE 159 AA; 17593 MW; 6590EACBFCF151C CRC64;
 Query Match 33.64; Score 46; DB 1; Length 159;
 Best Local Similarity 33.38; Pred. No. 7.2;
 Matches 7; Conservative 7; Mismatches 7; Indels 0; Gaps 0
 Oy 7 MIAHAAVGDSMDRSPICL 27
 Db 128 SLVEIAKPGSVHLYVPSI 148

RESULT 7
 ID PCN2_SULOH STANDARD; PRT: 248 AA.
 AC P57763;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE DNA polymerase sliding clamp B (proliferating cell nuclear antigen
 DNA polymerase sliding clamp B) (PCNA B).
 DE PCNA OR PCNA B.
 GN Sulfolobus solfataricus.
 OS Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.
 OC Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.
 OX NCBI_TaxID:69656;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-TA-1;
 RX MEDLINE:2102025; PubMed:11139078;
 RA Iwai T., Kurosawa N., Itoh Y.H., Horikuchi T.;
 RT Phylogenetic analysis of archaeal PCNA homologues.*;
 RL Exonuclease 4:357-364(2000).
 CC -1- CATALYTIC ACTIVITY: RESPONSIBLE FOR TETHERING THE
 CC REPLICATING SHIELD OF DNA POLYMERASE TO DNA DURING HIGH-SPEED
 CC REPLICATION (BY SIMILARITY).
 CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE PCNA FAMILY.
 CC -----
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 CC -----
 DR EMBL: A045090; BAB19662.1; .
 DR InterPro: IPR00730; PCNA.
 DR Pfam: PF00705; PCNA. 1.
 DR PROSITE: PD002673; PCNA. 1.
 DR PROSITE: PS01251; PCNA. 1; FALSE-NEG.
 DR PROSITE: PS00293; PCNA. 2; FALSE-NEG.
 KW DNA-binding; DNA replication.
 KW DNA-binding; DNA replication.
 SQ SEQUENCE 248 AA; 27681 MW; B6E200C3047E6E89 CRC64;

Query Match 33.64; Score 46; DB 1; Length 248;
 Best Local Similarity 33.08; Pred. No. 32;
 Matches 9; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
 Oy 3 DIIINIRHAAVGDSMDRSPICL 22
 Db 141 DIIKDIARLDSLVEEVEIS 160

RESULT 8
 ID B3A2_RABIT STANDARD; PRT: 1237 AA.
 AC P48746;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Antion exchange protein 2 (non-erythroid band 3-like protein) (B3BP)

GN SLC4A2 OR AE2.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NEW ZEALAND WHITE;
 RA MEDLINE=93035730; PubMed=1415547;
 RX Chow A., Dobbins J.W., Aronson P.S., Igarashi P.;
 RT "cDNA cloning and localization of a band 3-related protein from
 RT ileum.";
 RL Am. J. Physiol. 263:G345-G352(1992).
 CC -1- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE
 CC DISTRIBUTION.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
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 CC EMBL: S45791; AAB34488.1; -
 CC DR HSP: P02730; ISTR.
 CC DR InterPro: IPR001717; Anion exchanger.
 CC DR InterPro: IPR003020; HCO3 cotransp.
 CC DR Pfam: PF00955; HCO3 cotransp. 1.
 CC DR PRINTS: PR01231; HCO3TRNSPORT.
 CC DR PROSITE: PS00219; ANION_EXCHANGER_1; 1.
 CC DR PROSITE: PS00220; ANION_EXCHANGER_2; 1.
 CC KW Transmembrane; Glycoprotein; Anion exchange; Lipoprotein; Palmitate.
 FT DOMAIN 1 703
 FT TRANSMEM 704 1237
 FT TRANSMEM 704 727
 FT TRANSMEM 733 770
 FT TRANSMEM 790 812
 FT TRANSMEM 822 843
 FT TRANSMEM 844 896
 FT TRANSMEM 897 914
 FT DOMAIN 915 929
 FT TRANSMEM 930 950
 FT TRANSMEM 984 1006
 FT TRANSMEM 1032 1053
 FT TRANSMEM 1087 1132
 FT TRANSMEM 1159 1195
 FT DOMAIN 1195 1237
 FT DOMAIN 1237 1237
 FT CARBOHYD 855 855
 FT CARBOHYD 864 864
 FT CARBOHYD 878 878
 FT LIPID 1169 1169
 FT SEQUENCE 1237 AA; 136535 MW; 2811D1051552B2 CRC64;

Query Match 33.2%; Score 45.5; DB 1; Length 1237;
 Best Local Similarity 31.0%; Pred. No. 77;
 Matches 9; Conservative 9; Mismatches 8; Indels 3; Gaps 1;

OY 2 EDITRINIA--RHIAOVGSDMSRIPGL 27
 DB 616 EELLRSVAHROQLMKRREGORLAPGL 644

RESULT 9
 ID YU87_MYCTU STANDARD; PRT; 472 AA.
 AC 053304;
 DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical 52.6 kDa protein Rv3087.
 GN Rv3087 OR MT3172 OR MTV013.08.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RA MEDLINE=96295987; PubMed=9634230;
 RX Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holtroyd S.,
 RA Hornsby T., Jagers K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sulston J.E., Taylor K., Whitehead S., Barrall B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.";
 RL Nature 393:537-544(1998).
 CC [2]
 CC SEQUENCE FROM N.A.
 CC STRAIN=CDC 1551 / Oshkosh;
 CC RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 CC RA Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
 CC RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 CC RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 CC RA Bishal W.;
 CC RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 CC laboratory strains.";
 CC RL Submitted (APR-2001) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE UPF0089 FAMILY.
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 CC EMBL: AL021309; CA16145.1; -
 CC DR EMBL: AE007134; AAK47508.1; ALT_INIT.
 CC DR TIGR: MT3172; -
 CC DR TubercuList; Rv3087; -
 CC DR InterPro: IPR004255; UPF0089.
 CC DR Pfam: PF03007; UPF0089; 1.
 CC KW Hypothetical protein; Complete proteome.
 CC SO SEQUENCE 472 AA; 52597 MW; AC03BDDA970FC0 CRC64;

Query Match 32.8%; Score 45; DB 1; Length 472;
 Best Local Similarity 44.8%; Pred. No. 33;
 Matches 13; Conservative 3; Mismatches 7; Indels 6; Gaps 2;

OY 3 DIIIRIAHIAOVGD-----SMDRSIPG 26
 DB 204 DRRV-IEREFANDGRVPPFTRDSAPG 231

RESULT 10
 ID KEIL_YEAST STANDARD; PRT; 1164 AA.
 AC P38853;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Kelch repeats protein 1.
 GN KEIL OR YHR158C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=5288C / AB972;
 RA MEDLINE=94378003; PubMed=8091229;
 RA Johnson M., Andrews S., Blinkman R., Cooper J., Ding H., Dover J.,
 Du Z., Favella A., Fulton L., Galtung S., Geisel C., Kirsten J.,
 Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
 Larrelle P., Louis E.J., Macri C., Mardis E., Meneses S., Mouser L.,
 Nhan M., Riffin L., Riles L., St Peter H., Trevisan E., Vaughan K.,
 Vignati D., Wilcox L., Woldman P., Waterston R., Wilson R.,
 Vaudin M.;
 RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
 VII";
 RL Science 265:2077-2082(1994).
 CC [2]
 CC CHARACTERIZATION.
 CC MEDLINE=99003296; PubMed=9786949;
 CC Phillips J., Herskowitz I.;
 CC "Identification of Kel1p, a kelch domain-containing protein involved
 CC in cell fusion and morphology in Saccharomyces cerevisiae";
 CC J. Cell Biol. 143:375-389(1998).
 CC -1- FUNCTION: HAS A ROLE IN CELL MORPHOGENESIS AND CELL FUSION AND MAY
 CC ANTAGONIZE THE PKC1 PATHWAY.
 CC -1- SUBUNIT: INTERACTS WITH KEL2.
 CC -1- SIMILARITY: CONTRAINS 5 KELCH REPEATS.
 CC -1- SIMILARITY: TO YEAST KEL2.
 CC -----
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 CC -----
 CC EMBL: U10397; AAB68991.1; -
 CC DR PIR: S46769; S46769.
 CC DR COMPUYEAST-2DPAGE: P38853; -
 CC DR SGD: S0001201; KEL1.
 CC DR InterPro: IPR001798; Kelch.
 CC DR Pfam: PF01344; Kelch; 3.
 CC DR Repeat: Coiled coil.
 CC KM Repeat: 139 186 KELCH 1.
 CC FT REPEAT 253 307 KELCH 2.
 CC FT REPEAT 308 357 KELCH 3.
 CC FT REPEAT 359 409 KELCH 4.
 CC FT REPEAT 411 460 KELCH 5.
 CC FT DOMAIN 777 931 COILED COIL (POTENTIAL).
 CC FT DOMAIN 974 1163 COILED COIL (POTENTIAL).
 CC SQ SEQUENCE 1164 AA; 131093 MW; 43D0FC570F105E4D CRC64;
 CC -----
 CC Query Match 32.8%; Score 45; DB 1; Length 1164;
 CC Best Local Similarity 53.3%; Pred. No. 86;
 CC Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 CC
 CC 2 EDITORIAL:AOVG 16
 CC Db 920 EDITORIAL:AOVG 934
 CC
 CC RESULT 11
 CC DPOA_OXYTR STANDARD; PRT; 1513 AA.
 CC AC 027152;
 CC DT 15-DEC-1998 (Rel. 37, Created)
 CC DT 15-DEC-1998 (Rel. 37, Last sequence update)
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
 CC DE DNA polymerase alpha catalytic subunit (EC 2.7.7.7).
 CC OX Oxytricha trifallax.
 CC OS Eukaryota; Alveolata; Ciliophora; hypotrichs; Stichotrichidae;

OC Oxytrichidae; Oxytricha.
 OX NCBI_TaxID=5946;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=97451043; PubMed=9302325;
 RA Hoffman D.C., Prescott D.M.;
 RT "Phylogenetic relationships among hypotrichous ciliates determined
 RT with the macronuclear gene encoding the large, catalytic subunit of
 RT DNA polymerase alpha";
 CC J. Mol. Evol. 45:301-310(1997).
 CC -1- FUNCTION: POLYMERASE ALPHA IN A COMPLEX WITH DNA PRIMEASE IS A
 CC REPLICATIVE POLYMERASE.
 CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate - N diphosphate
 CC + (DNA)(N).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- MISCELLANEOUS: IN EUKARYOTES THERE ARE FIVE DNA POLYMERASES:
 CC ALPHA, BETA, GAMMA, DELTA, AND EPSILON WHICH ARE RESPONSIBLE FOR
 CC DIFFERENT REACTIONS OF DNA SYNTHESIS.
 CC -1- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.
 CC -----
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 CC -----
 CC EMBL: U59426; AAB57771.1; -
 CC DR InterPro: IPR002064; DNA_POL_B.
 CC DR Pfam: PF00136; DNA_POL_B; 1.
 CC DR Pfam: PF03104; DNA_POL_B_exo; 1.
 CC DR PRINTS: PR00106; DNAPOLB.
 CC DR SMART: SM00486; POLB; 1.
 CC DR PROSITE: PS00116; DNA_POLYMERASE_B; 1.
 CC KW Transferrase; DNA-directed DNA polymerase; DNA replication;
 CC DNA-binding; Nuclear protein.
 CC SQ SEQUENCE 1513 AA; 173059 MW; 4DF832EDCFC4416E CRC64;
 CC -----
 CC Query Match 32.8%; Score 45; DB 1; Length 1513;
 CC Best Local Similarity 31.6%; Pred. No. 11e+02;
 CC Matches 6; Conservative 8; Mismatches 5; Indels 0; Gaps 0;
 CC
 CC 1 OEDIRNIA:RLAOGVDSM 19
 CC Db 1151 REDVLAN:RLNEDYLDIGEM 1169
 CC
 CC RESULT 12
 CC G6PD_EMENT
 CC ID G6PD_EMENT STANDARD; PRT; 511 AA.
 CC AC P41764; Q92408;
 CC DT 01-NOV-1995 (Rel. 32, Created)
 CC DT 01-NOV-1997 (Rel. 35, Last sequence update)
 CC DT 15-DEC-1998 (Rel. 37, Last annotation update)
 CC DE Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) (G6PD).
 CC GN G6PD OR G6PD.
 CC OS Emericella nidulans (Aspergillus nidulans).
 CC OX Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 CC Eurotiiales; Trichocomaceae; Emericella.
 CC OX NCBI_TaxID=5072;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=FGSC 4;
 CC RA Schaap P.J., Muller Y., Visser J.;
 CC RL Submitted (Jan-1995) to the EMBL/Genbank/DBJ databases.
 CC [2]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=WG96;
 CC RA van den Broek P., Goosen T., Wennekes B., van den Broek H.;
 CC submitted (Sep-1996) to the EMBL/Genbank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: D-glucose 6-phosphate + NADP(+) -> D-glucose-

```
CC 1.5-lactone 6-phosphate + NADP.
CC -1- PATHWAY: FIRST STEP IN PENTOSE PHOSPHATE PATHWAY.
CC -1- SIMILARITY: BELONGS TO THE GLUCOSE-6-PHOSPHATE DEHYDROGENASE
CC FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X84001; CAA58825.1; -
DR HSSP: X77830; CAA5841.1; -
DR InterPro: IPR001282; G6PD.
DR Pfam: PF00479; G6PD.1.
DR PRINTS: PR00781; G6PD.C.1.
DR PRODOM: PR001129; G6PD.1.
DR PROSITE: PS00069; G6P_DEHYDROGENASE.1.
DR Oxioreductase; NADP; Glucose metabolism.
RW ACT_SITE 198 198 BY SIMILARITY.
FT CONFLICT 15 20 MISSING (IN REF. 1).
FT CONFLICT 76 85 R51KTPKE -> DTLRPROR (IN REF. 1).
FT CONFLICT 352 352 L -> LP (IN REF. 1).
SQ SEQUENCE 511 AA; 58977 MW; 66BC15B72878A475 CRC64;

Query Match 32.58; Score 44.5; DB 1; Length 511;
Best Local Similarity 23.58; Pred. No. 42;
Matches 8; Conservative 10; Mismatches 9; Indels 7; Gaps 1;

OY 1 OEDITRNARHLA0VGDSDMR-----STPGL 27
DB 106 QDSEKNAHKEIEKKNQKNRVYMLPPSV 139

RESULT 13
ID YPZX_METTF STANDARD: PRT; 148 AA.
AC P29587;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DE Hypothetical 16.7 kDa protein (ORF11).
OS Methanobacterium thermoformicum.
OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
OC Methanobacter.
OX NCBI_TaxID=145282;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN: DSM 3120 / Z-245;
RA MEDLINE: 93126090; PubMed: 1336177;
RA Nucleic Acids Res. 20:6501-6507 (1992);
RA Nucleic Acids Res. 20:6501-6507 (1992);
RA Restriction modification systems in Methanobacterium
thermoformicum.
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CC -----
DR EMBL: X68367; CAA48440.1; -
DR PIR: S26450; S26450.
DR PIR: S30316; S30316.
```

```
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 148 AA; 16658 MW; 77276336AA4853F CRC64;

Query Match 32.18; Score 44; DB 1; Length 148;
Best Local Similarity 38.18; Pred. No. 13;
Matches 8; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

OY 2 EDITRNARHLA0VGDSDMR 22
DB 106 KDTLRNAPALFALVSDIGDKN 126

RESULT 14
ID PROA_BACSU STANDARD: PRT; 415 AA.
AC P39821; Q35032;
DT 01-FEB-1995 (Rel. 31, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Gamma-glutamyl phosphate reductase (GPR) (EC 1.2.1.41) (Glutamate-5-semialdehyde dehydrogenase) (Glutamyl-gamma-semialdehyde dehydrogenase) (GSA dehydrogenase).
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN: 168;
RA MEDLINE: 94364946; PubMed: 8083159;
RA Ohtsu M, Kawata-Mukai M, Iraya M, Takio K, Tanaka T;
RT Multiple copies of the gpr gene enhance degs-dependent
RT extracellular protease production in Bacillus subtilis.
RT J. Bacteriol. 176:5673-5680 (1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN: 168;
RA Devine K.M.;
RT Sequence of the Bacillus subtilis genome between xlya and ykor.
RT submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CATALYZES THE NADPH DEPENDENT REDUCTION OF L-GAMMA-
CC GLUTAMYL-5-PHOSPHATE INTO L-GUTAMATE 5-SEMIALDEHYDE AND
CC PHOSPHATE. THE PRODUCT SPONTANEOUSLY UNDERGOES CYCLIZATION TO FORM
CC 1-PYRROLINE-5-CARBOXYLATE.
CC -1- CATALYTIC ACTIVITY: L-glutamate 5-semialdehyde + phosphate +
CC NAD(+) -> L-gamma-glutamyl 5-phosphate + NADH + H+.
CC -1- PATHWAY: PROLINE BIOSYNTHESIS PATHWAY (OF SEMIALDEHYDE).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).
CC -1- SIMILARITY: BELONGS TO THE GAMMA-GLUTAMYL PHOSPHATE REDUCTASE
CC FAMILY.
CC -----
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CC -----
DR EMBL: D26044; BAA05045.1; -
DR EMBL: A7002571; CAA0592.1; -
DR Subtilist; BG10964; proA.
DR InterPro: IPR002086; Aldehyde_dehydr.
DR InterPro: IPR000965; GPR.
DR Pfam: PF00171; aldehyd.1.
DR PROSITE: PS01223; PROA; 1.
RW Oxioreductase; Proline biosynthesis; NADP; Complete proteome.
FT CONFLICT 108 108 E -> Q (IN REF. 1).
FT CONFLICT 174 174 A -> F (IN REF. 1).
FT CONFLICT 271 271 H -> N (IN REF. 1).
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CC CONFLICT 359 359 R -> A (IN REF. 1).
CC FT CONFLICT 374 415 E -> EGIIRSRNRHONAKASCKRTDASCTDPYKIH
CC FT (IN REF. 1).
CC SEQUENCE 415 AA: 45336 MW: 6CA4BD035F9F62D0 CRC64:

Query Match
Best Local Similarity 32.1%; Score 44; DB 1; Length 415;
Matches 10; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

OY 2 EDIRNRHRLAOGVDSMDRSPG 26
DB 179 EDIRSRKELFTLNDGLVTPRG 203

RESULT 15
PROA_XYLFA STANDARD: PRT: 415 AA.
AC 09963:
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Gamma-glutamyl phosphate reductase (GPR) (EC 1.2.1.41) (Glutamate-5-
DE semialdehyde dehydrogenase) (Glutamy1-gamma-semialdehyde
DE dehydrogenase) (GSA dehydrogenase).
GN PROA OR XP1005.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xylella.
OX NCBI_TaxID=2371;
ON
RN
RP
SEQUENCE FROM N.A.
RC STRAIN=9ASC;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.C., Reimach F.C., Artuda P., Abreu F.A., Acencio M.,
RA Aliverenga R., Alves L.M.C., Araya J.E., Bala G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Brites M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carter H.,
RA Coutinho N.B., Colombo C., Costa F.B., Costa M.C.R., Costa Neto C.M.,
RA Fuchincini A.P., Fuchincini M.S., Fuchincini E., Docena C., El-Dorri H.,
RA Fraga J.S., Franco S.C., Franco M.C., Grohme M., Guzman L.R.,
RA Gertler M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hobeisel J.D., Junqueira M.L., Kemper E.L., Kishijima J.P.,
RA Klinger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhami A.Jr., Nodrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmeri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A.Jr., Peaquerio J.B.,
RA Queglio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva F.R., da Silva W.A.Jr.,
RA da Silva J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Trufi D., Tsai S.M., Tsuchioka M.H.,
RA Vallada H., Van Sluys M.A., Verjovsky-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Melandri J., Setubal J.C.;
RA "The genome sequence of the plant pathogen Xylella fastidiosa.";
RA Nature 406:151-159(2000).
RL
CC -1- FUNCTION: CATALYZES THE NADPH DEPENDENT REDUCTION OF L-GAMMA-
CC GLUTAMYL 5-PHOSPHATE INTO L-GLUTAMATE 5-SEMIALDEHYDE AND
CC PHOSPHATE. THE PRODUCT SPONTANEOUSLY UNDERGOES CYCLIZATION TO FORM
CC 1-PYRROLINE-5-CARBOXYLATE.
CC -1- NATURAL ACTIVITY: L-glutamate 5-semialdehyde + phosphate +
CC NADPH -> L-glutamate 5-semialdehyde + phosphate + NADP+
CC -1- PATHWAY: PHOTODIODESIS PATHWAY, SECOND STEP.
CC -1- SUBCELLULAR LOCATION: CYTOSOL (in plants)
CC -1- SIMILARITY: BELONGS TO THE GAMMA-GLUTAMYL PHOSPHATE REDUCTASE
CC FAMILY.

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CC -----
CC EMBL: AE003938; AAF83815.1; ALT_INIT.
CC InterPro: IPR000965; GPR.
CC DR PROSITE: PS01223; PROA: 1.
CC KW Oxidoreductase; Proline biosynthesis; NADP; Complete proteome.
CC SEQUENCE 415 AA: 44533 MW: 68F3A83D26BD454D CRC64:

```

```

Query Match
Best Local Similarity 32.1%; Score 44; DB 1; Length 415;
Matches 10; Conservative 7; Mismatches 6; Indels 4; Gaps 1;

OY 4 IIRNRHRLAOGVDSMDRSPG 26
DB 177 IYQDMARTWELTQLSDLIIVTPRG 203

```

Search completed: September 20, 2002, 11:04:31
Job time: 1628 sec

Fri Sep 20 11:03:05 2002

us-09-544-664-14.rsp

Page 9

Fri Sep 20 11:03:06 2002

us-09-544-664-14.rsp

Page 1

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 20, 2002, 11:03:39 : Search time 172.19 seconds
(without alignments)
27.126 Million cell updates/sec

Title: US-09-544-664-14
Sequence: 1 QEDIIINRIARHLAOGVDSMDRISPPGL 27

Scoring table: BLOSUM62
Gapop 10.0, Gapept 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP-archaea:
2: SP-bacteria:
3: SP-fungi:
4: SP-human:
5: SP-invertebrate:
6: SP-mammal:
7: SP-mhc:
8: SP-organelle:
9: SP-phage:
10: SP-plant:
11: SP-rodent:
12: SP-virus:
13: SP-vertebrate:
14: SP-unclassified:
15: SP-virus:
16: SP-bacteriophage:
17: SP-archaeop:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	137	100.0	467	4	Q9BRX3
2	99	72.3	195	11	Q9W39
3	92	67.2	196	11	Q9JL16
4	92	67.2	196	11	Q9JL16
5	36	40.9	336	2	Q9ALQ7
6	33	38.7	190	2	Q9JL16
7	33	37.6	190	2	Q9JL16
8	31	37.2	183	5	Q9JL16
9	31	37.2	183	5	Q9JL16
10	31	37.2	183	5	Q9JL16
11	49	35.8	939	8	Q9JL16
12	48.5	35.0	485	8	Q9JL16
13	48	35.0	485	8	Q9JL16
14	48	35.0	485	8	Q9JL16
15	47	34.3	273	16	Q9JL16
16	47	34.3	273	16	Q9JL16

17	47	34.3	484	8	Q9W39
18	47	34.3	513	10	Q9ZRX5
19	47	34.3	957	5	Q9W2N6
20	47	34.3	1107	10	Q9JL16
21	47	34.3	1129	5	Q9VPP3
22	46.5	33.9	209	5	Q9JL16
23	46.5	33.9	209	5	Q9JL16
24	46.5	33.9	209	5	Q9JL16
25	46.5	33.9	209	5	Q9JL16
26	46.5	33.9	209	5	Q9JL16
27	46.5	33.9	209	5	Q9JL16
28	46.5	33.9	209	5	Q9JL16
29	46.5	33.9	209	5	Q9JL16
30	46.5	33.9	209	5	Q9JL16
31	46.5	33.9	209	5	Q9JL16
32	46.5	33.9	209	5	Q9JL16
33	46.5	33.9	209	5	Q9JL16
34	46.5	33.9	209	5	Q9JL16
35	46.5	33.9	209	5	Q9JL16
36	46.5	33.9	209	5	Q9JL16
37	46.5	33.9	209	5	Q9JL16
38	46.5	33.9	209	5	Q9JL16
39	46.5	33.9	209	5	Q9JL16
40	46.5	33.9	209	5	Q9JL16
41	46.5	33.9	209	5	Q9JL16
42	46.5	33.9	209	5	Q9JL16
43	46.5	33.9	209	5	Q9JL16
44	46.5	33.9	209	5	Q9JL16
45	46.5	33.9	209	5	Q9JL16

ALIGNMENTS

RESULT	1		
Q9BRX3	PRELIMINARY:	PRT:	467 AA.
AC	Q9BRX3:		
DT	01-JUN-2001 (TReMBLrel. 17, Created)		
DR	01-JUN-2001 (TReMBLrel. 17, Last sequence update)		
DE	01-DEC-2001 (TReMBLrel. 19, Last annotation update)		
DI	HYPOTHETICAL 51.7 KDA PROTEIN.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OX	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
NCBI_TaxID	9606;		
RP	(1)		
RC	SEQUENCE FROM N.A.		
RA	TISSUE-JUNG CARCINOMA:		
RL	Strasbourg R.		
DR	Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BC005884; AA05884.1; .		
DR	HSSP; P5957; 2810.		
DR	Interpro: IPR000712; Bcl-2.		
DR	PROSITE: PS01259; BH3.1.		
KW	Hypothetical protein.		
SQ	SEQUENCE 467 AA; 51663 MW; 7D7121D47F8E9DAB CRC64;		
Query Match	100.0%;	Score 137;	DB 4; Length 467;
Best Local Similarity	100.0%;	Pred. No. 4;	5e-12;
Matches 27;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
DB	1 QEDIIINRIARHLAOGVDSMDRISPPGL 27		
QY			
DB	351 QEDIIINRIARHLAOGVDSMDRISPPGL 377		
RESULT	2		
Q9W39	PRELIMINARY:	PRT:	195 AA.
AC	Q9W39:		
DT	01-JUN-2001 (TReMBLrel. 17, Created)		

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DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)
DE BID INTERACTING DOMAIN DEATH AGONIST.
GN BID.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY TUMOR. MAP-TGF ALPHA MODEL. 7 MONTHS OLD. CROSS
RC TISSUE:
RL Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC002031; AA02031.1; -.
DR HSSP: P70444; 1DD8.
DR MCD: MGI108093; Bid.
DR InterPro: IPR000712; Bcl_2.
DR PROSITE: PS01259; BH3; 1.
SQ SEQUENCE 195 AA; 21951 MW; 52F412714FB867F3 CRC64;

Query Match 72.3%; Score 99; DB 11; Length 195;
Best Local Similarity 70.4%; Pred. No. 7.7e-07;
Matches 19; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 QEDIRNIRHIAQVDSMDRSPICL 27
Db 79 QEDIRNIRHIAQVDSMDRSPICL 105

RESULT 3
ID 09JLT6 PRELIMINARY; PRT; 196 AA.
AC 09JLT6;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE Apoptotic Death AGONIST BID.
GN BID.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RC Chen D.; Cao G.; Chen J.;
RT cloning of rat apoptotic death agonist (BID) and its different
RT expression in 19c6mle and normal rat brain.
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF136292; 1DD8.
DR HSSP: P70444; 1DD8.
DR InterPro: IPR000712; Bcl_2.
DR PROSITE: PS01259; BH3; UNKNOWN_1.
SQ SEQUENCE 196 AA; 22281 MW; C5F6AD3F442C02E3 CRC64;

Query Match 67.2%; Score 92; DB 11; Length 196;
Best Local Similarity 63.0%; Pred. No. 8.5e-06;
Matches 17; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 QEDIRNIRHIAQVDSMDRSPICL 27
Db 80 QEDIRNIRHIAQVDSMDRSPICL 106

RESULT 4
ID 09JUK60 PRELIMINARY; PRT; 196 AA.
AC 09JUK60;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)

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DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE BID PROTEIN.
GN BID.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RC Itoh T.; Itoh A.; Pleasure D.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF295503; AAF71759.1; -.
DR HSSP: P70444; 1DD8.
DR InterPro: IPR000712; Bcl_2.
DR PROSITE: PS01259; BH3; UNKNOWN_1.
SQ SEQUENCE 196 AA; 22249 MW; C5F6AD2F5D9B52B3 CRC64;

Query Match 67.2%; Score 92; DB 11; Length 196;
Best Local Similarity 63.0%; Pred. No. 8.5e-06;
Matches 17; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 QEDIRNIRHIAQVDSMDRSPICL 27
Db 80 QEDIRNIRHIAQVDSMDRSPICL 106

RESULT 5
ID 09AL07 PRELIMINARY; PRT; 336 AA.
AC 09AL07;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)
DE 01-OCT-2001 (TREMBlrel. 18, last annotation update)
DE METHYL-ACCEPTING CHEMORECEPTOR-LIKE PROTEIN ORF2 (FRAGMENT).
OS Pseudomonas fluorescens.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=294;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13625;
RC Feng S.F.; Rosebach S.;
RT "A locus involved in metal homeostasis in Pseudomonas fluorescens
RT encodes a proton/cation antiporter of the RND family and a two-
RT component system."
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY007258; AAC09634.1; -.
DR InterPro: IPR001610; PAC.
DR InterPro: IPR000700; PAS-asso_C.
DR Pfam: PF00785; PAC; 1.
DR SMART: SM00086; PAC; 2.
DR SMART: SM00091; PAS; 2.
KW Receptor.
FT NON-TER
SQ SEQUENCE 336 AA; 38039 MW; 867FBE095D4C4B38 CRC64;

Query Match 40.9%; Score 56; DB 2; Length 336;
Best Local Similarity 44.4%; Pred. No. 3.5;
Matches 8; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 3 DITRINIRHIAQVDSMD 20
Db 308 DVMKDLARHMDQAGDIE 325

RESULT 6
ID 09X2X0 PRELIMINARY; PRT; 190 AA.
AC 09X2X0;

```


RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt J.G., Nelson C.R., Milos G.L.G.,
 RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
 RA Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandal D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Botlinger P.,
 RA Burris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.M.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 *The genome sequence of *Drosophila melanogaster*.*;
 Science 287:2185-2195(2000).
 [3]
 RN SEQUENCE FROM N.A.
 RP STRAIN-BERKELEY.
 RC Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Munjal C.J.,
 RA Nuncio J., Pacle J., Paragas V., Park S., Phouanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
 Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 [4]
 RN SEQUENCE OF 793-849 FROM N.A.
 RP MEDLINE=92008631; PubMed=1915852;
 RA Shishido E., Emori Y., Saigo K.;
 RT *Identification of seven novel protein-tyrosine kinase genes of
 RT *Drosophila* by the polymerase chain reaction.*;
 RL Fests Lett. 289:235-238(1991).
 CC -1- FUNCTION: MAY BE INVOLVED IN SIGNAL TRANSDUCTION ON THE APICAL
 CC SURFACE OF ECTODERMAL EPITHELIA REGULATING THEIR POLARITY DURING
 CC IMAGINATION. CRUMBS (CRB) MAY BE THE INTRACELLULAR SIGNAL.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE -> ADP + PROTEIN
 CC TYROSINE PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC. APICAL EXPRESSION IN CEPHALIC
 CC FURROW AND TRACHEAL CELLS; LIMITED TO LUMINAL SURFACE AND ABSENT
 CC FROM THE BASAL SURFACE.
 CC -1- TISSUE SPECIFICITY: GASTRULATION EMBRYOS SHOW EXPRESSION IN
 CC ECTODERMAL CELLS ALONG THE CEPHALIC FURROW AND VENTRAL MIDLINE.
 CC PROCTODERM, STOMODERM AND THEIR DERIVED STRUCTURES (FOREGUT,
 CC INTSTIN, PHARYNX, ESOPHAGUS AND HINOGUT) CONTINUE TO SHOW
 CC EXPRESSION FROM STAGE 8-9 TO LATE EMBRYOS. OTHER ECTODERMALLY
 CC DERIVED STRUCTURES (FRONTAL SAC, SALIVARY GLAND AND LABIUM) AND
 CC DEVELOPING TRACHEAL SYSTEM ALSO SHOW EXPRESSION.
 CC -1- DEVELOPMENTAL STAGE: EMBRYOS ONLY.
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
 CC DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 SH2 DOMAINS.

CC -1- SIMILARITY: CONTAINS 3 ANK REPEATS.
 DR EMBL: U37773; AAA79851.1; -
 DR EMBL: AE003807; AAF58044.1; -
 DR EMBL: AY051937; AAK93361.1; -
 DR EMBL: S55962; AAB19909.1; -
 DR HSSP: P08631; IAD5.
 DR Flybase: Fggn0015295; shark.
 DR InterPro: IPR002110; ANK.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR000980; SH2_pkinase.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00023; ank; 3.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF00017; SH2; 2.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR PRINTS: PR00109; TYRKINASE.
 DR SMART: SM00248; ANK; 3.
 DR SMART: SM00252; SH2; 2.
 DR SMART: SM00219; TYRK; 1.
 DR PROSITE: PS50088; ANK_REPEAT; 3.
 DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS50001; SH2; 2.
 DR Transferrase: Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KW SH2 domain; ANK repeat; Repeat.
 FT DOMAIN 10 106 SH2 1.
 FT REPEAT 153 185 ANK 1.
 FT REPEAT 186 218 ANK 2.
 FT REPEAT 220 252 ANK 3.
 FT DOMAIN 288 403 SH2 2.
 FT DOMAIN 662 921 PROTEIN KINASE.
 FT NE_BIND 668 676 ATP (BY SIMILARITY).
 FT BINDING 668 698 ATP (BY SIMILARITY).
 FT ACT_SITE 789 789 BY SIMILARITY.
 FT MOD_RES 927 927 PHOSPHORYLATION (POTENTIAL).
 FT CONFLICT 19 19 A -> V (IN REF. 1).
 FT CONFLICT 39 39 S -> R (IN REF. 1).
 FT CONFLICT 50 50 L -> F (IN REF. 1).
 FT CONFLICT 85 85 D -> E (IN REF. 1).
 FT CONFLICT 129 129 S -> T (IN REF. 1).
 FT CONFLICT 199 199 P -> T (IN REF. 1).
 FT CONFLICT 341 341 C -> S (IN REF. 1).
 FT CONFLICT 505 506 GT -> RA (IN REF. 1).
 FT CONFLICT 597 597 M -> V (IN REF. 1).
 FT CONFLICT 611 611 A -> V (IN REF. 1).
 FT CONFLICT 732 732 A -> S (IN REF. 1).
 FT CONFLICT 898 898 A -> P (IN REF. 1).
 FT CONFLICT 935 939 QTVH -> KRFTFNVSITFFPRC (IN REF. 1).
 SQ SEQUENCE 939 AA; 104272 MW; 37CC2C3DA25D3F52 CRC64;
 Query Match 35.8%; Score 49; DB 5; Length 939;
 Best Local Similarity 52.0%; Pred. No. 1.2e+02;
 Matches 13; Conservative 3; Mismatches 5; Indels 4; Gaps 2;
 QY 6 NNI---ARHLAOGVD-SMRSIPG 26
 DB 793 RNILTLARHQAKISDFGMSRLRPG 817
 RESULT 12
 ID 098590 PRELIMINARY; PRT; 485 AA.
 AC 098590;
 DP 01-MAY-1999 (TREMblrel. 10, Created)
 DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE ATP SYNTHASE BETA SUBUNIT (FRAGMENT).
 GN ATPB.
 OS Pleiospermium alatum.
 OC Chloroplast.

Query Match	35.0%	Score 48	DB 2	Length 401
Best Local Similarity	27.8%	Pred. No. 66		
Matches 10	Conservative 8	Mismatches 6	Indels 12	Gaps 1
Oy	2	EDITININAR-----HLAOGVGSMDRSLRP 25		
Db	352	EDALERLARGSTPESTLRLRIEVAACGALDRNVP 387		
RESULT 14				
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BT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DE	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
GN	MANNOSYLTRANSFERASE.			
OS	Xp0608			
OC	Xyella fastidiosa.			
CC	Bacteria: Proteobacteria; gamma subdivision: Xanthomonas group;			
OX	Xyella.			
NCBI	taxid:2371;			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-9A5C:			
RX	MEDLINE-20365717; PubMed-10910347;			
RA	Simpson A.J.G., Relnach F.C., Arruda P., Abreu F.A., Acencio M.,			
RA	Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,			
RA	Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,			
RA	Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrier H.,			
RA	Colauco N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,			
RA	Costinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,			
RA	Faelencani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,			
RA	Fraga J.S., Franca S.C., Franco M.C., Frohne M., Furlan L.R.,			
RA	Ganier J.M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,			
RA	Ho P.L., Hohelsel J.D., Junqueira M.L., Kemper E.L., Kitaizima J.P.,			
RA	Kriegler J.E., Kuramae E.E., Lalret F., Lambais M.R., Leite L.C.C.,			
RA	Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,			
RA	Machado M.V., Madeira A.M.B.N., Martins E.M.F., Matsukuma C.L.,			
RA	Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma C.L.,			
RA	Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,			
RA	Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,			
RA	Nhani A.Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,			
RA	de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,			
RA	Pelxoto B.R., Pereira G.A.G., Pereira H.A., Jr., Pesquero J.B.,			
RA	Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,			
RA	de Rosa V.E., Jr., de Sa R.G., Sartelli R.V., Sawasaki H.E.,			
RA	da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A., Jr.,			
RA	da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,			
RA	de Souza A.A., Terenzi M.F., Truffi D., Tsai S.M., Tsubako H.L.,			
RA	Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.M.,			
RA	Zago M.A., Zatz M., Meidanis J., Setubal J.C.,			
RT	"The genome sequence of the plant pathogen Xylella fastidiosa.";			
RL	Nature 406:151-159(2000).			
DR	EMBL: AE003906; AAF83418.1;			
DR	InterPro: IPR001296; Glycos_transf_1.			
DR	Pfam: PF00534; Glycos_transf_1; 2.			
KW	Complete proteome.			
SO	SEQUENCE 849 AA; 95463 MW; 28FAACCT1C5726C CRC64;			

GenCore version 4.5
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OK protein - protein search, using sw model

Run on: September 20, 2002, 10:35:56 ; Search time 228.86 Seconds
(without alignments)
12.619 Million cell updates/sec

Title: US-09-544-664-2
Sequence: 1 NLMAAQRGRRLRMSDEFESFKGL 26

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 747574 seqs, 111073796 residues
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	138	100.0	26	21	AA837001 Bcl2 polypeptide B
2	138	100.0	26	21	AA837002 Bcl2 polypeptide B
3	138	100.0	27	21	AA837003 Bcl2 polypeptide B
4	138	100.0	27	21	AA837056 Bcl2 polypeptide B
5	138	100.0	28	21	AA837055 Bcl2 polypeptide B
6	138	100.0	162	22	AA870370 Shorter murine BAD
7	138	100.0	204	17	AA895168 bcl-x(l)/Bcl-2 ass
8	138	100.0	204	19	AA861315 Murine BCL-XL/BCL-
9	138	100.0	204	19	AA861316 Mutant BCL-XL/BCL-
10	138	100.0	204	19	AA861317 Mutant BCL-XL/BCL-
11	138	100.0	204	19	AA861318 Mutant BCL-XL/BCL-

12	138	100.0	204	19	AA858832 Murine BAD protein
13	138	100.0	204	22	AA870369 Longer murine BAD
14	138	100.0	567	22	AAU00220 Bad-DPFR apoptosis
15	114	82.6	166	18	AA832476 Bcl6 protein for r
16	114	82.6	168	19	AA855779 Human Bcl-xl/Bcl-2
17	114	82.6	168	21	AA813512 Human cell prolif
18	114	82.6	168	22	AA870368 Human BAD mutant a
19	114	82.6	168	22	AA848287 Human BAD protein.
20	114	82.6	168	22	AA867688 Amino acid sequenc
21	113	81.9	23	17	AA895165 bcl-x(l)/Bcl-2 ass
22	102	73.9	59	19	AA861319 Mutant BCL-XL/BCL-
23	102	73.9	59	19	AA861320 Mutant BCL-XL/BCL-
24	102	73.9	59	19	AA861321 Mutant BCL-XL/BCL-
25	102	73.9	59	19	AA861322 Mammalian Bad Bcl-
26	93	67.4	26	21	AA896321 BAD BH3 consensus
27	93	67.4	26	22	AA870371 bcl-x(l)/Bcl-2 ass
28	86	62.3	16	17	AA895163 Mouse BAD BH3 doma
29	84	60.9	16	21	AA895432 Bcl2 polypeptide B
30	84	60.9	16	21	AA837028 Human BAD BH3 doma
31	73	52.9	16	20	AA805421 Bcl2 polypeptide B
32	73	52.9	16	20	AA837029 Bcl2 polypeptide B
33	72	52.2	18	22	AA870379 BAD BH3 domain reg
34	72	52.2	20	22	AA870380 Arabidopsis thalia
35	51	37.0	125	21	AA825219 Arabidopsis thalia
36	51	37.0	171	21	AA825218 Arabidopsis thalia
37	51	37.0	181	21	AA825217 Arabidopsis thalia
38	51	37.0	186	21	AA825578 Arabidopsis thalia
39	51	37.0	186	21	AA854030 Arabidopsis thalia
40	51	37.0	232	21	AA825577 Arabidopsis thalia
41	51	37.0	232	21	AA854029 Arabidopsis thalia
42	51	37.0	236	21	AA854679 Arabidopsis thalia
43	51	37.0	241	21	AA854028 Arabidopsis thalia
44	51	37.0	242	21	AA825576 Arabidopsis thalia
45	50	36.2	516	21	AA852445 Arabidopsis thalia

ALIGNMENTS

RESULT 1
ID AA837001 standard; peptide: 26 AA.
XX AA837001;
XX 28-FEB-2001 (first entry)
XX Bcl2 polypeptide BH3 domain peptide #1.
XX Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;
XX cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;
XX apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;
XX colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;
XX melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
XX stroke; myocardial infarction.
XX
XX Homo sapiens.
XX WO200059526-A1.
XX 12-OCT-2000.
XX 06-APR-2000; 2000WO-US09352.
XX 07-APR-1999; 99US-0128202.
XX (UYZE) UNIV JEFFERSON THOMAS.
XX Huang Z, Wang J, Zhang Z, Shan S, Lu Z;
XX WPI: 2000-679325/66.
XX New peptide conjugates for modulating apoptosis or for inhibiting B

PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for
 XX treating neurodegenerative disorders, stroke, or cancer
 PS
 XX Claim 18: Page 17; 74pp; English.

CC The invention relates to a peptide conjugate having the formula:
 CC (R-X)n-peptide where n = 1-10; X = C=O, when the R-X group is attached
 CC to the N-terminus of the peptide, or a side chain of the peptide where
 CC the functional group of the side chain is NH₂ or OH; or X = O or NH,
 CC when the R-X group is attached to the C-terminus of the peptide, or a
 CC side chain of the peptide, where the side chain functional group is COOH
 CC or CONH₂; and R = 2-18C alkyl or alkoxy, 2-14C alkenyl containing one
 CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain
 CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples
 CC of the peptide portion of the conjugate. The peptides represent analogues
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of
 CC the B3 domain of the cell death agonist Bad. The peptide conjugate is
 CC useful for modulating apoptosis in the cells of a subject, or for
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2
 CC function. In particular, the peptide conjugate is useful for treating a
 CC subject afflicted with a cancer characterized by cancer cells that
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric,
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
 CC conjugate is also useful for treating disorders characterized by
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
 XX Sequence 26 AA:

Query Match 100.0%; Score 138; DB 21; Length 26;
 Best Local Similarity 100.0%; Pred. No. 1.4e-14;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 YY 1 NLMAAORYGRELRRMSDEFGSKGL 26
 DB 1 nlwaagrygrellrmsdefgsfkgl 26

RESULT 2
 AAB37002 AAB37002 standard; peptide: 26 AA.

AC AAB37002;

DT 28-FEB-2001 (first entry)

DE Bcl2 polypeptide B3 domain peptide #2.

XX Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;
 XX cardiant; Bcl-2 superfamily; B3 domain; cell death agonist; Bad;
 XX apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;
 XX colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;
 XX melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
 XX stroke; myocardial infarction.

OS Homo sapiens.

PN W0200059526-A1.

PD 12-OCT-2000.

PF 06-APR-2000; 2000WO-US09352.

PR 07-APR-1999; 99US-0128202.

PA (UIE-) UNTV JEFFERSON THOMAS.

PI Huang Z, Wang J, Zhang Z, Shan S, Lu Z;

XX
 DR WPI; 2000-679325/66.

PT New peptide conjugates for modulating apoptosis or for inhibiting B
 PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for
 PT treating neurodegenerative disorders, stroke, or cancer
 PS
 XX Claim 18: Page 17; 74pp; English.

CC The invention relates to a peptide conjugate having the formula:
 CC (R-X)n-peptide where n = 1-10; X = C=O, when the R-X group is attached
 CC to the N-terminus of the peptide, or a side chain of the peptide where
 CC the functional group of the side chain is NH₂ or OH; or X = O or NH,
 CC when the R-X group is attached to the C-terminus of the peptide, or a
 CC side chain of the peptide, where the side chain functional group is COOH
 CC or CONH₂; and R = 2-18C alkyl or alkoxy, 2-14C alkenyl containing one
 CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain
 CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples
 CC of the peptide portion of the conjugate. The peptides represent analogues
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of
 CC the B3 domain of the cell death agonist Bad. The peptide conjugate is
 CC useful for modulating apoptosis in the cells of a subject, or for
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2
 CC function. In particular, the peptide conjugate is useful for treating a
 CC subject afflicted with a cancer characterized by cancer cells that
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric,
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
 CC conjugate is also useful for treating disorders characterized by
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
 XX Sequence 26 AA:

Query Match 100.0%; Score 138; DB 21; Length 26;
 Best Local Similarity 100.0%; Pred. No. 1.4e-14;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

YY 1 NLMAAORYGRELRRMSDEFGSKGL 26
 DB 1 nlwaagrygrellrmsdefgsfkgl 26

RESULT 3

AAB37003 AAB37003 standard; peptide: 27 AA.

AC AAB37003;

DT 28-FEB-2001 (first entry)

DE Bcl2 polypeptide B3 domain peptide #3.

XX Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;
 XX cardiant; Bcl-2 superfamily; B3 domain; cell death agonist; Bad;
 XX apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;
 XX colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;
 XX melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
 XX stroke; myocardial infarction.

OS Homo sapiens.

PN W0200059526-A1.

PD 12-OCT-2000.

PF 06-APR-2000; 2000WO-US09352.

PR 07-APR-1999; 99US-0128202.

PA	(UYJE-) UNIV JEFFERSON THOMAS.
XX	
PI	Huang Z, Wang J, Zhang Z, Shan S, Lu Z;
XX	
DR	WPI: 2000-679325/66.
XX	
PT	New peptide conjugates for modulating apoptosis or for inhibiting B
PT	cell lymphoma/leukemia 2 (bcl-2) function, especially useful for
PT	treating neurodegenerative disorders, stroke, or cancer
PS	Claim 18: Page 17; 74pp; English.
CC	The invention relates to a peptide conjugate having the formula:
CC	(R-X) ⁿ -peptide where n = 1-10; X = C=O, when the R-X group is attached
CC	to the N-terminus of the peptide, or a side chain of the peptide where
CC	the functional group of the side chain is NH ₂ or OH; or X = O or NH,
CC	when the R-X group is attached to the C-terminus of the peptide, or a
CC	side chain of the peptide, where the side chain functional group is COOH
CC	or CONH ₂ ; and R = 2-18C alkyl or alkoxy, 2-14C alkylphenyl containing one
CC	or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally
CC	monosubstituted with a 1-5C straight or branched chain alkyl group,
CC	phenyl optionally monosubstituted with a 1-5C straight or branched chain
CC	alkyl group, or benzyl. The peptides AAB37001-B37058 represent analogues
CC	of the peptide portion of the conjugate. The peptides represent analogues
CC	of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of
CC	the B3 domain of the cell death agonist Bad. The peptide conjugate is
CC	useful for modulating apoptosis in the cells of a subject, or for
CC	reversing B cell lymphoma/leukemia 2 (bcl-2)-mediated blockage of
CC	apoptosis in cancer cells. It is also useful for inhibiting Bcl-2
CC	function. In particular, the peptide conjugate is useful for treating a
CC	subject afflicted with a cancer characterized by cancer cells that
CC	express Bcl-2. The cancer includes prostate, colorectal, gastric, or
CC	non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or
CC	acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
CC	conjugate is also useful for treating disorders characterized by
CC	increased apoptosis, e.g. neurodegenerative disorders, acquired
CC	immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
XX	
SO	Sequence 27 AA:
QY	1 NMAAQRVGRRLRMSDFEGSGFRG 26
Db	1 n1waagrygrelrmsdfegsfkg1 26
RESULT 4	
AAAB37056	AAAB37056 standard; peptide; 27 AA.
XX	
AC	AAAB37056:
XX	
DT	28-FEB-2001 (first entry)
DE	
XX	
Bcl2	polypeptide B3 domain peptide #56.
KV	Cytostatic; neuroprotective; anti-HIV; viroinhib; cerebroprotective;
KV	cardiant; Bcl-2 superfamily; B3 domain; cell death agonist; Bad;
KV	apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;
KV	colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;
KV	melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
KV	stroke; myocardiad infarction.
XX	
OS	Homo sapiens.
XX	
FN	WO200059526-A1.
XX	
DD	12-OCT-2000.

PF	XX	06-APR -2000:	2000MO-US09352.
PR	XX	07-APR -1999:	99US-0128202.
PA	(UYJE-) UNIV JEFFERSON THOMAS.		
PI	Huang Z., Wang J., Zhang Z., Shan S., Lu Z;		
P1	WPI; 2000-679325/66.		
DR			
XX	New peptide conjugates for modulating apoptosis or for inhibiting B		
PM	cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for		
PN	treating neurodegenerative disorders, stroke, or cancer		
PS			
X5	Claim 18; Page 19; 74pp; English.		
XX	The invention relates to a peptide conjugate having the formula:		
CC	(R-X)n-peptide where n = 1-10; X = C=O, when the R-X group is attached		
CC	to the N-terminals of the peptide, or a side chain of the peptide where		
CC	the functional group of the side chain is NH2 or OH; or X = O or NH,		
CC	when the R-X group is attached to the C-terminals of the peptide, or a		
CC	side chain of the peptide, where the side chain functional group is COOH		
CC	or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one		
CC	or two double bonds, cyclobutyl, cyclopentyl, cyclohexenyl optionally		
CC	monosubstituted with a 1-5C straight or branched chain alkyl group,		
CC	phenyl optionally monosubstituted with a 1-5C straight or branched chain		
CC	alkyl group, or benzyl. The peptides AAB37001-B37058 represent analogues		
CC	of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of		
CC	the B3 domain of the cell death agonist Bad. The peptide conjugate is		
CC	useful for modulating apoptosis in the cells of a subject, or for		
CC	reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockade of		
CC	apoptosis in cancer cells. It is also useful for inhibiting Bcl-2		
CC	function. In particular, the peptide conjugate is useful for treating a		
CC	subject afflicted with a cancer characterized by cancer cells that		
CC	express Bcl-2. The cancer includes prostate, colorectal, gastric,		
CC	non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or		
CC	acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide		
CC	conjugate is also useful for treating disorders characterized by		
CC	increased apoptosis, e.g. neurodegenerative disorders, acquired		
CC	immunodeficiency syndrome (AIDS), stroke or myocardial infarction.		
XX			
S0	Sequence 27 AA:		
Query Match	100.0%; Score 138; DB 21; Length 27;		
Best Local Similarity	100.0%; Pred. No. 1.4e-14;		
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0.			
OY	1 NLMAAGRYGRELIRMSDEFESFGKL 26		
	(((((((((((((((((((((((
DB	2 nlwaagrygrelirmsdefesfgskyl 27		
RESULT 5			
AAB37055	AAB37055 standard; peptide; 28 AA.		
XX	AAB37055;		
XX			
DT	28-FEB-2001 (first entry)		
XX			
DE	Bcl2 polypeptide BH3 domain peptide #55.		
XX			
KM	Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;		
KM	candidant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;		
KM	apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;		
KM	colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;		
KM	melanoma; myelocytic leukemia; neurodegenerative disorder; AIDS;		
XX	stroke; myocardial infarction.		
XX			
OS	Homo sapiens.		

XX WO20059526-A1.
 XX 12-OCT-2000.
 XX 06-APR-2000: 2000WO-US09352.
 XX 07-APR-1999: 99US-0128202.
 XX (UYJE-) UNIV JEFFERSON THOMAS.
 XX Huang Z, Mang J, Zhang Z, Shan S, Lu Z;
 XX WPI: 2000-679325/66.
 XX New peptide conjugates for modulating apoptosis or for inhibiting B
 XX cell lymphoma/leukemia 2 (bcl-2) function, especially useful for
 XX treating neurodegenerative disorders, stroke, or cancer
 XX
 XX Claim 18: Page 19; 74pp: English.
 XX The invention relates to a peptide conjugate having the formula:
 CC (R-X)n-peptide where n = 1-10; X = C=O when the R-X group is attached
 CC to the N-terminus of the peptide, or a side chain of the peptide where
 CC the functional group of the side chain is NH2 or OH, or X=O or NH
 CC when the R-X group is attached to the C-terminus of the peptide, or a
 CC side chain of the peptide, where the side chain functional group is COOH
 CC or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylaryl optionally
 CC or two double bonds, cyclohexyl, cyclopentyl, cyclohexyl optionally
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain
 CC alkyl group, or benzyl. The peptides AAB37001-837058 represent examples
 CC of the peptide portion of the conjugate. The peptides represent analogues
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of
 CC the Bcl-2 domain of the cell death agonist Bad. The peptide conjugate is
 CC useful for modulating apoptosis in the cells of a subject, or for
 CC reversing B cell lymphoma/leukemia 2 (bcl-2)-mediated blockage of
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2
 CC function. In particular, the peptide conjugate is useful for treating a
 CC subject afflicted with a cancer characterized by cancer cells that
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric,
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
 CC conjugate is also useful for treating disorders characterized by
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
 XX
 XX Sequence 28 AA:
 SO
 Query Match 100.0%; Score 138; DB 21; Length 28;
 Best Local Similarity 100.0%; Pred. NO. 1,5e-14;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 NMAAQRGRLRMSPDEPGSFKGL 26
 DB 2 nlwaagrygrelrmssdelegskgl 27
 RESULT 6
 AAB70370
 ID AAB70370 standard; protein: 162 AA.
 XX
 AC AAB70370;
 XX
 DT 02-MAY-2001 (first entry)
 XX
 DE Shorter murine BAD mutant amino acid sequence SEQ ID NO:3.
 XX
 KM Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;
 KM immunostimulant; neuroprotective; neurotrophic; antischismatic; vulnery;
 KM cytoskeletal; antiviral; antitumor; antineoplastic; wound healing;
 KM immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;

KM immunodeficiency disease; neurodegenerative disease; viral infection;
 KM ischaemic cell death; reperfusion cell death; arthritis; infertility;
 KM lymphoproliferative condition; inflammation; autoimmune disease.
 XX
 XX Mus musculus.
 XX Synthetic.
 XX WO200110868-A1.
 XX 15-FEB-2001.
 XX 30-MAY-2000: 2000WO-US11864.
 XX 28-MAY-1999: 99US-0136783.
 XX (APOF-) APOPTOSIS TECHNOLOGY INC.
 XX Zhou X;
 XX WPI: 2001-138734/14.
 XX New mutant Bcl-XL/Bcl-2 Associated cell death Regulator polypeptide,
 XX useful for screening for candidate compounds which induce or inhibit
 XX apoptosis, comprises amino acid substitutions at Ser118, Ser155 or
 XX Ser113 -
 XX Claim 7: Page 148-149; 157pp: English.
 XX The present invention describes an isolated or synthetic polypeptide
 XX (1) comprising a less than full length amino acid sequence of a mutant
 XX Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its
 XX fragment, which contains amino acid substitutions at Ser118 of a human
 XX BAD. Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine
 XX BAD (shorter murine BAD). (1) has immunostimulant, neuroprotective,
 XX neurotrophic, antischismatic, vulnery, cytoskeletal, antiviral,
 XX antitumor, antineoplastic, antitumor, antineoplastic, antineoplastic,
 XX and can be used as an apoptosis inducer or inhibitor. BAD polypeptides and
 XX polynucleotides can be used for screening candidate compounds and drugs
 XX for activating or promoting apoptosis in a cell. Candidate compounds
 XX inducing or inhibiting apoptosis in a cell. Candidate compounds
 XX identified and (mutant) BAD polypeptides are useful in treating
 XX immunodeficiency diseases, neurodegenerative diseases, ischaemic cell
 XX death, reperfusion cell death, wound healing, cancer, viral infections,
 XX lymphoproliferative conditions, arthritis, infertility, inflammation and
 XX autoimmune diseases. The present sequence represents a specifically
 XX claimed shorter murine BAD mutant amino acid sequence from the present
 XX invention.
 XX
 XX Sequence 162 AA:
 SO
 Query Match 100.0%; Score 138; DB 22; Length 162;
 Best Local Similarity 100.0%; Pred. NO. 1.1e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 NMAAQRGRLRMSPDEPGSFKGL 26
 DB 98 nlwaagrygrelrmssdelegskgl 123
 RESULT 7
 AAR95168
 ID AAR95168 standard; protein: 204 AA.
 XX
 AC AAR95168;
 XX
 DT 06-JAN-1997 (first entry)
 XX
 DE bcl-x(L)/bcl-2 associated death promoter protein.
 XX
 KM Bcl-XL/Bcl-2 associated cell death promoter; Bad; stroke;
 KM polypeptide; bcl-x(L)/bcl-2 associated death promoter; viral infections;
 KM cytokine deprivation; IL-3 dependent cell line; immunodeficiency; AIDS;

KM neurodegenerative disease; senescence; Ischaemia; neoplasia.
 XX Mus musculus.
 OS
 XX
 XX Key Location/Qualifiers
 XX 147..149
 FT Region /note="B1 conserved amino acids"
 FT 191..192
 FT Domain /note="B2 conserved amino acids"
 FT 38..61
 FT Domain /note="PEST sequence"
 FT 111..130
 FT /note="PEST sequence"
 PN W09613614-A1.
 PD 09-MAY-1996.
 PF 31-OCT-1995; 95MO-US14246.
 PR 31-OCT-1994; 94US-0333565.
 PA (UNIW) UNIV WASHINGTON.
 PI Kormeyer SJ;
 PS WPI; 1996-251465/25.
 DR N-PSDB; AAV29479.
 XX
 XX Polynucleotide encoding bcl-x(l)/bcl-2 associated death promoter -
 PT useful to treat neoplasia and apoptosis and to identify agents
 PT inhibiting its binding to bcl-2 or bcl-x(l) to form heterodimers
 PS Claim 3; Fig 1; 130pp; English.
 XX
 XX This sequence represents the murine bcl-x(l)/bcl-2 associated death
 CC promoter (Bad) gene. Bad is a 22.1 kD protein which interacts with
 CC bcl-2 and bcl-x proteins and regulates cell death. It has homology
 CC to the bcl-2-related family clustered in the B1 and B2 domain. Bad
 CC has been found to hybridise to bcl-x(l) and bcl-2 in yeast two-hybrid
 CC assays and in vivo in mammalian cells. Overexpressed Bad counters the
 CC death inhibitory activity of bcl-x(l), but is much less effective at
 CC countering the death inhibitory activity of bcl-2. Bad expression can
 CC accelerate apoptotic cell death induced by cytokine deprivation in an
 CC IL-3 dependent cell line expressing bcl-x(l), and its also counters the
 CC death repressor activity of bcl-x(l). Bad competes with Bax for binding
 CC to bcl-x(l). Bad may be used to identify agents which inhibit its
 CC binding to bcl-2 or bcl-x(l) to form heterodimers. Such agents may be
 CC used to treat neurodegenerative diseases, immunodeficiency diseases,
 CC e.g. AIDS, senescence or Ischaemia.
 CC
 XX Sequence 204 AA;
 SQ
 Query Match 100.0%; Score 138; DB 17; Length 204;
 Best Local Similarity 100.0%; Pred. No. 1.4e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 NINAAORYGRELRRMSDEFGSFKGL 26
 Db 140 nlmaagrygrellrmdelegsfkgl 165
 RESULT 8
 AAW61315 standard; Protein: 204 AA.
 ID AAW61315;
 AC AAW61315;
 XX
 XX 07-OCT-1998 (first entry)
 DT Murine BCL-XL/BCL-2 associated cell death regulator.
 DE
 XX

KM Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;
 KW serine substituted mutant; apoptosis; cancer; viral infection.
 XX Mus sp.
 XX
 XX W09817682-A1.
 PN 30-APR-1998.
 PD 17-OCT-1997; 97MO-US19175.
 PF 18-OCT-1996; 96US-0733505.
 PR (UNIW) UNIV WASHINGTON.
 PA Kormeyer SJ;
 PS WPI; 1998-261422/23.
 DR N-PSDB; AAV27833.
 XX
 XX New mutant BAD polypeptide with phosphorylatable serine replaced -
 PT useful for, e.g. treating reduced apoptosis such as in cancer or
 PT viral infection
 PS Claim 1; Fig 10; 95pp; English.
 XX
 XX The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
 CC death regulator) proteins, having an amino acid other than Ser at
 CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
 CC present sequence is the murine BAD protein. Also described are: (1)
 CC fragments of mutant BAD protein able to decrease cell viability; (2)
 CC fusion proteins of mutant BAD with a heterologous polypeptide that
 CC increases intracellular delivery. Mutant BAD proteins are used to treat
 CC or prevent diseases associated with reduced apoptosis, e.g. cancer,
 CC viral infection, lymphoproliferation, arthritis, infertility,
 CC inflammation and autoimmune disease. Polynucleotide sequences encoding
 CC mutant BAD proteins can be used similarly by gene therapy or to produce
 CC transgenic animals for use as disease models or in drug screening. BAD
 CC proteins phosphorylated at specified Ser are used to screen for enhancers
 CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful
 CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,
 CC aging or ischemic cell death. The apoptotic status of cells is
 CC determined by measuring relative amounts of phosphorylated and non-
 CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
 CC greater death-promoting activity than wild-type BAD which can become
 CC phosphorylated on the specified Ser, forming a product that does not
 CC heterodimerise with BCL-2 or BCL-XL, but instead binds to 14-3-3 family
 CC proteins in the cytosol, thus promoting cell survival. The mutants with
 CC Ser substituted cannot bind 14-3-3.
 CC
 XX Sequence 204 AA;
 SQ
 Query Match 100.0%; Score 138; DB 19; Length 204;
 Best Local Similarity 100.0%; Pred. No. 1.4e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 NINAAORYGRELRRMSDEFGSFKGL 26
 Db 140 nlmaagrygrellrmdelegsfkgl 165
 RESULT 9
 AAW61316 standard; Protein: 204 AA.
 ID AAW61316;
 AC AAW61316;
 XX
 XX 07-OCT-1998 (first entry)
 DT Mutant BCL-XL/BCL-2 associated cell death regulator #1.
 DE Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;
 XX

KM serine substituted mutant; apoptosis; cancer; viral infection.
 XX Mus sp.
 OS Synthetic.
 XX WO9817682-A1.
 XX 30-APR-1998.
 XX 17-OCT-1997: 97MO-US19175.
 XX 18-OCT-1996: 96US-0733505.
 XX (UNITV) UNIV WASHINGTON.
 XX Korsmeyer SJ:
 XX WP1: 1998-261422/23.
 XX DR N-PSDB: AAV27834.
 XX
 PT New mutant BAD polypeptide with phosphorylatable serine replaced -
 PT useful for, e.g. treating reduced apoptosis such as in cancer or
 PT viral infection
 XX
 PS Claim 7: Page 59: 95pp: English.
 XX
 CC The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
 CC death regulator) proteins, having an amino acid other than Ser at
 CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
 CC present sequence represents a mutant BAD protein. Also described are: (1)
 CC fragments of mutant BAD protein able to decrease cell viability; (2)
 CC fusion proteins of mutant BAD with a heterologous polypeptide that
 CC increases intracellular delivery. Mutant BAD proteins are used to treat
 CC or prevent diseases associated with reduced apoptosis, e.g. cancer,
 CC viral infection, lymphoproliferation, arthritis, infertility,
 CC inflammation and autoimmune disease. Polynucleotide sequences encoding
 CC mutant BAD proteins can be used similarly by gene therapy or to produce
 CC transgenic animals for use as disease models or in drug screening. BAD
 CC proteins phosphorylated at specified Ser are used to screen for enhancers
 CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful
 CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,
 CC aging or ischemic cell death. The apoptotic status of cells is
 CC determined by measuring relative amounts of phosphorylated and non-
 CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
 CC greater death-promoting activity than wild-type BAD which can become
 CC phosphorylated on the specified Ser, forming a product that does not
 CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family
 CC proteins in the cytosol, thus promoting cell survival. The mutants with
 CC Ser substituted cannot bind 14-3-3.
 XX
 SO Sequence 204 AA:

Query Match 100.0%; Score 138; DB 19; Length 204;
 Best Local Similarity 100.0%; Pred. No. 1,4e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLMAAQRVGRRLRRMSDEFGSFKGL 26
 Db 140 nlwaagrygrelrrmsdefgsfkgl 165

RESULT 10
 AAM61317
 ID AAM61317 standard; Protein: 204 AA.
 XX
 AC AAM61317;
 XX 07-OCT-1998 (first entry)
 XX Mutant BCL-XL/BCL-2 associated cell death regulator #2.
 DE Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;
 XX

KM serine substituted mutant; apoptosis; cancer; viral infection.
 XX Mus sp.
 OS Synthetic.
 XX WO9817682-A1.
 XX 30-APR-1998.
 XX 17-OCT-1997: 97MO-US19175.
 XX 18-OCT-1996: 96US-0733505.
 XX (UNITV) UNIV WASHINGTON.
 XX Korsmeyer SJ:
 XX WP1: 1998-261422/23.
 XX DR N-PSDB: AAV27835.
 XX
 PT New mutant BAD polypeptide with phosphorylatable serine replaced -
 PT useful for, e.g. treating reduced apoptosis such as in cancer or
 PT viral infection
 XX
 PS Claim 7: Page 60: 95pp: English.
 XX
 CC The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
 CC death regulator) proteins, having an amino acid other than Ser at
 CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
 CC present sequence represents a mutant BAD protein. Also described are: (1)
 CC fragments of mutant BAD protein able to decrease cell viability; (2)
 CC fusion proteins of mutant BAD with a heterologous polypeptide that
 CC increases intracellular delivery. Mutant BAD proteins are used to treat
 CC or prevent diseases associated with reduced apoptosis, e.g. cancer,
 CC viral infection, lymphoproliferation, arthritis, infertility,
 CC inflammation and autoimmune disease. Polynucleotide sequences encoding
 CC mutant BAD proteins can be used similarly by gene therapy or to produce
 CC transgenic animals for use as disease models or in drug screening. BAD
 CC proteins phosphorylated at specified Ser are used to screen for enhancers
 CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful
 CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,
 CC aging or ischemic cell death. The apoptotic status of cells is
 CC determined by measuring relative amounts of phosphorylated and non-
 CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
 CC greater death-promoting activity than wild-type BAD which can become
 CC phosphorylated on the specified Ser, forming a product that does not
 CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family
 CC proteins in the cytosol, thus promoting cell survival. The mutants with
 CC Ser substituted cannot bind 14-3-3.
 XX
 SO Sequence 204 AA:

Query Match 100.0%; Score 138; DB 19; Length 204;
 Best Local Similarity 100.0%; Pred. No. 1,4e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLMAAQRVGRRLRRMSDEFGSFKGL 26
 Db 140 nlwaagrygrelrrmsdefgsfkgl 165

RESULT 11
 AAM61318
 ID AAM61318 standard; Protein: 204 AA.
 XX
 AC AAM61318;
 XX 07-OCT-1998 (first entry)
 XX Mutant BCL-XL/BCL-2 associated cell death regulator #3.
 DE Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;
 XX

```

XX serine substituted mutant; apoptosis; cancer; viral infection.
XX Mus sp.
OS Synthetic.
XX WO9817682-A1.
XX 30-APR-1998.
XX 17-OCT-1997. 97WO-US19175.
XX 18-OCT-1996. 96US-0733505.
XX (UNIM ) UNIV WASHINGTON.
XX Korsmeyer SJ.
XX WPI: 1998-261422/23.
XX N-PSDB: AAV27836.
XX New mutant BAD polypeptide with phosphorylatable serine replaced
XX useful for, e.g. treating reduced apoptosis such as in cancer or
XX viral infection
XX Claim 7: Page 60-61, 95pp: English.
XX
XX The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
XX death regulator) proteins, having an amino acid other than Ser at
XX position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
XX present sequence represents a mutant BAD protein. Also described are: (1)
XX fragments of mutant BAD protein able to decrease cell viability; (2)
XX fragments of mutant BAD protein that induce apoptosis in cells; (3)
XX isolated polyclonal and monoclonal antibodies that bind to BAD protein
XX or prevent diseases associated with reduced apoptosis, e.g. cancer,
XX viral infection, lymphoproliferation, arthritis, infertility,
XX inflammation and autoimmune disease. Polynucleotide sequences encoding
XX mutant BAD proteins can be used similarly by gene therapy or to produce
XX transgenic animals for use as disease models or in drug screening. BAD
XX and inhibitors of serine-phosphatase. Inhibitors are potentially useful
XX in treatment of excessive apoptosis such as AIDS, neurodegeneration,
XX aging or ischemic cell death. The apoptotic status of cells is
XX determined by measuring relative amounts of phosphorylated and non-
XX phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
XX greater death-promoting activity than wild-type BAD which can become
XX heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family
XX proteins in the cytosol, thus promoting cell survival. The mutants with
XX Ser substituted cannot bind 14-3-3.
XX
XX Sequence 204 AA:
XX
XX Query Match 100.0%; Score 138; DB 19; Length 204;
XX Best Local Similarity 100.0%; Pred. No. 1,4e-13;
XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 NMAAORYGRELRRMSDEPGSGFKL 26
XX |||||||||||||||||||
XX Db 140 nlwaagrygrellrmdepgsfkyl 165
XX
XX RESULT 12
XX ID AAM58832 standard: protein; 204 AA.
XX AAM58832:
XX 23-JUL-1998 (first entry)
XX Murine BAD protein.
XX BAD protein; Bcl-XL/Bcl-2 associated cell death regulator; 14-3-3;

```

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XX serine phosphorylation; post-translational modification; apoptosis;
XX signal transduction regulator; phosphoserine phosphatase; senescence;
XX immunodeficiency disease; neurodegenerative disease; infertility;
XX cancer; viral infection; lymphoproliferative condition; arthritis;
XX inflammation; autoimmune diseases.
XX Mus sp.
XX WO9809643-A1.
XX 12-MAR-1998.
XX 09-SEP-1997. 97WO-US15871.
XX 09-SEP-1996. 96US-0707868.
XX (UNIM ) UNIV WASHINGTON.
XX Korsmeyer SJ.
XX WPI: 1998-207049/18.
XX Serine-phosphorylated Bcl-X-L/Bcl-2 Associated cell Death regulator
XX polypeptide - useful for modulation of apoptosis associated with,
XX e.g. cancer and immunodeficiency diseases
XX Claim 3: Fig 8; 61pp: English.
XX
XX This sequence represents a novel serine-phosphorylated protein, BAD
XX (Bcl-XL/Bcl-2 associated cell death regulator). The serine residue is
XX phosphorylated in a post-translational modification and allows binding
XX of BAD protein to 14-3-3 family proteins which act through inhibition/activation
XX of a phosphoserine phosphatase, are useful for preventing/treating
XX increased/decreased apoptosis in a cell. The increased apoptosis may
XX result from immunodeficiency diseases, senescence, neurodegenerative
XX disease, ischemic cell death, reperfusion cell death, infertility and
XX wound-healing. Decreased apoptosis may result from cancer, viral
XX infection, lymphoproliferative conditions, arthritis, infertility,
XX inflammation and autoimmune diseases. Measuring the amount of
XX phosphorylated compared to unphosphorylated BAD polypeptide and/or total
XX BAD in a cell is useful for determining the apoptotic state of a cell.
XX
XX Sequence 204 AA:
XX
XX Query Match 100.0%; Score 138; DB 19; Length 204;
XX Best Local Similarity 100.0%; Pred. No. 1,4e-13;
XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 NMAAORYGRELRRMSDEPGSGFKL 26
XX |||||||||||||||||||
XX Db 140 nlwaagrygrellrmdepgsfkyl 165
XX
XX RESULT 13
XX ID AAB70369 standard: protein; 204 AA.
XX AAB70369:
XX 02-MAY-2001 (first entry)
XX Longer murine BAD mutant amino acid sequence SEQ ID NO:2.
XX Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;
XX immunosuppressant; neuroprotective; nontropic; antischismatic; vulnerrary;
XX cytosolic; antiviral; antiarthritis; antinflammatory; wound healing;
XX immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;
XX immunodeficiency disease; neurodegenerative disease; viral infection;
XX ischemic cell death; reperfusion cell death; arthritis; infertility;
XX lymphoproliferative condition; inflammation; autoimmune disease.
XX

```

OS	Mus musculus.
XN	Synthetic.
PN	WO200110888-A1.
PD	15-FEB-2001.
PF	30-MAY-2000; 2000MO-US11864.
XX	28-MAY-1999; 99US-0136783.
XX	(APOP-) APOPTOSIS TECHNOLOGY INC.
PA	Zhou X;
PI	WPI: 2001-138734/14.
PM	New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide useful for candidate compounds which induce or inhibit apoptosis, comprises amino acid substitutions at Ser118, Ser155 or Ser113 -
PT	Ser113 -
PS	Claim 4: Page 148; 157P; English.
XX	The present invention describes an isolated or synthetic polypeptide (I) comprising a less than full length amino acid sequence of a mutant Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its fragment, which contains amino acid substitutions at Ser118 of a human BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective, anticarcinogenic, antischistosomal, cytotoxic, antiviral, antiapoptotic, anti-inflammatory and immunosuppressive activities, and can be used as an apoptosis inducer or inhibitor. BAD polypeptides and polynucleotides can be used for screening candidate compounds and drugs for activity that promote cell survival or apoptosis. Other uses include inducing or inhibiting apoptosis in a cell. Candidate compounds identified and (mutant) BAD polypeptides are useful in treating immunodeficiency diseases, neurodegenerative diseases, ischemic cell damage, cancer, autoimmune diseases, infectious diseases, inflammatory lymphoproliferative conditions, arthritis, infertility, inflammation and autoimmune diseases. The present sequence represents a specifically claimed longer murine BAD mutant amino acid sequence from the present invention.
CC	Sequence 204 AA:
SO	Query Match 100.0%; Score 138; DB 22; Length 204; Best Local Similarity 100.0%; Pred. No. 1,46-13; Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 NLMAARVGRLEKRMSEDFGSPFKGL 26 140 nlwagqrgyrelrmsedefgskgl 165
Ob	RESULT 14 TANU00220 XN TANU00220 standard; Protein: 567 AA. XX AAU00220: AC DT 31-MAY-2001 (first entry) XT DE Bad-DTRR apoptosis-modifying fusion protein. XX XX Mouse; Bad-DTRR: apoptosis; cancer; spinal muscular atrophy; XX diphtheria toxin receptor binding domain; DTR; neoplasm; tumor; XX hyper-proliferation; Alzheimer's disease; neurodegenerative disorder; XX transient ischaemic neuronal injury; stroke; spinal cord injury; XX Huntington's disease. XX XS Chimeric - Mus sp.

[illegible]

XX BRC6 gene; cell death; cell cycle; Bcl2; human.
 XX Homo sapiens.
 OS
 XX
 XX US5663316-A.
 PN
 XX
 XX 02-SEP-1997.
 PD
 XX
 XX 18-JUN-1996; 96US-0665617.
 PF
 XX
 XX 18-JUN-1996; 96US-0665617.
 PR
 XX
 XX (CLON-) CLONTECH LAB INC.
 PA
 XX
 XX Xudong Y;
 PI
 XX
 XX WPI; 1997-447980/41.
 DR
 XX N-PSDB; AAT91561.
 DR
 XX
 XX Isolated BRC6 gene - encodes a protein that regulates cell death
 PT through interaction with Bcl-2
 PT
 XX
 XX Claim 1: Column 11-12; 7pp; English.
 PS
 XX
 XX The present sequence represents a protein of 166 amino acids. The
 CC sequence is disclosed as being a protein called BRC6 which regulates
 CC cell death through interaction with Bcl-2. The DNA may be used for the
 CC production of the recombinant protein, which can be used in unspecified
 CC therapeutic or diagnostic procedures, as a molecular weight marker, and
 CC to raise antibodies that can be used in unspecified diagnostic or
 CC therapeutic applications and to reduce or eliminate the biological
 CC activity of the BRC6 protein in vivo.
 CC
 XX
 SO Sequence 166 AA:

Query Match 82.6%; Score 114; DB 18; Length 166;
 Best Local Similarity 91.7%; Pred. No. 6.1e-10;
 Matches 22: Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 NLMAGRYGRELRRMSDEFGCSFK 24
 ||||||||||||||||
 Db 101 nlwaagrygrelrrmsdefvdfsk 124

Search completed: September 20, 2002, 10:35:56
 Job time: 424 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 20, 2002, 10:37:18 ; Search time 75.64 Seconds
(without alignments)
8.396 Million cell updates/sec

Title: US-09-544-664-2

Perfect score: 138

Sequence: 1 NLMAQRYGRELRLMSDFEFGSKCL 26

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*
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3: /cgn2.6/ptodata/2/1aa/6a.COMB.pep:*
4: /cgn2.6/ptodata/2/1aa/6b.COMB.pep:*
5: /cgn2.6/ptodata/2/1aa/PCITUS.COMB.pep:*
6: /cgn2.6/ptodata/2/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	138	100.0	204	1	US-08-333-565-2
2	138	100.0	204	2	US-08-661-479-2
3	138	100.0	204	2	US-08-733-505A-1
4	138	100.0	204	2	US-08-733-505A-12
5	138	100.0	204	2	US-08-733-505A-13
6	138	100.0	204	2	US-08-733-505A-14
7	135	97.8	204	2	US-08-717-123-3
8	114	82.6	166	1	US-08-665-617-2
9	114	82.6	168	2	US-08-717-123-2
10	114	82.6	168	3	US-08-985-335-1
11	114	82.6	168	3	US-08-985-335-7
12	114	82.6	168	4	US-09-410-372-1
13	114	82.6	168	4	US-09-410-372-7
14	113	81.9	23	1	US-08-333-565-10
15	113	81.9	23	2	US-08-661-479-10
16	102	73.9	59	2	US-08-733-505A-55
17	102	73.9	59	2	US-08-733-505A-56
18	102	73.9	59	2	US-08-733-505A-57
19	102	73.9	59	2	US-08-733-505A-58
20	102	73.9	59	2	US-08-733-505A-59
21	86	62.3	16	1	US-08-333-565-26
22	86	62.3	16	1	US-08-661-479-26
23	61	44.2	11	2	US-08-733-505A-34
24	61	44.2	11	2	US-08-706-741B-69
25	37.0	11	2	2	US-08-924-695A-69
26	33.3	66	3	2	US-08-867-087B-40
27	33.3	946	4	4	US-09-074-579-3
					Sequence 3, Appl

28	44	31.9	263	4	US-09-651-656-27	Sequence 27, Appl
29	43	31.2	81	1	US-08-497-312-19	Sequence 19, Appl
30	43	31.2	213	3	US-08-718-738-18	Sequence 18, Appl
31	43	31.2	213	4	US-09-221-844-18	Sequence 18, Appl
32	43	31.2	380	1	US-08-153-848-40	Sequence 40, Appl
33	43	31.2	380	3	US-09-299-843A-40	Sequence 40, Appl
34	43	31.2	380	4	US-09-088-337B-40	Sequence 40, Appl
35	43	31.2	380	5	PCT-US93-11153-40	Sequence 40, Appl
36	42	30.4	322	4	US-09-359-161-7	Sequence 7, Appl
37	42	30.4	348	2	US-08-997-080-170	Sequence 170, App
38	42	30.4	348	2	US-08-997-362-170	Sequence 170, App
39	42	30.4	348	2	US-09-095-855-170	Sequence 170, App
40	42	30.4	348	4	US-09-324-542-170	Sequence 170, App
41	42	30.4	393	2	US-08-997-080-94	Sequence 94, Appl
42	42	30.4	393	2	US-08-997-362-94	Sequence 94, Appl
43	42	30.4	393	3	US-08-873-970-94	Sequence 94, Appl
44	42	30.4	393	4	US-09-095-855-94	Sequence 94, Appl
45	42	30.4	393	4	US-09-324-542-94	Sequence 94, Appl

ALIGNMENTS

RESULT 1
US-08-333-565-2
Sequence 2, Application US/08333565
Patent No. 5622852
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl-X/Bcl-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend Kourile and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,565
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ. ID NO.: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: protein
LOCATION: 1..204
OTHER INFORMATION:
OTHER INFORMATION: of mouse BAd.
US-08-333-565-2

Query Match 100.0%; Score 138; DB 1; Length 204;
Best Local Similarity 100.0%; Pred. No. 4e-14;
Matches 26; Conservative 0; Mismatches 0; Indels 0;

OY 1 NLMAAORYGRELRRMSDEFECSFKGL 26
DB 140 NLMAAORYGRELRRMSDEFECSFKGL 165

RESULT 2:

US-08-661-479-2
Sequence 2, Application US/08661479
Patent No. 5834209
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: BCL-X/BCL-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,479
FILING DATE: 11-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/333,565
FILING DATE: 31-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..204
OTHER INFORMATION: /note="Deduced amino acid sequence
OTHER INFORMATION: of mouse BAD."

Query Match 100.0%; Score 138; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 4e-14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLMAAORYGRELRRMSDEFECSFKGL 26
DB 140 NLMAAORYGRELRRMSDEFECSFKGL 165

RESULT 3

US-08-733-505A-1
Sequence 1, Application US/08733505A
Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR

NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-733-505A-1

Query Match 100.0%; Score 138; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 4e-14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLMAAORYGRELRRMSDEFECSFKGL 26
DB 140 NLMAAORYGRELRRMSDEFECSFKGL 165

RESULT 4

US-08-733-505A-12
Sequence 12, Application US/08733505A
Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:

TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-733-505A-12

Query Match 100.0%; Score 138; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 4e-14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLMAAORYGRELRRMSDEFGSFKGL 26
|||||
Db 140 NLMAAORYGRELRRMSDEFGSFKGL 165

RESULT 5
US-08-733-505A-13
Sequence 13, Application US/08733505A
Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
NUMBER OF SEQUENCES: 60
BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-733-505A-13

Query Match 100.0%; Score 138; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 4e-14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLMAAORYGRELRRMSDEFGSFKGL 26
|||||
Db 140 NLMAAORYGRELRRMSDEFGSFKGL 165

RESULT 6

US-08-733-505A-14
Sequence 14, Application US/08733505A
Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
NUMBER OF SEQUENCES: 60
BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-733-505A-14

Query Match 100.0%; Score 138; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 4e-14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLMAAORYGRELRRMSDEFGSFKGL 26
|||||
Db 140 NLMAAORYGRELRRMSDEFGSFKGL 165

RESULT 7
US-08-717-123-3
Sequence 3, Application US/08717123
Patent No. 5965703
GENERAL INFORMATION:
APPLICANT: Horne, William A.
TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
NUMBER OF SEQUENCES: 15
ACIDS AND METHODS OF USE
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/717,123
FILING DATE: 20-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 1929
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-717-123-3

Query Match 97.8%; Score 135; DB 2; Length 204;
Best Local Similarity 96.2%; Pred. No. 1.2e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 NMAAQRGRLRMSDFEGSFKGL 26
DB 140 NMAAQRGRLRMTDFEGSFKGL 165

RESULT 8
US-08-665-617-2
Sequence 2, Application US/08665617
Patent No. 5663316
GENERAL INFORMATION:
APPLICANT: Xudong, Yin
TITLE OF INVENTION: Gene and Protein for Regulation of Cell Death
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,617
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: CL-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-665-617-2

Query Match 82.6%; Score 114; DB 1; Length 166;
Best Local Similarity 91.7%; Pred. No. 1.8e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 NMAAQRGRLRMSDFEGSFK 24

DB 101 NMAAQRGRLRMSDFEYDSFK 124

RESULT 9
US-08-717-123-2
Sequence 2, Application US/08717123
Patent No. 5965703
GENERAL INFORMATION:
APPLICANT: Horne, William A.
APPLICANT: Oltendorf, Yllman
TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
Acids and Methods of Use
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/717,123
FILING DATE: 20-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 1929
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-717-123-2

Query Match 82.6%; Score 114; DB 2; Length 168;
Best Local Similarity 91.7%; Pred. No. 1.8e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 NMAAQRGRLRMSDFEGSFK 24
DB 103 NMAAQRGRLRMSDFEYDSFK 126

RESULT 10
US-08-985-335-1
Sequence 1, Application US/08985335
Patent No. 6080847
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Ial, Preeti
APPLICANT: Shah, Puryi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
PROLIFERATION
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSER: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA

COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSD for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,335
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SYNORAB01
CLONE: 358673
US-08-985-335-1

Query Match 82.6%; Score 114; DB 3; Length 168;
Best Local Similarity 91.7%; Pred. No. 1.8e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NMAAORYGRELIRMSDEFGSK 24
DB 103 NMAAORYGRELIRMSDEFGSK 126

RESULT 11
US-08-985-335-7
Sequence 7, Application US/08985335
Patent No. 6080847
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purni
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
PROLIFERATION
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSD for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,335
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 1683637
US-08-985-335-7

Query Match 82.6%; Score 114; DB 3; Length 168;
Best Local Similarity 91.7%; Pred. No. 1.8e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NMAAORYGRELIRMSDEFGSK 24
DB 103 NMAAORYGRELIRMSDEFGSK 126

RESULT 12
US-09-410-372-1
Sequence 1, Application US/09410372
Patent No. 6281334
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purni
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
PROLIFERATION
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSD for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/410,372
FILING DATE:
PRIOR APPLICATION DATA: 08/985,335
APPLICATION NUMBER: 08/985,335
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SYNORAB01

CLONE: 358673
US-09-410-372-1

Query Match 82.6% Score 114; DB 4; Length 168;
Best Local Similarity 91.7% Pred. No. 1.8e-10;
Matches 22: Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 NMAAORYGRELRLMSDEFGSFK 24
DB 103 NMAAORYGRELRLMSDEFGSFK 126

RESULT 13
US-09-410-372-7
Sequence 7, Application US/09410372
Patent No. 628134
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/410,372
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985,335
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ. ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 1683637
US-09-410-372-7

Query Match 82.6% Score 114; DB 4; Length 168;
Best Local Similarity 91.7% Pred. No. 1.8e-10;
Matches 22: Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 NMAAORYGRELRLMSDEFGSFK 24
DB 103 NMAAORYGRELRLMSDEFGSFK 126

RESULT 14

US-08-333-565-10
Sequence 10, Application US/08333565
Patent No. 5622852
GENERAL INFORMATION:

APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,565
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ. ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-333-565-10

Query Match 81.9% Score 113; DB 1; Length 23;
Best Local Similarity 100.0% Pred. No. 2.8e-11;
Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NMAAORYGRELRLMSDEFGS 21
DB 3 NMAAORYGRELRLMSDEFGS 23

RESULT 15
US-08-661-479-10
Sequence 10, Application US/08661479
Patent No. 5831203
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,479

Fri Sep 20 11:03:06 2002

us-09-544-664-2.rai

Page 7

FILED DATE: 11-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/333,565
FILING DATE: 31-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-661-479-10

Query Match 81.9%; Score 113; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 NLMAAQRGRLRRMSDEFEG 21
|||||
Db 3 NLMAAQRGRLRRMSDEFEG 23

Search completed: September 20, 2002, 10:37:19
Job time: 407 sec

Fri Sep 20 11:03:07 2002

us-09-544-664-2.rpt

ge 1

GenCore version 4.5
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OW protein - protein search, using SW model

Run on: September 20, 2002, 10:39:02 ; Search time 55.59 Seconds
(without alignments)
26.136 Million cell updates/sec

Title: US-09-544-664-2

Perfect score: 138

Sequence: 1 NMAAQRGRRLRMSDEFSGFKGL 26

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched:

283138 seqs, 9608934 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

Listing first 45 summaries
1: PIR-71:
2: PIR-1:
3: PIR-2:
4: PIR-4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	138	100.0	204	2	AS5671
2	34	39.1	223	2	JC5575
3	33	38.4	223	2	D70760
4	32	37.0	223	2	S53384
5	32	37.0	223	2	S53384
6	32	37.0	223	2	S53384
7	32	37.0	223	2	S53384
8	32	37.0	223	2	S53384
9	32	37.0	223	2	S53384
10	32	37.0	223	2	S53384
11	32	37.0	223	2	S53384
12	32	37.0	223	2	S53384
13	32	37.0	223	2	S53384
14	32	37.0	223	2	S53384
15	32	37.0	223	2	S53384
16	32	37.0	223	2	S53384
17	32	37.0	223	2	S53384
18	32	37.0	223	2	S53384
19	32	37.0	223	2	S53384
20	32	37.0	223	2	S53384
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23	32	37.0	223	2	S53384
24	32	37.0	223	2	S53384
25	32	37.0	223	2	S53384
26	32	37.0	223	2	S53384
27	32	37.0	223	2	S53384
28	32	37.0	223	2	S53384
29	32	37.0	223	2	S53384

30	45	32.6	155	2	S53384
31	39	32.6	155	2	S53384
32	39	32.6	155	2	S53384
33	39	32.6	155	2	S53384
34	39	32.6	155	2	S53384
35	39	32.6	155	2	S53384
36	39	32.6	155	2	S53384
37	39	32.6	155	2	S53384
38	39	32.6	155	2	S53384
39	39	32.6	155	2	S53384
40	39	32.6	155	2	S53384
41	39	32.6	155	2	S53384
42	39	32.6	155	2	S53384
43	39	32.6	155	2	S53384
44	39	32.6	155	2	S53384
45	39	32.6	155	2	S53384

ALIGNMENTS

RESULT 1
bad protein - mouse
C:Species: Mus musculus (house mouse)
C>Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 05-Nov-1995
C:Accession: A55671
R:Yang, E.; Zha, J.; Jockel, J.; Boise, L.H.; Thompson, C.B.; Korsmeyer, S.J.
Cell 80, 285-291, 1995
A:Title: Bad, a heterodimeric partner for Bcl-xL and Bcl-2, displaces Bax and promotes apoptosis.
A:Reference number: A55671; MUID:95136361
A:Accession: A55671
A:Status: preliminary: not compared with conceptual translation
A:Molecule type: mRNA
A:Accession: A55671
A:Cross-references: CB:137296; NID:9639778; PIDN:AAA64455.1; PID:9639779
C:Keywords: heterodimer

Query Match 100.0% Score 138; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 7.1e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 NMAAQRGRRLRMSDEFSGFKGL 165
|||
RESULT 2
bad protein - mouse
C:Species: Mus musculus (house mouse)
C>Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 05-Nov-1995
C:Accession: A55671
R:Yang, E.; Zha, J.; Jockel, J.; Boise, L.H.; Thompson, C.B.; Korsmeyer, S.J.
Cell 80, 285-291, 1995
A:Title: Bad, a heterodimeric partner for Bcl-xL and Bcl-2, displaces Bax and promotes apoptosis.
A:Reference number: A55671; MUID:95136361
A:Accession: A55671
A:Status: preliminary: not compared with conceptual translation
A:Molecule type: mRNA
A:Accession: A55671
A:Cross-references: CB:137296; NID:9639778; PIDN:AAA64455.1; PID:9639779
C:Keywords: heterodimer

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Query Match      39.1% Score 54 DB 2 Length 946;
Best local similarity 34.6% pred. No. 8.8
Matches 9; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

Qy      1 NLMAAOBYGRELRLRMSDEFGSGFKGL 26
       1 1 1 : : | 1 1 1 1 1 :
Db      212 NWAVLELQGMARFLVPRDTEGHPCGV 237

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RESULT **3**

D70760
hypothetical protein RV2014 - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 **Sequence_revision** 17-Jul-1998 **Stext_change** 22-Oct-1999
C:Accession: D70760
R:ColE, S.T.: Brosch, R., Parkhill, J., Garnier, T., Churcher, C., Harris, D., Gordon, S., Cole, M.A., de Lencastre, E., Archer, G.F., Berrington, J., Brown, K.E., Cherepanin, P., et al.: Nature 393:525-544, 1998
R:Authors: Segre, R., Salton, J.R., Taylor, J.R., Whittambs, S., Barrall, R.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; NCID:98295987
A:Accession: D70760
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-223 <COL>
A:Cross-references: GB:574025; GB:ALJ23456; NID:93261586; PIDN:CAA98415.1; PID:ej299111
A:Experimental source: strain H37RV
G:Genetics:
G:Gene: RV2014

5

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Oy      1 NMAAORYGRLRPMSD 17
         ||||| ||| : : |
Db      165 NMAADRYKRALRGHD 181

Query Match      38.4%; Score 53; DB 2; length 223;
Best Local Similarity 58.8%; Pred. No. 2.8;
Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

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RESULT 4

Inter-alpha-Inhibitor H2 chain - mouse
S54354

C:Species: Mus musculus (house mouse)
C:Date: 15-Jul-1993 sequence-revision 01-Sep-1995 #text-change 20-Aug-1999
C:Accession: S54354

R:Chan, P.; Risler, J.L.; Raguenez, G.; Saller, J.P.
Biochem. J. 306, 505-513, 1995

A:Title: The three heavy-chain precursors for the inter-alpha-inhibitor family in mouse
A:Reference number: S54353; MUID:95194326

A:Accession: S54354

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residue: 1,946 <CNA>

A:Cross-References: EMBL:X70392; NID:g695633; PIDD:CAA9842.1; PID:g695634

A:Superfamily: Inter-alpha-trypsin inhibitor complex component II

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Query Match      38.4%; Score 53; DB 2; Length 946;
Best Local Similarity 34.6%; Pred. No. 12;
Matches 9; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

Qy      1 NMAAQRYRELRMSDEFGSGKL 26
      1:1 1 1 1 1 1 1 1
Db      212 NWMIIEQGMRLNPDTGEGHPOV 237

```

RESULT 3
S38185
2-dehydro-3-deoxyphosphonate aldolase (EC 4.1.2.15) ARO4 - yeast (Saccharomyces cerevisiae)
N Alternate names: 3-deoxy-D-arabino-heptulosonate-7-phosphate synthase; DAHP synthase;
C Species: Saccharomyces cerevisiae

C:Idate: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
C:Accession: S38185 #S46126: S46130: J060322: P48651
R:Dolignon, P.; Bileau, N.; Aigle, M.; Crowzet, M.
Yeast 9, 1131-1137, 1993
A:Title: The complete sequence of a 6794 bp segment located on the right arm of chr.
A:Reference number: S38185; M01D:94078675
A:Accession: S38185
A:Status: translation not shown

A:Residues: 1-370 <AD>
A:Cross-references: EMBL:Z26118; NID:933666; PIRN:CAA85212.1; PTD:g33665; MIPS:YBR222.1; RAL1novic, G.; Pohl, F.M.; Pohl, T.M.
Submitted to the Protein Sequence Database, August 1994
A:Reference number: S45906
A:Accession: S46126
A:Molecule type: DNA
A:Residues: 1-370 <AD>
A:Cross-references: EMBL:Z26118; NID:933666; PIRN:CAA85212.1; PTD:g33665; MIPS:YBR222.1; RAL1novic, G.; Pohl, F.M.; Pohl, T.M.
Submitted to the Protein Sequence Database, August 1994
A:Reference number: S45940
A:Accession: S46130
A:Molecule type: DNA
A:Residues: 1-370 <AD>
A:Cross-references: EMBL:Z26118; NID:933666; PIRN:CAA85212.1; PTD:g33665; MIPS:YBR222.1; Rikienzi, M.; Paravaychi, G.; Egli, C.M.; Tringer, S.; Braus, G.H.
Gene 113, 67-74, 1992
A:Title: Cloning, primary structure and regulation of the ARO4 gene, encoding the Cys4
A:Reference number: JN0322; M01D:92225349
A:Accession: JN0322

A:Cross-references: EMBL:X61107
R:Kienzlner, M.; Balmelli, T.; Egli, C.M.; Parvizi, G.; Bruns, G.H.
J. Bacteriol. 175, 5548-5558, 1993
A:Title: Cloning, primary structure, and regulation of the H17 gene encoding a b1un
A:Reference number: A48651, MIMD:5374850
A:Accession: B48651
A>Status: preliminary

A:Cross-references: GB:X61107
A:Comment: This enzyme catalyzes the condensation of phosphoenolpyruvate and D-erythr
C:Genetics:
A:Gene: SGD:ARO4
A:Cross-references: SGD:S0000453; MIPS:YBR249C
A:Map position: 2R
Function:
A:Pathway: aldohyde-lyase: carbon-carbon lyase
A:Pathway: aromatic amino acid biosynthesis; shikimate pathway
A:Note: first step in shikimate pathway
C:Superfamily: phospho-2-dehydro-3-deoxyheptonate aldolase
C:Keywords: aldohyde-lyase; aromatic amino acid biosynthesis; carbon-carbon lyase; cy

Query Match 37.7%; Score 52; DB 2; Length 370;
Best Local Similarity 47.6%; Pred. NO. 6.7;
Matches 10; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy	1	N	A	A	O	R	V	G	R	E	L	R	M	S	D	E	F	E	G	21
Db	80	D	L	F	A	A	O	E	T	A	L	R	K	T	S	D	E	L	K	100

C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994
C:Accession: A42095: S52633: T4753 #text_change 21-Jul-2000
R:Jack, T.: Brockman, L.L.: Meyerowitz, E M
Cell 86, 685-697, 1992

A:Title: The homeotic gene *APETALA3* of *Arabidopsis thaliana* encodes a MADS-box and is ex
A:Reference number: A42095; MUID:92154682
A:Accession: A42095
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-232 <JAC>
A:Cross-references: GB:M6357; NID:q166607; PIDN:AAA32740.1; PID:q166608
A:Experimental source: petals, stamens
A:Note: sequence extracted from NCBI backbone (NCBIN:82520, NCBI:P:82521)
R:Okamoto, H.; Yano, A.; Shirasahi, H.; Okada, K.; Shimura, Y.
Plant Mol. Biol. 26, 465-472, 1994
A:Title: Genetic complementation of a floral homeotic mutation, *apetala3*, with an *Arabid*
A:Reference number: S52633; MUID:95036018
A:Accession: S52633
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-63 <OKA>
A:Cross-references: GB:ID21125
R:Blocker, H.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Queller, F.; Salanoubat M.Mewes,
submitted to the Protein Sequence Database, March 2000
A:Reference number: 224469
A:Accession: 247593
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-232 <DLO>
A:Cross-references: EMBL:AL132971
A:Experimental source: cultivar Columbia; BAC clone T12P18
C:Genetics:
A:Map position: 3
A:introns: 63/2; 106/2; 139/3; 153/3; 168/3
A:Note: T12P18.30
C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
C:Keywords: DNA binding; nucleus; transcription regulation
F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 37.0%; Score 51; DB 2; Length 232;
Best Local Similarity 44.4%; Pred. No. 5.8;
Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;

OY 6 OMVG-----RLRRMSDEFGSFK 24
DB 107 ORLGCLEDDLDLRLRRLEDEMTFK 133

RESULT 7
C84338
Spermidine/putrescine ABC transporter [imported] - *Halobacterium* sp. NRC-1
C:Species: *Halobacterium* sp. NRC-1
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: C84338
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.
; Leihhauser, B.; Keller, K.; Cruz, R.; Dawson, M.J.; Hough, D.W.; Maddocks, D.G.; Jaldic
Jung, K.H.; Alam, S.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Ng, W.V.; Daniels, C.; Dennis, P.F.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li
A:Title: Genome sequence of *Halobacterium* species NRC-1.
A:Reference number: A84160; MUID:20504483
A:Accession: C84338
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-374 <STO>
A:Cross-references: GB:AE004437; NID:q1058134; PIDN:AGC20071.1; GSPDB:GN00138
C:Genetics:
A:Gene: *potA2*

Query Match 36.2%; Score 50; DB 2; Length 374;
Best Local Similarity 76.9%; Pred. No. 13;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 11 ELRRMSDEFGSF 23
||||| |||

DB 197 ELRRLSDAVBGSF 209

RESULT 8
A96753
Probable threonine synthase [imported] - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cross)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: A96753
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Com, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, T.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Matzla
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A:Reference number: A86141; MUID:21016719
A:Accession: A96753
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-516 <STO>
A:Cross-references: GB:AE005173; NID:q5903070; PIDN:AA55628.1; GSPDB:GN00141
C:Genetics:
A:Gene: *ERN3.1*
A:Map position: 1

Query Match 35.2%; Score 50; DB 2; Length 516;
Best Local Similarity 35.3%; Pred. No. 19;
Matches 12; Conservative 7; Mismatches 7; Indels 8; Gaps 1;

OY 1 NMAAORYGRELRMSD-----EFGSFKGL 26
DB 163 NMAAORYGKGYLDMDLVKKGISHTGSKDL 196

RESULT 9
E83517
Conserved hypothetical protein PA1031 [imported] - *Pseudomonas aeruginosa* (strain PAO
C:Species: *Pseudomonas aeruginosa*
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: E83517
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lapid, K.; L
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pa
A:Reference number: A82950; MUID:20437337
A:Accession: E83517
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-453 <STO>
A:Cross-references: GB:AE004535; GB:AE004091; NID:q9944636; PIDN:AA04420.1; GSPDB:GN
A:Experimental source: strain PA01
C:Genetics:
A:Gene: *PA1031*

Query Match 35.5%; Score 49; DB 2; Length 453;
Best Local Similarity 55.6%; Pred. No. 23;
Matches 10; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

OY 3 WMAORYGR--ELRRMSDE 18
DB 65 WMSRGGREELRLRIASF 82
||||| |||

RESULT 10
S40376
Ig kappa chain - human

C:Species: Homo sapiens (man)
 C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C:Accession: S40376
 R:Klein, R.; Jaenichen, R.; Zachau, H.G.
 R:Klein, R.; Jaenichen, R.; Zachau, H.G.
 A:Title: Expressed human immunoglobulin cH1 genes and their hypermutation.
 A:Reference number: S40376; MUID:94080891
 A:Accession: S40376
 A:Status: preliminary; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-134 <K1E>
 A:Cross-references: EMBL:X72486; NID:g441440; PIDN:CAA51154.1; PID:g441441
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:34-113/Domain: Immunoglobulin homology <1MM>

Query Match 35.18; Score 48.5; DB 2; Length 134;
 Best Local Similarity 38.28; Pred. No. 7.8;
 Matches 13; Conservative 1; Mismatches 9; Indels 11; Gaps 1;
 Oy 3 MAARYGRLRRM-----SDEFGSFGK 25
 Db 58 WFRQRPGRSPRLIYNVSKRDSGVSRSGSG 91

RESULT 11
 T02975
 C:Species: Zea mays (maize)
 C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
 C:Accession: T02975
 R:Bartley, N.H.; James, N.C.; Greenland, A.J.
 R:Plant Physiol. 112, 1391-1396, 1996
 A:Title: CDNA isolation and gene expression of maize annexins P33 and P35.
 A:Reference number: 214796; MUID:97092863
 A:Accession: T02975
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-314 <BAY>
 A:Cross-references: EMBL:X98245; NID:g3370602; PIDN:CAA66901.1; PID:g3370603
 A:Experimental source: cultured clipper root tip
 C:Superfamily: annexin I; annexin repeat homology
 F:14-85/Domain: annexin repeat homology <AKR>

Query Match 35.18; Score 48.5; DB 2; Length 314;
 Best Local Similarity 47.68; Pred. No. 19;
 Matches 10; Conservative 4; Mismatches 6; Indels 1; Gaps 1;
 Oy 5 AQRVGR-LRMSDFEGSFGK 24
 Db 54 AEAVGKELRALGDEIRKPE 74

RESULT 12
 C36365
 C:Species: Rhizomucor racemosus
 C:Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 19-Jan-2001
 C:Accession: C36365
 R:Casale, M.L.; McConnell, D.G.; Wang, S.Y.; Lee, Y.J.; Linz, J.E.
 R:Mol. Cell. Biol. 10, 6654-6663, 1990
 A:Title: Expression of a gene family in the dimorphic fungus Mucor racemosus which exhibit
 A:Reference number: A56365; MUID:91061774
 A:Accession: C36365
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-206 <CAS>
 A:Cross-references: GB:M55117
 C:Superfamily: ras transforming protein; translation elongation factor Tu homology
 C:Keywords: GTP binding; nucleotide binding; P-loop
 F:11-126/Domain: translation elongation factor Tu homology <ETU>

F:17-24/Region: nucleotide-binding motif A (P-loop)
 F:123-126/Region: GTP-binding NKXD motif
 F:153-155/Region: GTP-binding SAK/L motif
 F:23,24,42,123,124,126,153/Binding site: Mg-GTP (Lys, Ser, Thr, Asn, Lys, Asp, Ser) #

Query Match 34.88; Score 48; DB 2; Length 206;
 Best Local Similarity 62.58; Pred. No. 14;
 Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 Oy 10 REIRMSDFEGSFGK 25
 Db 169 REIRRMKEDBSRSG 184

RESULT 13
 F72289
 C:Species: Thermotoga maritima
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
 C:Accession: F72289
 R:Neelson, K.E.; Cleyton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hic
 Carrell, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
 C.M.
 A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
 A:Reference number: A72200; MUID:99287316
 A:Accession: F72289
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-220 <AR>
 A:Cross-references: GB:AE001772; GB:AE000512; NID:g4981693; PIDN:AA036230.1; PID:g498
 A:Experimental source: strain MS8
 C:Genetic: TM1154
 C:Superfamily: yeast SOL3 protein

Query Match 34.88; Score 48; DB 2; Length 220;
 Best Local Similarity 34.88; Pred. No. 15;
 Matches 8; Conservative 8; Mismatches 7; Indels 0; Gaps 0;
 Oy 4 MAQRGRLRRMSDFEGSFGK 26
 Db 111 ACERYEREIRSAVDFDLALIGM 133

RESULT 14
 T08545
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 07-Dec-1999
 C:Accession: T08545; S71362; S74307
 R:Bevan, M.; Zimmermann, W.; Gruenisen, A.; Wandut, R.; Bancroft, I.; Mewes, H.W.;
 submitted to the Protein Sequence Database, May 1999
 A:Reference number: 216442
 A:Accession: T08545
 A:Molecule type: DNA
 A:Residues: 1-526 <BEV>
 A:Cross-references: EMBL:A1050352; GSPDB:GN00062; ATSP:F72813.80
 A:Experimental source: cultured Columbia; BAC clone F72813
 R:Curien, G.; Dumas, R.; Ravanet, S.; Douce, R.
 R:FEBS Lett. 390, 85-90, 1996
 A:Title: Characterization of an Arabidopsis thaliana cDNA encoding an S-adenosylmethi
 A:Reference number: S71362; MUID:96314555
 A:Accession: S71362
 A:Molecule type: mRNA
 A:Residues: 1-3-526 <CUR>
 A:Cross-references: EMBL:L41666; NID:g1448916; PIDN:AA04607.1; PID:g1448917
 A:Accession: S74307
 A:Molecule type: protein
 A:Residues: 40-54 <CUR>

C, Genetics:
A, Gene: ATSP:F27B13.80

A map position: 4
A: Genomic nucleayA, uellome: uacreat
C. Kaywonds: carbh

Casey records: 1940-1941

E: A0=526/Product: threonine synthase #status experimental <MAT>

[illegible]

Query Match	34.88;	Score 48;	DB 2;	Length 526
Best local similarity	35.38;	Pred. No. 37;		

Matches 12: Conservative 6: Mismatches 8: Indels

[illegible]

QY 1 NLWAAQRYGRELRRMSD-----EFGSFKGL 26

Db 172 NLFWAERFGKQELGMNDLWKHCISHTGSFKDL 209

RESULT 15

682306
Johns Hopkins Univ. - Vibrio cholerae (strain NI

Reaction: with cholesterol
 Oxaloacetate decarboxylase, alpha chain (similarity)
 Oxaloacetate decarboxylase (beta chain)

```

c:species: WDPIO endietae
c:date: 18-Aug-2000 #sequence revision 20-Aug-2000 #text change 02-Feb-2001

```

C:\data\10 Aug 2000 *sequence_revision 20 Aug 2000 *tunc_change 02 Aug 2000
C:\data\10 Aug 2000 *sequence_revision 20 Aug 2000 *tunc_change 02 Aug 2000

C/ACCESSION: 002309
 RAYDAID, I E : Eileen I A : Nelson, W C : Clayton, B A : Gwinn, M. L.: Dodson, B. J.:

Chardson D.: Ermolaeva M.D.: Yamathayan J.: Bass S.: Qin H.: Dragoi I.: Sellers F.
R./Heuvelvelg, D.: F.: Wilsen, D.M.: Nelson M.C.: Craigdon R.M.: Channing M.M.: Cohen, M.

1. P. R. : Mekalanos, J. J. : Venter, J. C. : Fraser, C. M.

Nature 406: 477-483, 2000

A: Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.

A:Reference number: A82035: MUID:20406833

A:Accession: G82308

A: Status: preliminary

A: molecule type: DNA

A;Residues: 1-597 <HEI>

A; Cross-references: GB:AE004141; GB:AE003852; MID:q9654976; PIDN:AAF93718.1; GSPDB:GN001

A; Experimental source: serogroup O1; strain N16961; biotype El Tor

C;Genetics:

A;Gene: VC0550

A:Map position: 1
C:Superfamily: Klebsiella pneumoniae oxaloacetate decarboxylase alpha chain; Lipoyl/biotin

Query Match	34.1%;	Score 47;	DB 2;	length 597;
Best Local Similarity	47.4%;	Pred. No. 60;		

Matches	9;	Conservative	4;	Mismatches	6;	Indels	0;	Gaps	0;
---------	----	--------------	----	------------	----	--------	----	------	----

QY 8 YGRELRMSDEEFGSFKJL 26
| | : : : | | :
010 YHRELRMSDEEFGSFKJL 200

DB 212 YFREVRKKKXAKFEGQLNGV 290

100

100

100

100

100

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 20, 2002, 11:04:28 : Search time 44.99 Seconds

(without alignments)
22.376 Million cell updates/sec

Title: US-09-544-664-2

Perfect score: 138

Sequence: 1 NIMAAQRYGRIEIRMSDEPESFKGL 26

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt.40.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	ID	Description
1	138	100.0	204	1	BAD_MOUSE
2	138	100.0	205	1	BAD_MOUSE
3	114	82.6	168	1	BAD_HUMAN
4	54	39.1	946	1	ITRH2_MOUSE
5	53	38.4	946	1	ITRH2_MOUSE
6	52	37.7	370	1	AROG_YEAST
7	51	37.0	232	1	AP3_ARATH
8	49	35.5	453	1	RMC_PSEAE
9	48	34.8	205	1	RAS3_RHRA
10	48	34.8	220	1	GPGL_THEMA
11	48	34.8	519	1	THRC_SOTU
12	48	34.8	526	1	THRC_SOTU
13	47	34.1	198	1	BIM_HUMAN
14	46.5	33.7	429	1	FMRL2_MOUSE
15	46.5	33.7	435	1	FMRL2_MOUSE
16	46	33.3	946	1	ITRH2_HUMAN
17	46	33.3	1378	1	ITRH2_HUMAN
18	45.5	33.0	287	1	PRPA_CAME
19	45.5	33.0	334	1	FMRL2_MOUSE
20	45	32.6	328	1	SNR4_CALPA
21	45	32.6	590	1	DCOA_SALTY
22	45	32.6	595	1	DCOA_SALTY
23	45	32.6	653	1	DCOA_SALTY
24	45	32.6	653	1	DCOA_SALTY
25	45	32.6	653	1	DCOA_SALTY
26	44.5	32.2	907	1	NUOG_ECOLI
27	44.5	32.2	907	1	NUOG_ECOLI
28	44	31.9	196	1	BIM_MOUSE
29	44	31.9	196	1	BIM_MOUSE
30	44	31.9	262	1	ENDR_ECOLI
31	44	31.9	768	1	ENV_SIVAG
32	44	31.9	877	1	ENV_SIVAG
33	43.5	31.5	217	1	UREF_SIVAG

ALIGNMENTS

RESULT	ID	Sequence	Score	Match Length	Description
1	BAD_MOUSE	US-09-544-664-2	138	204	BAD_MOUSE
2	BAD_MOUSE	US-09-544-664-2	138	205	BAD_MOUSE
3	BAD_HUMAN	US-09-544-664-2	114	168	BAD_HUMAN
4	ITRH2_MOUSE	US-09-544-664-2	54	946	ITRH2_MOUSE
5	ITRH2_MOUSE	US-09-544-664-2	53	946	ITRH2_MOUSE
6	AROG_YEAST	US-09-544-664-2	52	370	AROG_YEAST
7	AP3_ARATH	US-09-544-664-2	51	232	AP3_ARATH
8	RMC_PSEAE	US-09-544-664-2	49	453	RMC_PSEAE
9	RAS3_RHRA	US-09-544-664-2	48	205	RAS3_RHRA
10	GPGL_THEMA	US-09-544-664-2	48	220	GPGL_THEMA
11	THRC_SOTU	US-09-544-664-2	48	519	THRC_SOTU
12	THRC_SOTU	US-09-544-664-2	48	526	THRC_SOTU
13	BIM_HUMAN	US-09-544-664-2	47	198	BIM_HUMAN
14	FMRL2_MOUSE	US-09-544-664-2	46.5	429	FMRL2_MOUSE
15	FMRL2_MOUSE	US-09-544-664-2	46.5	435	FMRL2_MOUSE
16	ITRH2_HUMAN	US-09-544-664-2	46	946	ITRH2_HUMAN
17	ITRH2_HUMAN	US-09-544-664-2	46	1378	ITRH2_HUMAN
18	PRPA_CAME	US-09-544-664-2	45.5	287	PRPA_CAME
19	FMRL2_MOUSE	US-09-544-664-2	45.5	334	FMRL2_MOUSE
20	SNR4_CALPA	US-09-544-664-2	45	328	SNR4_CALPA
21	DCOA_SALTY	US-09-544-664-2	45	590	DCOA_SALTY
22	DCOA_SALTY	US-09-544-664-2	45	595	DCOA_SALTY
23	DCOA_SALTY	US-09-544-664-2	45	653	DCOA_SALTY
24	DCOA_SALTY	US-09-544-664-2	45	653	DCOA_SALTY
25	DCOA_SALTY	US-09-544-664-2	45	653	DCOA_SALTY
26	NUOG_ECOLI	US-09-544-664-2	44.5	907	NUOG_ECOLI
27	NUOG_ECOLI	US-09-544-664-2	44.5	907	NUOG_ECOLI
28	BIM_MOUSE	US-09-544-664-2	44	196	BIM_MOUSE
29	BIM_MOUSE	US-09-544-664-2	44	196	BIM_MOUSE
30	ENDR_ECOLI	US-09-544-664-2	44	262	ENDR_ECOLI
31	ENV_SIVAG	US-09-544-664-2	44	768	ENV_SIVAG
32	ENV_SIVAG	US-09-544-664-2	44	877	ENV_SIVAG
33	UREF_SIVAG	US-09-544-664-2	43.5	217	UREF_SIVAG

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CC Ser-136 is the major site of AKT/PKB phosphorylation, Ser-155 the
CC major site of protein kinase A (CAPK) phosphorylation.
CC -1- SIMILARITY: CONTAINS A BCL-3 HOMOLGY DOMAIN 3 (BH3).
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L37296; AAC64465.1;
DR MGD: MGI:1096330; Bcl-2
DR InterPro: IPR000712; Bcl-2
DR PROSITE: PS01259; BH3; FALSE_NEG.
KW Apoptosis; Phosphorylation.
FT DOMAIN 147 161 BH3.
FT MOD_RES 112 112 PHOSPHORYLATION (BY CAPK AND PKB).
FT MOD_RES 136 136 PHOSPHORYLATION (BY CAPK AND PKB).
FT MOD_RES 155 155 PHOSPHORYLATION (BY CAPK AND PKB).
FT MUTAGEN 112 112 S->A: NO PHOSPHORYLATION.
FT MUTAGEN 136 136 S->A: NO PHOSPHORYLATION.
FT MUTAGEN 155 155 S->A: NO PHOSPHORYLATION; INTERACTS WITH
FT BCL-X(L).
SO SEQUENCE 204 AA; 22080 MW; 6C2BA910205053F7 CRC64;

Oy 1 NLMAAGRYGRLRRMSDEFGSKGL 26
Db 140 NLMAAGRYGRLRRMSDEFGSKGL 165
|||||
Query Match 100.0%; Score 138; DB 1; Length 204;
Best Local Similarity 100.0%; Pred. No. 8.6e-14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
ID BAD_RAT STANDARD: PRT; 205 AA.
AC Q35147; Q70256; Q9JHX1;
DT 16-OCT-2001 (Rel. 40; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 01-MAR-2002 (Rel. 41; Last annotation update)
DE Bcl2-antagonist of cell death (BAD) (Bcl-2 binding component
DE 6) (Bcl-xL/Bcl-2 associated death promoter).
GN BAD.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN (1)
RP SEQUENCE FROM N.A. AND MUTAGENESIS OF SER-113 AND SER-137.
RC TISSUE-Ovary;
RX MEDLINE=98034386; PubMed=9369453;
RA Hsu S.Y., Kaipia A., Zhu L., Hsueh A.J.W.;
RT "Interference of BAD (Bcl-xL/Bcl-2-associated death promoter)-induced
RT apoptosis in mammalian cells by 14-3-3 isoforms and p11."
RL Mol. Endocrinol. 11:1858-1867(1997).
RN (2)
RP SEQUENCE FROM N.A.
RC TISSUE-Brain;
RX MEDLINE=98194755; PubMed=9535132;
RA D'Agata V., Negro G., Trevaill S., Musco S., Cavallaro S.;
RT "Cloning and expression of the programmed cell death regulator BAD in
RT the rat brain."
RL Neurosci. Lett. 243:137-140(1998).
RN (3)
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RC TISSUE-Brain;
RX MEDLINE=21109372; PubMed=11161472;
RA Hamner S., Atunue D., Yu L.-Y., Sun Y.-F., Saarna M., Lindholm D.;

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RT "Functional characterization of two splice variants of rat BAD and
RT their interaction with Bcl-w in sympathetic neurons."
RL Mol. Cell. Neurosci. 17:97-106(2001).
CC -1- FUNCTION: Promotes cell death. Successfully competes for the
CC binding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level
CC of heterodimerization of these proteins with BAX. Can reverse the
CC death repressor activity of Bcl-x(L), but not that of Bcl-2 (By
CC similarity). Appears to act as a link between growth factor
CC receptor signaling and the apoptotic pathways.
CC SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-
CC x(L), Bcl-2 and Bcl-w. Also binds protein S100A10. The Ser-
CC 113/Ser-137 phosphorylated form binds 14-3-3 proteins.
CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon
CC phosphorylation, locates to the cytoplasm (By similarity).
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; alpha (shown here) and beta; are
CC produced by alternative splicing. They differ only in their C-
CC terminal regions.
CC -1- TISSUE SPECIFICITY: Expressed in all tissues tested, including
CC brain, liver, spleen and heart. In the brain, restricted to
CC epithelial cells of the choroid plexus. Isoform alpha is the more
CC abundant form.
CC -1- DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND
CC BAX for their pro-apoptotic activity and for their interaction
CC with anti-apoptotic members of the Bcl-2 family.
CC -1- PTM: Phosphorylation on Ser-113 in response to survival stimuli.
CC Subsequent phosphorylation on Ser-137 promotes heterodimerization
CC with 14-3-3 proteins. This interaction then facilitates the
CC phosphorylation at Ser-156, a site within the BH3 domain, leading
CC to the release of Bcl-x(L) and the promotion of cell survival.
CC Ser-137 is the major site of AKT/PKB phosphorylation, Ser-156 the
CC major site of protein kinase A (CAPK) phosphorylation (By
CC similarity).
CC -1- SIMILARITY: CONTAINS A BCL-3 HOMOLGY DOMAIN 3 (BH3).
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF003523; AAC53374.1;
DR EMBL: AF031227; AAC15100.1;
DR EMBL: AF279910; AAP91427.1;
DR EMBL: AF279911; AAP91428.1;
DR InterPro: IPR000712; Bcl-2
DR PROSITE: PS01259; BH3; FALSE_NEG.
KW Apoptosis; Phosphorylation; Alternative splicing.
FT DOMAIN 148 162 BH3.
FT MOD_RES 113 113 PHOSPHORYLATION (BY CAPK AND PKB) (BY
FT SIMILARITY).
FT MOD_RES 137 137 PHOSPHORYLATION (BY CAPK AND PKB) (BY
FT SIMILARITY).
FT MOD_RES 156 156 PHOSPHORYLATION (BY CAPK AND PKB) (BY
FT SIMILARITY).
FT VARSPIC 166 205 LPPKSGRTQKQKASATRTIGSWDRNKGKSTPSO
FT ~> BELTYSVEPLPVAVLAMEKPLNSFSPPTPTTPE
FT EVAMFPLRYWTALRRIC (IN ISOFORM BETA).
FT S->A: NO EFFECT ON HETERODIMERIZATION
FT WITH 14-3-3 PROTEINS.
FT S->A: NO HETERODIMERIZATION WITH 14-3-3
FT PROTEINS. NO EFFECT ON HETERODIMERIZATION
FT WITH BCL2 NOR WITH PROTEIN P11.
FT SDAGGR -> ERNGRK (IN REF. 1).
FT CONFLICT 29 34
SO SEQUENCE 205 AA; 22228 MW; 7AFAT1DAE9CF4A81 CRC64;

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Query Match 100.0%; Score 138; DB 1; Length 205;
Best Local Similarity 100.0%; Pred. No. 8.7e-14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 NMAAQRGRLRRMSDFEESFKGL 26
 DB 141 NMAAQRGRLRRMSDFEESFKGL 166

RESULT 3
 BAD_HUMAN STANDARD: PRT: 168 AA.

AC O92934; 014803; 16-NOV-1997 (Rel. 35, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Bcl-2-antagonist of cell death (BAD) (Bcl-2 binding component 6) (Bcl-XL/Bcl-2 associated death promoter).
 DE BAD OR BRC6 OR BCL2L8.
 GN Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Xin D.X., Li Z., Huang B., Chen S., Zhou H.;
 RT "A human protein that interacts with Bcl-2 and have homology to mouse BAD."
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A., AND PHOSPHORYLATION BY RAF-1.
 RX MEDLINE=97083574; PubMed=8929532;
 RA Wang H.-G., Rapp U.R., Reed J.C.;
 RT "Bcl-2 targets the protein kinase Raf-1 to mitochondria."
 RL Cell 87:629-638(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Takeyama S., Reed J.C.;
 RT Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 RL [4]
 RP SEQUENCE FROM N.A., AND DIMERIZATION.
 RC TISSUE=Bone marrow;
 RX MEDLINE=98049554; PubMed=9388232;
 RA Ohtsuka S., Diaz J.-L., Horne W., Chang J., Wang Y., Wilson G.,
 RT Chang S., Weeks S., Fritz L.C., Oltersdorf T.;
 RL "Dimerization properties of human BAD."
 RL J. Biol. Chem. 272:30866-30872(1997).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Strausberg R.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP STRUCTURE BY NMR OF 103-127.
 RX MEDLINE=21073561; PubMed=11206074;
 RA Petros A.M., Nettesheim D.G., Wang Y., Olejniczak E.T., Meadows R.P.,
 RA Mack J., Swift K., Matayoshi E.D., Zhang H., Thompson C.B.,
 RA Fesik S.W.;
 RT "Rationale for Bcl-XL/Bad peptide complex formation from structure, mutagenesis, and biophysical studies."
 RL Protein Sci. 9:2528-2534(2000).
 CC -1- FUNCTION: Promotes cell death. Successfully competes for the binding to Bcl-X(L), Bcl-2 and Bcl-w, thereby affecting the level of heterodimerization of these proteins with BAX. Can reverse the death repressor activity of Bcl-X(L), but not that of Bcl-2 (by similarity). Appears to act as a link between growth factor receptor signaling and the apoptotic pathways.
 CC -1- SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-X(L), Bcl-2 and Bcl-w. Also binds protein S100A10 (by similarity). The Ser-75/Ser-99 phosphorylated form binds 14-3-3 proteins (by similarity).
 CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon phosphorylation, localizes to the cytoplasm.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
 CC -1- DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND BAX for their pro-apoptotic activity and for their interaction with anti-apoptotic members of the Bcl-2 family.

CC -1- PPM: Phosphorylated on Ser-75 in response to survival stimuli.
 CC Subsequent phosphorylation on Ser-99 promotes heterodimerization with 14-3-3 proteins. This interaction then facilitates the phosphorylation at Ser-118, a site within the BH3 domain, leading to the release of Bcl-X(L) and the promotion of cell survival.
 CC Ser-99 is the major site of AKT/PKB phosphorylation, Ser-118 the major site of protein kinase A (CAK) phosphorylation (by similarity).
 CC -1- SIMILARITY: CONTAINS 1 BCL-3 HOMOLOG DOMAIN 3 (BH3).
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
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 CC -----
 DR EMBL; U66879; AAB36516.1; -;
 DR EMBL; AF021792; AAB72092.1; -;
 DR EMBL; AF031523; AAB88124.1; -;
 DR EMBL; BC001901; AAR01901.1; -;
 DR PDB; 1G50; 07-FEB-01.
 DR MIM; 603167; -;
 DR InterPro; IPR000712; Bcl-2.
 DR PROSITE; PS01259; BH3; FALSE_NEG.
 KW Apoptosis; Phosphorylation; 3D-structure.
 FT DOMAIN 110 124 BH3
 FT MOD_RES 75 75 PHOSPHORYLATION (BY CAK AND PKB) (BY SIMILARITY).
 FT MOD_RES 99 99 PHOSPHORYLATION (BY CAK AND PKB) (BY SIMILARITY).
 FT MOD_RES 118 118 PHOSPHORYLATION (BY CAK AND PKB) (BY SIMILARITY).
 FT CONFLICT 64 91 AGAVEIRSRHSSTIPATEDDEGGEERS -> RMGGDPES POLLPKDGGRRRDGGGAG (IN REF. 1).
 FT FT
 SQ SEQUENCE 168 AA; 18392 MW; 69F8D27DDEE3241 CRC64;

OY 1 NMAAQRGRLRRMSDFEESFKGL 24
 DB 103 NMAAQRGRLRRMSDFEESFKGL 126

RESULT 4
 ITH2_MESAU STANDARD: PRT: 946 AA.

AC P97279;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITI heavy chain H2) (HC2).
 DE ITH2.
 GN Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 OC NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=97420688; PubMed=9276673;
 RA Nakatani T., Suzuki Y., Yamamoto T., Sinoihara H.;
 RT "Molecular cloning and sequencing of cDNAs encoding three heavy-chain precursors of the inter-alpha-trypsin inhibitor in Syrian hamster: implications for the evolution of the inter-alpha-trypsin inhibitor heavy chain family."
 RT

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RL J. Blochem. 122:71-82(1997).
RP SEQUENCE OF 55-64; 140-146; 151-156; 424-447; 500-528 AND 577-605,
RP AND SUBUNITs.
RX TISSUE=Plasma;
RA MEDLINE=97018241; PubMed=8864857;
RT Yamamoto T., Yamamoto K., Sinochira H.;
RT "Inter-alpha-trypsin inhibitor and its related proteins in Syrian
RT hamster urine and plasma";
RL J. Blochem. 120:145-152(1996).
CC -I- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A
CC BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,
CC INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE
CC LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE
CC ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
CC SIMILARITY).
CC -I- SUBUNIT: 1-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM
CC ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,
CC BIKININ. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2
CC AND BIKININ, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND
CC BIKININ, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKININ.
CC -I- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKININ VIA A CHONDROITIN
CC 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY
CC SIMILARITY).
CC -I- SIMILARITY: BELONGS TO THE ITTH FAMILY.
CC -I- SIMILARITY: CONTAINS 1 WMFA DOMAIN.
-----
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CC
DR EMBL: D89286; BAA13939.1; -
DR InterPro: IPR002035; WMFA.
DR Pfam: PF00092; vwa; 1.
DR SMART: SM00327; VWA; 1.
DR PROSITE: PS50234; WMFA; 1.
KW Serine protease inhibitor; Repeat; Signal; Multigene family;
KW Glycoprotein.
FT SIGNAL 1 18
FT PROPEP 19 54
FT CHAIN 55 702
FT
FT PROPER 703 946
FT DOMAIN 308 468
FT CARBOHYD 118 118
FT CARBOHYD 263 263
FT CARBOHYD 445 445
FT CARBOHYD 578 578
FT BINDING 702 702
FT
FT CONFLICT 510 510
FT CONFLICT 595 595
SQ SEQUENCE 946 AA; 106580 MM; CA8BF555458E7B2E CRC64;
Query Match 39.1%; Score 54; DB 1; Length 946;
Best Local Similarity 34.6%; Pred. No. 2.6;
Matches 9; Conservative 5; Mismatches 12; Indels 0; Gaps 0;
Oy 1 NLMAAORYGRELRRMSDEFGSKGL 26
Db 212 NWAIYELQGMRLHVPDTFECHFGCV 237
RESULT 5
ID ITTH_MOUSE STANDARD: PRT: 946 AA.
IC 061703:
DT 15-JUL-1998 (Rel. 36, Created)

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DT 15-JUL-1998 (Rel. 36, last sequence update)
DE 15-JUL-1999 (Rel. 38, last annotation update)
DR Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITI heavy
DE chain H2).
GN ITIH2
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6N; TISSUE=Liver;
RA MEDLINE=95194326; PubMed=7534067;
RX Chan P., Risler J.-L., Raguenes G., Sallier J.-P.;
RT "The three heavy-chain precursors for the inter-alpha-inhibitor
RT family in mouse: new members of the multicopier oxidase protein group
RT with differential transcription in liver and brain.";
RL Biochem. J. 306:505-512(1995).
CC -1- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A
CC BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,
CC INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE
CC LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE
CC ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
CC SIMILARITY).
CC -1- SUBUNIT: 1-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM
CC ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,
CC BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-1) IS COMPOSED OF H1, H2
CC AND BIKUNIN. INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND
CC BIKUNIN. AND PRE-ALPHA-INHIBITOR (P-ALPHA-1) OF H3 AND BIKUNIN..
CC -1- TISSUE SPECIFICITY: EXPRESSED IN BOTH LIVER AND BRAIN.
CC -1- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN
CC 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ITIH FAMILY.
CC -1- SIMILARITY: CONTAINS 1 VFMA DOMAIN.
CC -----
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CC -----
DR EMBL: X70382; CAA49842.1; -
DR MGD: MGI:96619; Itih2.
DR InterPro: IPR002035; VFMA.
DR Pfam: PF00092; vwa: 1.
DR SMART: SM00327; VWA: 1.
DR PROSITE: PSS0234; VFMA: 1.
DR Serine protease inhibitor; Repeat; Signal; Multigene family;
KW Glycoprotein.
FT SIGNAL 1 18
FT PROPEP 19 54
FT CHAIN 55 702
FT -----
FT PROPEP 703 946
FT DOMAIN 308 468
FT CARBOHYD 118 118
FT CARBOHYD 263 263
FT CARBOHYD 445 445
FT BINDING 702 702
FT -----
SQ SEQUENCE 946 AA; 105927 MW; 40DB6716433ED9DC CRC64;
      (BY SIMILARITY).
      (BY SIMILARITY).
      INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN
      H2.
      BY SIMILARITY.
      BY SIMILARITY.
      N-LINKED (GLCNAC. . .) (POTENTIAL).
      N-LINKED (GLCNAC. . .) (POTENTIAL).
      N-LINKED (GLCNAC. . .) (POTENTIAL).
      CHONDROITIN 4-SULFATE, CROSS-LINK SITE
      (BY SIMILARITY).

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RESULT 6
AR06_YEAST STANDARD; PRT; 370 AA.
ID AR06_YEAST
AC P32449;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Phospho-2-dehydro-3-deoxyheptone aldolase, tyrosine-inhibited
DE (EC 4.1.2.15) (Phospho-2-keto-3-deoxyheptone aldolase) (DHP
DE synthetase) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase).
GN AR04 OR YBR249C OR YBR1701.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
[1]
SEQUENCE FROM N.A.
MEDLINE=92225349; PubMed=1348717;
RX Kuenzler M., Paravicini G., Egli C., Irniger S., Braus G.H.;
RT "Cloning, primary structure and regulation of the AR04 gene, encoding
RT the tyrosine-inhibited 3-deoxy-D-arabino-heptulosonate-7-phosphate
RT synthase from Saccharomyces cerevisiae.";
RL Gene 113:67-74(1992).
[2]
REVISIONS TO 205-207.
RX Kuenzler M.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A.
STRAIN=5288C;
RX MEDLINE=94078675; PubMed=8256522;
RT Doignon F., Biteau N., Aigle M., Crouzet M.;
RT "The complete sequence of a 6794 bp segment located on the right arm
RT of chromosome II of Saccharomyces cerevisiae. Finding of a putative
RT duplicate in a yeast.";
RL Yeast 9:1131-1137(1993).
[4]
SEQUENCE FROM N.A.
STRAIN=5288C;
RX Aljinovic G., Pohl F.M., Pohl T.M.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: STEREOSPECIFIC CONDENSATION OF PHOSPHOENOLPYRUVATE (PEP)
CC AND D-ERYTHROSE-4-PHOSPHATE (E4P) GIVING RISE TO 3-DEOXY-D-
CC ARABINO-HEPTULOSONATE-7-PHOSPHATE (DHP).
CC -1- CATALYTIC ACTIVITY: 2-dehydro-3-deoxy-D-arabino-heptone 7-
CC phosphate + phosphate -> phosphoenolpyruvate + D-erythrose 4-
CC phosphate + H(2)O.
CC -1- ENZYME REGULATION: INHIBITED BY TYROSINE.
CC -1- PATHWAY: FIRST STEP IN THE BIOSYNTHESIS OF CHORISMATE WITHIN
CC THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE PATHWAY).
CC -1- INDUCTION: BY AMINO ACID STARVATION.
CC -1- SIMILARITY: BELONGS TO CLASS-1 DHP SYNTHETASE FAMILY.
CC -----
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CC -----
DR EMBL: X61107; CAA43419.1; -
DR EMBL: L20296; AAA65607.1; -
DR EMBL: L26118; CAA85212.1; -
DR PIR: S38185; S38185.
DR HSSP: P00886; 10R7.
DR SGD: S0000453; AR04.
DR InterPro: IPR001785; DHP_synth_1.
DR Pfam: PF00793; DHP_synth_1; 1.
DR ProDom: PD005060; DHP_synth_1; 1.
KW Aromatic amino acid biosynthesis; Lyase; Multigene family.

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SQ SEQUENCE 370 AA; 39749 MW; 594EDA8F24175979 CRC64;
Query Match 37.7%; Score 52; DB 1; Length 370;
Best Local Similarity 47.68; Pred. No. 1.8;
Matches 10; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
Oy 1 NLMAORYGRELRRMSDEFG 21
Db 80 DLFAOEYALRLKKLSDELKG 100
RESULT 7
AP3_ARATH STANDARD; PRT; 232 AA.
ID AP3_ARATH
AC P35632; Q39003;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Floral homeotic protein APETALA3.
DE AP3 OR AT3G54340 OR T12E18.30.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustoids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
[1]
SEQUENCE FROM N.A.
TISSUE=Petal;
RX MEDLINE=92154682; PubMed=1346756;
RA Jack T., Brockman L.L., Meyerowitz E.M.;
RT "The homeotic gene APETALA3 of Arabidopsis thaliana encodes a MADS
RT box and is expressed in petals and stamens.";
RL Cell 68:683-697(1992).
[2]
SEQUENCE FROM N.A.
STRAIN=CV. LANDSBERG ERECTA;
RX MEDLINE=95036018; PubMed=794893;
RA Okamoto H., Yano A., Shiraiishi H., Okada K., Shimura Y.;
RT "Genetic complementation of a floral homeotic mutation, apetala3,
RT with an Arabidopsis thaliana gene homologous to DEFICIENS of
RT Antirrhinum majus.";
RL Plant Mol. Biol. 26:465-472(1994).
[3]
SEQUENCE FROM N.A.
STRAIN-VARIOUS STRAINS;
RX MEDLINE=99126449; PubMed=9927474;
RA Putuganan M.D., Suddith J.I.;
RT "Molecular population genetics of floral homeotic loci. Departures
RT from the equilibrium-neutral model at the APETALA3 and PISTILLATA
RT genes of Arabidopsis thaliana.";
RL Genetics 151:839-848(1999).
[4]
SEQUENCE FROM N.A.
STRAIN=CV. COLOMBIA;
RX MEDLINE=21016720; PubMed=11130713;
RA Salanoubat M., Lemcke K., Rieger M., Ansoorge W., Unsel M.,
RA Fatnani B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
RA Deleney M., Boutry M., Grivell L.A., Mache R., Puidgomech P.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Winkler P., Catolico L., Weissenbach J., Saurin W., Quetier F.,
RA De Simone V., Choisme N., Artiguenave F., Robert C., Brothier P.,
RA Mumbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
RA Widelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simonati B.,
RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordstiek G.,
RA Reichelt J., Scharfe M., Schoen O., Barues M., Terol J., Climent J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
RA Cooke R., Landie M., Berger-Liauro C., Purnelle B., Masuy D.,
RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
RA Monfort A., Argirou A., Flores M., Liguori R., Vitale D.,
RA Mannhapt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Talon L.J., Jenkins J.,

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RA Rooney T., Rizzo M., Wals A., Utterback T., Fujii C.Y., Shea T.P.,
 RA Creasy T.H., Hasas B., Maiti R., Wu D., Peterson J., Van Aken S.,
 RA Pai G., Miltscher J., Sellers P., Gill J.E., Feldbyum T.V.,
 RA Preuss D., Lin X., Nierman W.C., Salzborg S.L., White O., Venter J.C.,
 RA Fraser C.M., Kaneo T., Nakamura Y., Sato S., Kato T., Asamizu E.,
 RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
 RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakayama S., Nakazaki N., Shino S., Takeuchi C., Wada T.,
 RA Matanabe A., Yamada M., Yasuda M., Tabata S.,
 RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
 thaliana";
 RT Nature 408:820-822(2000).
 RL -1- FUNCTION: TRANSCRIPTION FACTOR INVOLVED IN THE GENETIC CONTROL OF
 CC FLOWER DEVELOPMENT.
 CC -1- SUBUNIT: FORMS AN HETERODIMER WITH PISTILLATA.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN PETALS AND STAMENS.
 CC -1- MISCELLANEOUS: MUTATIONS IN AP3 CAUSE TRANSFORMATION OF PETALS
 CC INTO SEPALs AND STAMINA INTO CARPELS.
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
 CC FACTORS.
 CC -1- SIMILARITY: CONTAINS A PROBABLE DIMERIZATION DOMAIN FOUND IN
 CC SRF-TYPE TRANSCRIPTION FACTORS (K-BOX).
 CC -----
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 CC -----
 CC EMBL: M6357; AAA2740.1; -
 CC EMBL: D1125; BAA0465.1; -
 CC EMBL: AF115799; AAD51888.1; -
 CC EMBL: AF115800; AAD51889.1; -
 CC EMBL: AF115802; AAD51891.1; -
 CC EMBL: AF115804; AAD51893.1; -
 CC EMBL: AF115811; AAD51900.1; -
 CC EMBL: AF115814; AAD51903.1; -
 CC EMBL: AL134971; CAB81799.1; -
 CC PIR: A42095; A42095.
 CC HSP: P11746; 1NMN.
 CC TRANSFAC: T01776; -
 CC InterPro: IPR002487; K-box.
 CC InterPro: IPR002100; MADS-box.
 CC Pfam: PF01486; K-box; 1.
 CC Pfam: PF00319; SRF-TF; 1.
 CC PRINTS: PR00404; MADSDOMAIN.
 CC SMART: SM00432; MADS; 1.
 CC PROSITE: PS00350; MADS_BOX_1; 1.
 CC PROSITE: PS50066; MADS_BOX_2; 1.
 CC Transcription regulation; DNA-binding; Activator; Nuclear protein;
 CC Developmental protein.
 CC KW DOMAIN 3 57 MADS.
 CC FT DOMAIN 93 165 K-BOX.
 CC FT CONFLICT 199 199 A -> R (IN REF. 2).
 CC SEQUENCE 232 AA; 27341 MW; 669070319F9857C3 CRC64;

Query Match 37.0%; Score 51; DB 1; Length 232;
 Best Local Similarity 44.4%; Pred. No. 1.5;
 Matches 12: Conservative 3; Mismatches 4; Indels 8; Gaps 1;

OY 6 ORYG-----RELIRMSDEFGSK 24
 DB 107 ORIGCELDLDIOELRLREDEMENTFK 133

RESULT 8
 RMUC_PSEAE STANDARD: PRT; 453 AA.
 AC 091403;

DT 01-MAR-2002 (Rel. 41, Last Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE DNA recombination protein rmuc homolog.
 GN RMUC OR PA1031.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=20437337; PubMed=10984043;
 RA Stoyer C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 RA Hickey M.J., Brickman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garner R.L., Colty L., Tolentino E., Westbrook-Wedman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Laidig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.,
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 RT opportunistic pathogen";
 RT Nature 406:959-964(2000).
 RL -1- FUNCTION: Involved in DNA recombination (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE RMUC FAMILY.
 CC -----
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 CC -----
 CC EMBL: AE004535; AAG04420.1; -
 CC InterPro: IPR003798; DUF195.
 CC Pfam: PF02646; DUF195; 1.
 CC DNA recombination; Coiled coil; Complete proteome.
 CC KW DOMAIN 16 COILED COIL (POTENTIAL).
 CC FT DOMAIN 16 201
 CC SEQUENCE 453 AA; 51539 MW; 1E7EA97EB2EC5E4B CRC64;

Query Match 35.5%; Score 49; DB 1; Length 453;
 Best Local Similarity 55.6%; Pred. No. 6.5;
 Matches 10: Conservative 4; Mismatches 2; Indels 2; Gaps 1;

OY 3 WAAORYGR--ELRMSDE 18
 DB 65 WASEROGREELRLASE 82

RESULT 9
 RAS3_RHIRA STANDARD: PRT; 205 AA.
 ID RAS3_RHIRA
 AC P22280;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Ras-like protein 3.
 GN RAS3.
 OS Rhizomucor racemosus (Mucor circinelloides f. lusitanicus).
 OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;
 OC Mucor.
 OX NCBI_TaxID=4841;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 1216B;
 RX MEDLINE=91061774; PubMed=1701021;
 RA Casale W.L., McConnell D.G., Wang S.-Y., Lee Y.-J., Linz J.E.,
 RT "Expression of a gene family in the dimorphic fungus Mucor racemosus
 RT which exhibits striking similarity to human ras genes";
 RL Mol. Cell. Biol. 10:6654-6663(1990).
 CC -1- ENZYME REGULATION: ALTERNATE BETWEEN AN INACTIVE FORM BOUND TO GTP
 CC AND AN ACTIVE FORM BOUND TO GTP. ACTIVATED BY A GUANINE

```
CC NUCLEOTIDE-EXCHANGE FACTOR (GEF) AND INACTIVATED BY A GTPASE-  
CC ACTIVATING PROTEIN (GAP).  
CC -1- SUBCELLULAR LOCATION: PLASMA MEMBRANE.  
CC -1- DEVELOPMENTAL STAGE: IN SPOROBLASTING MYCELIAL AND MUCH LESS IN  
CC GERMLING AND YEAST.  
CC -1- SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RAS FAMILY.  
CC -----  
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CC -----  
DR EMBL; M55177; AAA83379.1; -.  
DR PIR; C36365; C36365.  
DR HSSP; P01112; LPLI.  
DR InterPro; IPR003577; Ras_tnsftrng.  
DR InterPro; IPR001806; Ras_tnsftrng.  
DR Pfam; PF00071; ras; 1.  
DR PRINTS; PRD0449; RASTRNSFRNG.  
DR SMART; SM00173; RAS; 1.  
KW GTP-binding; Prenylation; Lipoprotein.  
FT NP_BIND 16 23 GTP (BY SIMILARITY).  
FT NP_BIND 63 67 GTP (BY SIMILARITY).  
FT NP_BIND 122 125 GTP (BY SIMILARITY).  
FT DOMAIN 38 46 EFFECTOR REGION (PROBABLE).  
FT LIPID 202 202 FARNESYL (BY SIMILARITY);  
SO SEQUENCE 205 AA; 23408 MW; DBF08B466F09F50 CRC64;  
  
Query Match 34.8%; Score 48; DB 1; Length 205;  
Best Local Similarity 62.5%; Pred. No. 3.8;  
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
  
Oy 10 RELRRMSDEFGSGFKG 25  
||:||||: ||| ||  
Db 168 RELRRMRKEQGRSKG 183  
  
RESULT 10  
6PGL_THEME  
AC ID 6PGL_THEME STANDARD; PROT: 220 AA.  
AD OGYON8:  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE 6-phosphogluconolactonase (EC 3.1.1.31) (6PGL).  
GN PGL OR DEVB OR TM1154.  
OS Thermotoga maritima.  
OC Bacteria; Thermotogales; Thermotoga.  
OX NCBI_TaxID=2336;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MSB8 / DSM 3109;  
RX MEDLINE=99287316; PubMed=10360571;  
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,  
RA Hatt D.H., Hickey E.K., Peterson J.D., Nelson W.C., Garrett M.M.,  
RA McDonald L., Utterback T.R., Malek J.A., Inher K.D., Richard D.,  
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,  
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,  
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;  
RT "Evidence from a lateral gene transfer between Archaea and Bacteria from  
RL genome sequence of Thermotoga maritima";  
RL Nature 399:323-329(1999).  
CC -1- FUNCTION: HYDROLYSIS OF 6-PHOSPHOGLUCONOLACTONE TO 6-  
CC PHOSPHOGLUCONATE.  
CC -1- CATALYTIC ACTIVITY: 6-phospho-D-glucono-1,5-lactone + H(2)O = 6-  
CC phospho-D-gluconate.  
CC -1- PATHWAY: SECOND STEP IN PENTOSE PHOSPHATE PATHWAY.  
CC -1- SIMILARITY: BELONGS TO THE GLUCOSAMINE/GALACTOSAMINE-6-PHOSPHATE  
CC ISOMERASE FAMILY. 6-PHOSPHOGLUCONOLACTONASE SUPERFAMILY.
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CC -----
DR DR EMBL: AF081772; MAD36230.1; -.
DR TRIC: TM1154; -.
DR InterPro: IPR000457; Glucosamine_iso.
DR Pfam: PF01182; Glucosamine_iso.1.
RW Hydrolase; Complete proteome.
SQ SEQUENCE 220 AA; 25325 MW; 980FD07E01E60C3 CRC64;

Query Match 34.8%; Score 48; DB 1; Length 220;
Best Local Similarity 34.8%; Pred. No. 4.1;
Matches 8; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Oy 4 AAOYGRGLRMSDEFGSEFKGI 26
   1::1111::111::11
Db 111 ACEYEREIRSATDQFDLATIGM 133

RESULT 11
THRC SOLUTU
1D THRC SOLUTU STANDARD; PRT; 519 AA.
AC Q9WTJ28;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Threonine synthase, chloroplast precursor (EC 4.2.99.2) (TS).
OS Solanum tuberosum (Potato)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN (1)
RP SEQUENCE FROM N.A.
RA Caazaza P., Kaiser S., Willmitzer L., Hoefgen R., Hesse H.;
RT "Isolation and characterization of a cDNA encoding threonine synthase
RT from Solanum tuberosum.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: O-phospho-L-homoserine + H(2O) = L-threonine +
CC phosphate.
CC -1- COFACTOR: Pyridoxal phosphate (By similarity).
CC -1- ENZYME REGULATION: Allosterically activated by S-adenosyl-
CC methionine (SAM) (By similarity).
CC -1- PATHWAY: Threonine biosynthesis; last step.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Chloroplast (By similarity).
CC -1- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
CC -----
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CC -----
DR DR EMBL: AF082894; AAF74384.1; -.
DR InterPro: IPR001926; B6_enzyme_beta.
DR Pfam: PF00291; PALP; 1.
DR PROSITE: PS00165; DEHYDRATASE_SER_THR; 1.
KW Threonine biosynthesis; Lyase; Pyridoxal phosphate; Allosteric enzyme;
KW Chloroplast; Transil peptide.
FT TRANSIT 1 40 CHLOROPLAST (BY SIMILARITY).
FT CHAIN 41 519 THREONINE SYNTHASE.
FT BINDING 196 196 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 519 AA; 57412 MW; 114C0979CD231464 CRC64;

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Db      172 NLFMAERFGKQFLGMDLWVHCISHTGSEKDL 205

RESULT 13
BIM_HUMAN
ID      BIM_HUMAN      STANDARD;      PRT;      198 AA.
AC      043521; 043522;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Bcl2-like protein 11 (Bcl2 interacting mediator of cell death).
GN      BCL2L1 OR BIM.
OS      Homo sapiens (human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX      NCBI_TaxID=9606;
[1]
RP      SEQUENCE FROM N.A., FUNCTION, AND ALTERNATIVE SPLICING.
RC      TISSUE=peripheral blood, and spleen;
RX      MEDLINE=98094360; PubMed=9430630;
RA      O'Connor L., Strasser A., O'Reilly L.A., Hausmann G., Adams J.M.,
RA      Cory S., Huang D.C.S.;
RT      *Bim: a novel member of the Bcl-2 family that promotes apoptosis.*;
RL      EMBO J. 17:384-395(1998).
CC      -1- FUNCTION: INDUCES APOPTOSIS. ISOFORM BIML IS MORE POTENT THAN
CC      ISOFORM BIMEL.
CC      -1- SUBUNIT: FORMS HETERODIMERS WITH A NUMBER OF ANTIAPOTOTIC BCL-2
CC      PROTEINS INCLUDING MCL-1, BCL-2, BCL-XL, BFL-1, AND BHRF-1. DOES
CC      NOT HETERODIMERIZE WITH PROAPOPTOTIC PROTEINS SUCH AS BAD, BOK,
CC      BAX OR BAK (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: ASSOCIATED WITH INTRACITOPLASMIC MEMBRANES
CC      (BY SIMILARITY).
CC      -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: BimEL (SHOWN HERE) AND
CC      BimL; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC      -1- DOMAIN: THE BH3 DOMAIN IS REQUIRED FOR BCL-2 BINDING AND
CC      CYTOTOXICITY.
CC      -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 3 (BH3).
-----
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-----
CC      EMBL: AF032457; AAC39593.1; -.
CC      EMBL: AF032458; AAC39594.1; -.
CC      MIM: 603827; -.
DR      InterPro: IPR000712; Bcl_2.
DR      PROSITE: PS01259; BH3; FALSE_NEG.
DR      KMW: APOPTOSIS; Alternative splicing; Membrane.
FT      DOMAIN 148 162 BH3.
FT      VARSPLIC 42 101 MISSING (IN ISOFORM BIML).
FT      SEQUENCE 198 AA; 22171 MW; D75735B469CA6997 CRC64;

Query Match      34.1%; Score 47; DB 1; Length 198;
Best Local Similarity 45.5%; Pred. No. 5.1;
Matches 10; Conservative 3; Mismatches 5; Indels 4; Gaps 1;

Oy      2 LMAAQRGRELRLMSDEFGSF 23
Db      146 LIIAQ---ELRRIGDEFNAVY 163

RESULT 14
FMR2_ANTTEL      STANDARD;      PRT;      429 AA.
AC      Q16994;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      01-MAR-2002 (Rel. 41, Last annotation update)

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DE      Antho-Rfamidae neuropeptides type 2 precursor.
OS      Anthopleura elegantissima (Sea anemone).
OC      Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actinaria;
OC      Nynanthaeae; Actiniidae; Anthopleura.
OX      NCBI_TaxID=6110;
[1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=93054550; PubMed=14296603;
RA      Schmutzler C., Darmer D., Diekhoff D., Grimmelikhuijzen C.J.P.;
RT      Identification of a novel type of processing sites in the precursor
RT      for the sea anemone neuropeptide Antho-Rfamidae (<Glu-Gly-Arg-Phe-NH2)
RT      from Anthopleura elegantissima.*;
RL      J. Biol. Chem. 267:22534-22541(1992)
CC      -1- FUNCTION: NOT KNOWN BUT IT COULD ACT AS A TRANSMITTER AT
CC      NEUROUSCULAR SYNAPSES.
CC      -1- SUBCELLULAR LOCATION: Secreted.
-----
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-----
CC      EMBL: M99170; AAA27739.1; -.
DR      Neuropeptide; Amidation: Repeat; Signal.
FT      SIGNAL 1 22
FT      PEPTIDE 234 237 POTENTIAL.
FT      PEPTIDE 242 245 ANTHO-RFAMIDE.
FT      PEPTIDE 250 253 ANTHO-RFAMIDE.
FT      PEPTIDE 258 261 ANTHO-RFAMIDE.
FT      PEPTIDE 266 269 ANTHO-RFAMIDE.
FT      PEPTIDE 274 277 ANTHO-RFAMIDE.
FT      PEPTIDE 290 293 ANTHO-RFAMIDE.
FT      PEPTIDE 298 301 ANTHO-RFAMIDE.
FT      PEPTIDE 306 309 ANTHO-RFAMIDE.
FT      PEPTIDE 322 325 ANTHO-RFAMIDE.
FT      PEPTIDE 330 333 ANTHO-RFAMIDE.
FT      PEPTIDE 343 346 ANTHO-RFAMIDE.
FT      PEPTIDE 356 359 ANTHO-RFAMIDE.
FT      PEPTIDE 369 372 ANTHO-RFAMIDE.
FT      MOD_RES 237 237 ANTHO-RFAMIDE.
FT      MOD_RES 245 245 ANTHO-RFAMIDE.
FT      MOD_RES 253 253 ANTHO-RFAMIDE.
FT      MOD_RES 261 261 ANTHO-RFAMIDE.
FT      MOD_RES 269 269 ANTHO-RFAMIDE.
FT      MOD_RES 277 277 ANTHO-RFAMIDE.
FT      MOD_RES 293 293 ANTHO-RFAMIDE.
FT      MOD_RES 301 301 ANTHO-RFAMIDE.
FT      MOD_RES 309 309 ANTHO-RFAMIDE.
FT      MOD_RES 325 325 ANTHO-RFAMIDE.
FT      MOD_RES 333 333 ANTHO-RFAMIDE.
FT      MOD_RES 346 346 ANTHO-RFAMIDE.
FT      MOD_RES 359 359 ANTHO-RFAMIDE.
FT      MOD_RES 372 372 ANTHO-RFAMIDE.
FT      SEQUENCE 429 AA; 50564 MW; 7C54F5C606D537E4 CRC64;

Query Match      33.7%; Score 46.5; DB 1; Length 429;
Best Local Similarity 52.4%; Pred. No. 15;
Matches 11; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

Oy      4 AAOYRGRELRLMSDEFGSF 23
Db      209 AOGRFRELQGRFGREFQGRF 229

RESULT 15
FMR1_ANTTEL      STANDARD;      PRT;      435 AA.
AC      P10419;
DT      01-MAR-1989 (Rel. 10, Created)

```

DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Antho-Rfamide neuropeptides type 1 precursor.
 OS Anthopleura elegantissima (Sea anemone).
 OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actinaria;
 NC Nematode; Actinellidae; Anthopleura.
 NC NCUT_Taxid=6110;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93054550; PubMed=1429603;
 RA Schmittler C., Darmer D., Diekhoff D., Grimmalkhuizen C.J.P.;
 RT "Identification of a novel type of processing sites in the precursor
 RT for the sea anemone neuropeptide Antho-Rfamide (<Glu-Gly-Arg-Phe-NH2)
 RT from Anthopleura elegantissima";
 RL J. Biol. Chem. 267:22534-22541(1992).
 RL [2]
 RN SEQUENCE OF MATURE PEPTIDE.
 RX MEDLINE=87092339; PubMed=2879288;
 RA Grimmalkhuizen C.J.P., Graff D.;
 RT "Isolation of pyroglu-Gly-Arg-Phe-NH2 (Antho-Rfamide), a neuropeptide
 RT from sea anemones";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:9817-9821(1986).
 RL -1- FUNCTION: NOT KNOWN BUT IT COULD ACT AS A TRANSMITTER AT
 CC NEUROMUSCULAR SYNAPSES.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 DR EMBL: M98269; AAA27738.1; -
 DR PIR: A26666; ECXAA.
 DR PIR: A43308; A44308.
 DR InterPro: IPR002544; FARP.
 DR Pfam: PF01581; FARP; 13.
 KW Neuropeptide; Amidation; Repeat; Signal.
 FT SIGNAL 1 22
 FT PEPTIDE 194 197 ANTHO-RFAMIDE.
 FT PEPTIDE 202 205 ANTHO-RFAMIDE.
 FT PEPTIDE 210 213 ANTHO-RFAMIDE.
 FT PEPTIDE 218 221 ANTHO-RFAMIDE.
 FT PEPTIDE 226 229 ANTHO-RFAMIDE.
 FT PEPTIDE 234 237 ANTHO-RFAMIDE.
 FT PEPTIDE 242 245 ANTHO-RFAMIDE.
 FT PEPTIDE 250 253 ANTHO-RFAMIDE.
 FT PEPTIDE 258 261 ANTHO-RFAMIDE.
 FT PEPTIDE 266 269 ANTHO-RFAMIDE.
 FT PEPTIDE 274 277 ANTHO-RFAMIDE.
 FT PEPTIDE 282 285 ANTHO-RFAMIDE.
 FT PEPTIDE 290 293 ANTHO-RFAMIDE.
 FT PEPTIDE 298 301 ANTHO-RFAMIDE.
 FT PEPTIDE 306 309 ANTHO-RFAMIDE.
 FT PEPTIDE 314 317 ANTHO-RFAMIDE.
 FT PEPTIDE 322 325 ANTHO-RFAMIDE.
 FT PEPTIDE 330 333 ANTHO-RFAMIDE.
 FT PEPTIDE 343 346 ANTHO-RFAMIDE.
 FT PEPTIDE 356 359 ANTHO-RFAMIDE.
 FT PEPTIDE 369 372 ANTHO-RFAMIDE.
 FT DOMAIN 376 386 POLY-ALA.
 FT MOD_RES 194 194 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 197 197 AMIDATION (G-198 PROVIDE AMIDE GROUP).
 FT MOD_RES 205 205 AMIDATION (G-206 PROVIDE AMIDE GROUP).
 FT MOD_RES 213 213 AMIDATION (G-214 PROVIDE AMIDE GROUP).
 FT MOD_RES 221 221 AMIDATION (G-222 PROVIDE AMIDE GROUP).
 FT MOD_RES 229 229 AMIDATION (G-230 PROVIDE AMIDE GROUP).
 FT MOD_RES 237 237 AMIDATION (G-238 PROVIDE AMIDE GROUP).
 FT MOD_RES 245 245 AMIDATION (G-246 PROVIDE AMIDE GROUP).
 FT MOD_RES 253 253 AMIDATION (G-254 PROVIDE AMIDE GROUP).
 FT MOD_RES 261 261 AMIDATION (G-262 PROVIDE AMIDE GROUP).

FT MOD_RES 269 269 AMIDATION (G-270 PROVIDE AMIDE GROUP).
 FT MOD_RES 277 277 AMIDATION (G-278 PROVIDE AMIDE GROUP).
 FT MOD_RES 285 285 AMIDATION (G-286 PROVIDE AMIDE GROUP).
 FT MOD_RES 293 293 AMIDATION (G-294 PROVIDE AMIDE GROUP).
 FT MOD_RES 301 301 AMIDATION (G-302 PROVIDE AMIDE GROUP).
 FT MOD_RES 309 309 AMIDATION (G-310 PROVIDE AMIDE GROUP).
 FT MOD_RES 317 317 AMIDATION (G-318 PROVIDE AMIDE GROUP).
 FT MOD_RES 325 325 AMIDATION (G-326 PROVIDE AMIDE GROUP).
 FT MOD_RES 333 333 AMIDATION (G-334 PROVIDE AMIDE GROUP).
 FT MOD_RES 346 346 AMIDATION (G-347 PROVIDE AMIDE GROUP).
 FT MOD_RES 359 359 AMIDATION (G-360 PROVIDE AMIDE GROUP).
 FT MOD_RES 372 372 AMIDATION (G-373 PROVIDE AMIDE GROUP).
 SO SEQUENCE 435 AA; 50940 MW; B0C44020CDS58D61 CRC64;

Query Match 33.7%; Score 46.5; DB 1; Length 435;
 Best Local Similarity 52.4%; Pred. No. 15;
 Matches 11; Conservative 3; Mismatches 6; Indels 1; Gaps 1;
 Oy 4 AAQRYGRELR-RMSDEFGSF 23
 Db 209 AQGRFGRELQGRGREFQGRF 229

Search completed: September 20, 2002, 11:04:28
 Job time: 1625 sec

Fri Sep 20 11:03:08 2002

us-09-544-664-2.rsp

Page 11

GenCore version 4.5
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OM protein - protein search, using SW model

Run on: September 20, 2002, 11:03:36 : Search time 172.19 Seconds

(without alignments)
26.122 Million cell updates/sec

Title: US-09-544-664-2

Sequence: 1 NLMAAQRKRGRLRMSDFEGSRKGL 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 17294929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: SPTRMBL.19:*
2: sp.archaea:*
3: sp.bacteria:*
4: sp.fungi:*
5: sp.human:*
6: sp.invertebrate:*
7: sp.mammal:*
8: sp.mnc:*
9: sp.organelle:*
10: sp.phage:*
11: sp.plant:*
12: sp.potent:*
13: sp.virus:*
14: sp.vertbrate:*
15: sp.virus:*
16: sp.bacteriap:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	63.0	146	13 0919N2	0919N2 brachydanio
2	53	38.4	223	16 0108A3	0108A3 mycobacteri
3	51	37.0	231	10 0989G0	0989G0 arabidopsis
4	51	37.0	232	10 0987G3	0987G3 arabidopsis
5	51	37.0	232	10 0980Q2	0980Q2 arabidopsis
6	51	37.0	232	10 0980Q1	0980Q1 arabidopsis
7	51	37.0	232	10 0980Q0	0980Q0 arabidopsis
8	51	37.0	232	10 0980S19	0980S19 arabidopsis
9	51	37.0	232	10 0980S18	0980S18 arabidopsis
10	51	37.0	232	10 0980S17	0980S17 arabidopsis
11	51	37.0	232	10 0980S16	0980S16 arabidopsis
12	51	37.0	232	10 0980S15	0980S15 arabidopsis
13	50.5	36.6	904	2 09K6W3	09K6W3 pseudomonas
14	50	36.2	283	15 0370S6	0370S6 chimpanzee
15	50	36.2	374	17 09H2S9	09H2S9 halobacteri
16	50	36.2	516	10 09S5P5	09S5P5 arabidopsis

17	49.5	35.9	153	5 09UB33	09UB33 anopheles g
18	49.5	35.9	401	5 097407	097407 anopheles g
19	49.5	35.9	505	8 047148	047148 menziesia c
20	49.5	35.9	506	8 063960	063960 rhododendro
21	49.5	35.9	506	8 062972	062972 rhododendro
22	49.5	35.9	506	8 062973	062973 rhododendro
23	49.5	35.9	506	8 062974	062974 rhododendro
24	49.5	35.9	506	8 062975	062975 rhododendro
25	49.5	35.9	506	8 062977	062977 rhododendro
26	49.5	35.9	506	8 062978	062978 rhododendro
27	49.5	35.9	506	8 062980	062980 rhododendro
28	49.5	35.9	506	8 062981	062981 rhododendro
29	49.5	35.9	506	8 062982	062982 rhododendro
30	49.5	35.9	506	8 062983	062983 rhododendro
31	49.5	35.9	506	8 062984	062984 rhododendro
32	49.5	35.9	506	8 062985	062985 rhododendro
33	49.5	35.9	506	8 062986	062986 rhododendro
34	49.5	35.9	506	8 062987	062987 rhododendro
35	49.5	35.9	506	8 062988	062988 rhododendro
36	49.5	35.9	506	8 062989	062989 rhododendro
37	49.5	35.9	506	8 062990	062990 rhododendro
38	49.5	35.9	506	8 062991	062991 rhododendro
39	49.5	35.9	506	8 062992	062992 rhododendro
40	49.5	35.9	506	8 062993	062993 rhododendro
41	49.5	35.9	506	8 047152	047152 rhododendro
42	49.5	35.9	506	8 047155	047155 rhododendro
43	49.5	35.9	506	8 047168	047168 menziesia p
44	49.5	35.9	506	8 047170	047170 rhododendro
45	49.5	35.9	506	8 047171	047171 rhododendro
					047173 rhododendro
					047174 tsusitophyll

ALIGNMENTS

RESULT 1
ID 0919N2 PRELIMINARY: PRT: 146 AA.
AC 0919N2: 1
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE BAD.
GN BAD.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes; Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20373792; PubMed-10917738;
RA Inohara N., Nunez G.;
RT "Genes with homology to mammalian apoptosis regulators identified in zebrafish";
RL Cell death differ. 7:509-510(2000).
DR EMBL: AF231017; AAF65962.2;
SQ SEQUENCE 146 AA; 16546 MW; 28A5650BB5107ECB CRC64;

Query Match 63.0%; Score 87; DB 13; Length 146;
Best Local Similarity 65.2%; Pred No. 2; Re-05;
Matches 15; Conservative 5; Mismatches 3; Indels 0;
Gaps 0;
OY 2 LMAAQRKRGRLRMSDFEGSRK 24
DB 89 LMAAQRKRGRLRMSDFEGSRK 111
RESULT 2
ID 0108A3 PRELIMINARY: PRT: 223 AA.
AC 0108A3:
DT 01-NOV-1998 (TREMBLrel. 08, Created)

DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
 DE 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 GN HYPOTHEICAL 24.1 KDA PROTEIN CY33.03C.
 OS RV2014 OR MTCY33.03C.
 NC Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RA MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Barry C.E. III, Tekala F.,
 RA Gordon S.V., Eiglmeier K., Gas S., Chillingworth T., Connor R.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feldwell T., Gentles S., Hamlin N., Holtroyd S.,
 RA Hornsbury T., Jagels K., Kirogi A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.K., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sutcliffe J.E., Taylor K., Whittam S., Barrett B.G.,
 RA "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence."
 CC Nature 393:537-544(1998).
 RL -1- SIMILARITY: TO M. PARATUBERCULOSIS 15900.
 DR EMBL: 274025; CA98415.1; -
 DR Tuberculist; RV2014; -
 DR InterPro: IPR003346; Transposase.20.
 DR Pfam: PF02371; Transposase.20; 1.
 KW Hypothetical protein; Complete Proteome.
 SQ SEQUENCE 223 AA; 24132 MW; 7045675001PFF37 CRC64;

Query Match 38.4%; Score 53; DB 16; Length 223;
 Best Local Similarity 58.8%; Pred. No. 5.4;
 Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
 OY 1 N1MA0RYGRELKMSD 17
 DB 165 N1MA0RYGRELKMSD 181

RESULT 3
 ID 09SECO PRELIMINARY; PRT: 231 AA.
 AC 09SECO;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE APETALA3 (FRAGMENT).
 OS Arabidopsis lyrata.
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eutrosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=59689;
 RN 11
 RP SEQUENCE FROM N.A.
 RC MEDLINE=99404148; PubMed=10474900;
 RA Lawton-Rauh A.L., Buckler E.S. IV, Purugganan M.D.;
 RT "Patterns of molecular evolution among paralogous floral homeotic
 genes."
 RL Mol. Biol. Evol. 16:1037-1045(1999).
 DR EMBL: AF143380; AAF25590.1; -
 DR HSSP: P11746; 1MNW.
 DR InterPro: IPR002487; K-box.
 DR Pfam: PF01486; K-box; 1.
 DR PRINTS: PF00319; SRF-TF; 1.
 DR SMART: SM00404; MADSOMAIN.
 DR SMART: SM00432; MADS; 1.
 DR PROSITE: PS50066; MADS_BOX_2; 1.
 DR PROSITE: PS50066; MADS_BOX_2; 1.
 FT NON_TER 231 231
 SQ SEQUENCE 231 AA; 27176 MW; A67CAIEBDBFTAA CRC64;

Query Match 37.0%; Score 51; DB 10; Length 221;
 Best Local Similarity 44.4%; Pred. No. 11;
 Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;
 OY 6 ORYG-----RELKMSDEFGSFK 24
 DB 107 ORLGECDKLDIOLRLDEMENTFK 133

RESULT 4
 ID 09S703 PRELIMINARY; PRT: 232 AA.
 AC 09S703;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE FLORAL HOMEOTIC PROTEIN AP3.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eutrosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. GR-3, AND CV. CHI-1;
 RA MEDLINE=99126449; PubMed=9927474;
 RA Purugganan M.D., Sudduth J.I.;
 RT "Molecular population genetics of floral homeotic loci. Departures
 RT from the equilibrium-neutral model at the APETALA3 and PISTILLATA
 RT genes of Arabidopsis thaliana."
 RL Genetics 151:839-848(1999).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
 DR EMBL: AF115803; AAD51892.1; -
 DR EMBL: AF115798; AAD51887.1; -
 DR HSSP: P11746; 1MNW.
 DR InterPro: IPR002487; K-box.
 DR PRINTS: PF01486; K-box; 1.
 DR Pfam: PF00319; SRF-TF; 1.
 DR PRINTS: PF00404; MADSOMAIN.
 DR SMART: SM00432; MADS; 1.
 DR SMART: SM00350; MADS_BOX_1; 1.
 DR PROSITE: PS50066; MADS_BOX_2; 1.
 DR PROSITE: PS50066; MADS_BOX_2; 1.
 KW DNA-binding; Nuclear protein; Transcription regulation.
 SQ SEQUENCE 232 AA; 27340 MW; 6690703F9FCED63 CRC64;

Query Match 37.0%; Score 51; DB 10; Length 232;
 Best Local Similarity 44.4%; Pred. No. 11;
 Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;
 OY 6 ORYG-----RELKMSDEFGSFK 24
 DB 107 ORLGECDKLDIOLRLDEMENTFK 133

RESULT 5
 ID 09SQ22 PRELIMINARY; PRT: 232 AA.
 AC 09SQ22;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE FLORAL HOMEOTIC PROTEIN AP3.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eutrosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;

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RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-CV. 11-8;
RX MEDLINE-99126449; PubMed-9927474;
RX Purgunan M.D., Suddith J.I.;
RX "Molecular population genetics of floral homeotic loci. Departures
RX from the equilibrium-neutral model at the APTAL3 and PISTILATA
RX genes of Arabidopsis thaliana."
RX Genetics 151:839-848(1999).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC EMBL: AF115805.1; AAD51890.1;
DR HSSP: P11746; 1MMN.
DR InterPro: IPR002487; K-box.
DR InterPro: IPR002100; MADS-box.
DR Pfam: PF01486; K-box; 1.
DR Pfam: PF00319; SRF-TE; 1.
DR PRINTS: PR00404; MADSDOMAIN.
DR SMART: SM00432; MADS_1.
DR PROSITE: PS00350; MADS_BOX_1; 1.
DR PROSITE: PS50065; MADS_BOX_2; 1.
DR DNA-binding: Nuclear protein; Transcription regulation.
KW DNA-binding; Nuclear protein; Transcription regulation.
SQ SEQUENCE 232 AA; 2726 MW; 42A852DB97E2A465 CRC64;

Query Match 37.0%; Score 51; DB 10; Length 232;
Best local similarity 44.4%; Pval No. 11;
Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1

Oy 6 ORFY-----RELRRMSDFGSGFR 24
Db 107 QRLSECDLDTGELRLRLEDMENRFX 133
|||:||||:||||:
|||:||||:||||:

RESULT 6
098021 PRELIMINARY; PRT; 232 AA.
AC 098021.
DT 01-MAY-2000 (TRENHIREL 13, Created)
DT 01-MAY-2000 (TRENHIREL 13, Last sequence update)
DT 01-DEC-2001 (TRENHIREL 19, Last annotation update)
DE FLORAL HOMEOTIC PROTEIN AP3.
CN APTAL3.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Eudicotyledons; Core eudicots; Rosidae;
OC Eusteroideae; Brassicales; Brassicaceae; Arabidopsis.
OC NIT__taxid-3702;
RX NIT__taxid-3702;
RP SEQUENCE FROM N.A.
RX STRAIN-CV. KENT;
RX MEDLINE-99126449; PubMed-9927474;
RX Purgunan M.D., Suddith J.I.;
RX "Molecular population genetics of floral homeotic loci. Departures
RX from the equilibrium-neutral model at the APTAL3 and PISTILATA
RX genes of Arabidopsis thaliana."
RX Genetics 151:839-848(1999).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC EMBL: AF115805.1; AAD51894.1;
DR HSSP: P11746; 1MMN.
DR InterPro: IPR002487; K-box.
DR InterPro: IPR002100; MADS-box.
DR Pfam: PF01486; K-box; 1.
DR Pfam: PF00319; SRF-TE; 1.
DR PRINTS: PR00404; MADSDOMAIN.
DR SMART: SM00432; MADS_1.
DR PROSITE: PS00350; MADS_BOX_1; 1.
DR PROSITE: PS50065; MADS_BOX_2; 1.
DR DNA-binding: Nuclear protein; Transcription regulation.
KW DNA-binding; Nuclear protein; Transcription regulation.
SQ SEQUENCE 232 AA; 2726 MW; 66976505B8B63E3 CRC64;

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OY      6 QRYG-----RELRLMSDPEFGSKF 24
           |||::|||::|||::|||::|||::
DB      107 GRLSGCLDELDIOELRLEDEMENTPK 133

RESULT  7
09SQ020 PRELIMINARY; PRT: 232 AA.
ID       8
09SQ020
OC       09SQ020:
DT       01-MAY-2000 (TRENBLREL_13, Created)
DT       01-MAY-2000 (TRENBLREL_13, Last sequence update)
DT       01-DEC-2001 (TRENBLREL_19, last annotation update)
DE       FLORAL HOMEOTIC PROTEIN AP3.
GN       APTALA3.
OS       Arabidopsis thaliana (Mouse-ear cress).
OC       Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC       Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC       eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX       NCBI_TaxID=3702;
ON       (1)
RP       SEQUENCE FROM N.A.
RX       STRAIN=CV_CORSICALIA;
RX       MEDLINE=99126449; PubMed=9927474;
RA       PURUGENAN M.D. Suddith J.T.;
RA       "Molecular population genetics of floral homeotic loci. Departures
RA       from the equilibrium-neutral model at the APTALA3 and PISTILLATA
RA       genes of Arabidopsis thaliana.";
RL       Genetics 151:839-848(1999).
CC       -|- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC       -|- SIMILARITY: NO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR       HSBP: AF115805; MAD51895.1; -.
DR       HSBP: P11746; 1MNK.
DR       InterPro: IPR002487; K-box.
DR       InterPro: IPR002100; MADS-box.
DR       Pfam: PF01486; K-box_1.
DR       Pfam: PF00339; SRP-TF_1.
DR       PRINTS: PR00404; MADSDOMAIN.
DR       SMART: SM00432; MADS_box_1.
DR       PROSITE: PS00350; MADS_box_1; 1.
DR       PROSITE: PS00066; MADS_box_2; 1.
DR       DNA-binding; Nuclear Protein; Transcription regulation.
KM       DNABinding; Nuclear Protein; Transcription regulation.
SQ       SEQUENCE 232 AA; 27342 MW; BDFDC55B7FF4601 CAC66;

Query Match          37.0%; Score 51; DB 10; Length 232;
Best Local Similarity 44.4%; Freq. No. 11;
Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1.

OY      6 QRYG-----RELRLMSDPEFGSKF 24
           |||::|||::|||::|||::|||::
DB      107 GRLSGCLDELDIOELRLEDEMENTPK 133

RESULT  8
09SQ019 PRELIMINARY; PRT: 232 AA.
ID       8
09SQ019
OC       09SQ019:
DT       01-MAY-2000 (TRENBLREL_13, Created)
DT       01-MAY-2000 (TRENBLREL_13, Last sequence update)
DT       01-JUN-2001 (TRENBLREL_17, last annotation update)
DE       FLORAL HOMEOTIC PROTEIN AP3.
GN       APTALA3.
OS       Arabidopsis thaliana (Mouse-ear cress).
OC       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC       Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC       eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX       NCBI_TaxID=3702;
ON       (1)
RP       SEQUENCE FROM N.A.

```


DR HSSP: P11746; 1MM.
DR InterPro: IPR002487; K-box.
DR InterPro: IPR002100; MADS-box.
DR Pfam: PF01486; K-box; 1.
DR Pfam: PF00319; SRP-TE; 1.
DR PRINTS: PR00404; MADSOMAIN.
DR SMART: SM00432; MADS; 1.
DR PROSITE: PS00350; MADS_BOX_1; 1.
DR PROSITE: PS00066; MADS_BOX_2; 1.
KW DNA-binding; Nuclear Protein; Transcription regulation.
SQ SEQUENCE 232 AA; 27314 MW; DB8CA1FC83557D6 CRC64;

Query Match 37.0%; Score 51; DB 10; Length 232;
Best Local Similarity 44.4%; Pred. No. 11;
Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;

QY 6 ORYG-----RLRRMSDEFGSFK 24
DB 107 ORGECLELDIOELRLLEDEMENTFK 133

RESULT 12
ID 09S015 PRELIMINARY; PRT: 232 AA.
AC 09S015;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE FLORAL HOMEOTIC PROTEIN AP3.
GN APETALA3
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;
OC Eucoisids II; Brassicales; Brassicaceae; Arabidopsis.
OC NCBI_TaxID=3702;
RN 111
RP SEQUENCE FROM N.A.
RC STRAIN=CV_KNS-1;
RX MEDLINE=99126449; PubMed=997474;
RA Purganan M.D.; Sudduth J.I.;
RT Molecular population genetics of floral homeotic loci. Departures
RT from the equilibrium-neutral model at the APETALA3 and PISTILLATA
RT genes of Arabidopsis thaliana.
RL Genes 151:839-848(1999).
CC 1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC 1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR EMBL: AF115812; AAD51901.1; -
DR HSSP: P11746; 1MM.
DR InterPro: IPR002487; K-box.
DR InterPro: IPR002100; MADS-box.
DR Pfam: PF01486; K-box; 1.
DR Pfam: PF00319; SRP-TE; 1.
DR PRINTS: PR00404; MADSOMAIN.
DR SMART: SM00432; MADS; 1.
DR PROSITE: PS00350; MADS_BOX_1; 1.
DR PROSITE: PS00066; MADS_BOX_2; 1.
KW DNA-binding; Nuclear Protein; Transcription regulation.
SQ SEQUENCE 232 AA; 27300 MW; 5CA05FD4F824DF0 CRC64;

Query Match 37.0%; Score 51; DB 10; Length 232;
Best Local Similarity 44.4%; Pred. No. 11;
Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;

QY 6 ORYG-----RLRRMSDEFGSFK 24
DB 107 ORGECLELDIOELRLLEDEMENTFK 133

AC 09KGM3;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE NADH DEHYDROGENASE 1 SUBUNIT G.
GN NUOG.
OS Pseudomonas fluorescens.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OC NCBI_TaxID=294;
RN 111
RP SEQUENCE FROM N.A.
RC STRAIN=WCS365;
RA Camacho Carvajal M.M., Lugtenberg B.J.J., Bloembergen G.V.;
RT Characterization of NADH dehydrogenases of Pseudomonas fluorescens
RT WCS365 and their role in competitive root colonization.
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF281148; AAF97803.1; -75K.
DR InterPro: IPR000283; Complex1_75K.
DR PROSITE: PS00641; COMPLEX1_75K_1; 1.
DR PROSITE: PS00642; COMPLEX1_75K_2; 1.
DR PROSITE: PS00643; COMPLEX1_75K_3; 1.
SQ SEQUENCE 904 AA; 98157 MW; C25E86C6D4F4A57 CRC64;

Query Match 36.6%; Score 50.5; DB 2; Length 904;
Best Local Similarity 50.0%; Pred. No. 63;
Matches 11; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

QY 1 NIMAAORYGRELRRMSDEFGS 22
DB 236 NISPGERYG-ELRRIRNRNGS 256

RESULT 14
ID 037056 PRELIMINARY; PRT: 283 AA.
AC 037056;
DT 01-JAN-1998 (T-EMBLrel. 05, Created)
DT 01-JAN-1998 (T-EMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
GN ENV.
OS Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
OS Viruses; Retroid viruses; Retroviridae; Lentivirus.
OC NCBI_TaxID=11723;
RN 111
RP SEQUENCE FROM N.A.
RC STRAIN=SIAGMP1185;
RX MEDLINE=98343740; PubMed=9680146;
RA van Rensburg E.J., Engelbrecht S., Mwenda J., Laten J.D., Robson B.A.;
RT *Stander T., Chege G.K.;
RT Similar immunodeficiency viruses (SIVs) from eastern and southern
RT Africa: detection of a SIVgm variant from a chacma baboon.
RL J. Gen. Virol. 79:1809-1814(1998).
DR EMBL: AF015909; AAC59621.1; -
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
KW AIDS; Coat protein; Glycoprotein.
FT NON_TER 1
FT NON_TER 283
SQ SEQUENCE 283 AA; 32477 MW; 49ED545018BA2871 CRC64;

Query Match 36.2%; Score 50; DB 15; Length 283;
Best Local Similarity 42.9%; Pred. No. 20;
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 5 AORYGRELRRMSDEFGSFK 25
DB 74 SOKYRLRLRQNSCHFGNWK 94

```

RESULT 15
O9HNZ9 PRELIMINARY: PRT: 374 AA.
ID O9HNZ9
AC O9HNZ9;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 16, Last annotation update)
DE SPERMIDINE/PUTRESCINE ABC TRANSPORTER.
GN POTAZ OR VNG1871G.
OS Halobacterium sp. (strain NRC-1).
OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
OC Halobacterium.
OX NCBI_TaxID=64091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20504483; PubMed-11016950;
RA Ng W.V., Kennedy S.P., Mahafiras G.C., Berquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Weltl R., Goo Y.A.,
RA Leitbauer B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
RA Alem M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., Dasarma S.;
RT Genome sequence of Halobacterium species NRC-1.*;
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
CC -1- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
CC (ABC TRANSPORTERS).
CC EMBL: AE005086; AAC20071.1; -.
CC DR InterPro: IPR003593; AAA.
CC DR InterPro: IPR003439; ABC_Transport.
CC DR InterPro: IPR001687; ATP_GTP_A.
CC DR Pfam: PF00005; ABC_tran. 1.
CC DR SMART: SM00382; AAA. 1.
CC DR PROSITE: PS00211; ABC_TRANSPORTER. 1.
CC DR ATP-binding; Complete proteome: Transport.
CC SO SEQUENCE 374 AA; 39190 MW; 1442EF7823037E16 CRC64;

Query Match 36.2%; Score 50; DB 17; Length 374;
Best Local Similarity 76.9%; Pred. No. 27;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 11 ELRMSDFEGGSF 23
DB 197 ELRLSDAVEGSF 209

```

Search completed: September 20, 2002, 11:03:36
 Job time: 1653 sec

PS Example 1; Fig 4; 104pp: English.

CC This sequence represents the BH3 domain of human BAD.

CC The invention relates to a bcl homology domain 3 (BH3 domain),

CC derived from a proapoptotic member of the BCL-2 family. The

CC BH3 polypeptide can be used in a method for promoting apoptosis in a

CC target cell, especially where the cell is a cancer cell a virus infected

CC cell or an autointubody producing cell. The BH3 polypeptide can be used

CC in therapeutic compositions for treating disease including cancer, other

CC lymphoproliferative conditions, arthritis, inflammation, and autoimmune

CC diseases, which may result from the down regulation of cell death

CC regulation.

CC

XX Sequence 16 AA:

SQ

Query Match 100.0%; Score 83; DB 20; Length 16;

Best Local Similarity 100.0%; Pred. No. 9.3e-08;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QRYGRELRRMSDEFPD 16

DB 1 qrygrellrmsdefvd 16

RESULT 2

ID AAB37029 standard; peptide: 16 AA.

XX AAB37029;

XX 28-FEB-2001 (first entry)

XX

DE Bcl2 polypeptide BH3 domain peptide #29.

XX

XX Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;

XX cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;

XX apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;

XX colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;

XX melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;

XX stroke; myocardial infarction.

XX

OS Homo sapiens.

XX

XX WO200059526-A1.

XX

XX 12-OCT-2000.

XX

XX 06-APR-2000: 2000WO-US09352.

XX

XX 07-APR-1999: 99US-0128202.

XX

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX

XX Huang Z, Wang J, Zhang Z, Shan S, Lu Z;

XX

XX WPI: 2000-679325/66.

XX

XX New peptide conjugates for modulating apoptosis or for inhibiting B

XX cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for

XX treating neurodegenerative disorders, stroke, or cancer -

XX

XX

PS Claim 18; Page 18; 74pp: English.

XX

CC The invention relates to a peptide conjugate having the formula:

CC (R-X)n-peptide where n = 1-10; X = C=O, when the R-X group is attached

CC to the N-terminus of the peptide, or a side chain of the peptide where

CC the functional group of the side chain is NH2 or OH; or X = O or NH,

CC when the R-X group is attached to the C-terminus of the peptide, or a

CC side chain of the peptide, where the side chain functional group is COOH

CC or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one

CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally

CC monosubstituted with a 1-5C straight or branched chain alkyl group,

CC phenyl optionally monosubstituted with a 1-5C straight or branched chain

CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples

CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of

CC the BH3 domain of the cell death agonist Bad. The peptide conjugate is

CC useful for modulating apoptosis in the cells of a subject, or for

CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of

CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2

CC function, in particular, the peptide conjugate is useful for treating a

CC subject afflicted with a cancer characterized by cancer cells that

CC express Bcl-2. The cancer includes prostate, colorectal, gastric, or

CC non-small lung. renal or thyroid cancers, neuroblastoma, melanoma, or

CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide

CC conjugate is also useful for treating disorders characterized by

CC increased apoptosis, e.g. neurodegenerative disorders, acquired

CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.

XX

SQ

Sequence 16 AA:

Query Match 100.0%; Score 83; DB 21; Length 16;

Best Local Similarity 100.0%; Pred. No. 9.3e-08;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QRYGRELRRMSDEFPD 16

DB 1 qrygrellrmsdefvd 16

RESULT 3

ID AAY96321 standard; Peptide; 26 AA.

XX AAY96321;

XX 17-AUG-2000 (first entry)

XX

DE Mammalian Bad Bcl-2 homology domain 3 domain.

XX

XX Mammal; apoptosis; cell death; Bnc3; apoptosis promotion; Bad;

XX apoptosis inhibition; malignant cell; autoimmune disease.

XX

XX Mammalia.

XX

XX WO200026228-A1.

XX

XX 11-MAY-2000.

XX

XX 28-OCT-1999: 99WO-US25285.

XX

XX 02-NOV-1998: 98US-0184168.

XX

XX (CLON-) CLONTECH LAB INC.

XX

XX Zhu L, Yin X, Chittenden T;

XX

XX WPI: 2000-365560/31.

XX

XX Novel polynucleotide encoding a BBC3 protein which is useful for

XX modulating apoptosis, especially in the treatment of cancer and

XX autoimmune diseases -

XX

XX

PS Disclosure; Fig 4; 47pp: English.

XX

CC The present sequence is the mammalian Bad Bcl-2 homology domain 3

CC (BH3) domain, which was used in a sequence alignment with the same

CC domain of a putative version of the mammalian apoptosis

CC regulator Bbc3, which was designated BBC3-ORF2. The BBC3 protein,

CC nucleic acids and antibodies are suitable for use in promoting cell

CC death or for preventing apoptosis in malignant cells and those causing

CC autoimmune diseases.

XX

SQ

Sequence 26 AA:

Query Match 100.0%; Score 83; DB 21; Length 26;
 Best Local Similarity 100.0%; Pred. No. 1.6e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ORRGRLRRMSDEPVD 16
 |||||
 Db 3 qrygrellrmsdeivd 18

RESULT 4

AAW0371
 ID AAW0371 standard; Peptide; 26 AA.
 XX
 AC AAW0371;
 XX
 DT 02-MAY-2001 (first entry)
 XX
 DE BAD BH3 consensus peptide sequence SEQ ID NO:4.
 XX
 KW Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;
 KW immunostimulant; neuroprotective; nocitropic; antischismic; vulnery;
 KW cyrostatic; antiviral; antitumor; antitumor; wound healing;
 KW immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;
 KW immunodeficiency disease; neurodegenerative disease; viral infection;
 KW ischaemic cell death; reperfusion cell death; arthritis; infertility;
 KW lymphoproliferative condition; inflammation; autoimmune disease.
 XX
 OS Unidentified.
 XX
 PA WC200110888-A1.
 XX
 PD 15-FEB-2001.
 XX
 PF 30-MAY-2000; 2000MO-US11864.
 XX
 PR 28-MAY-1999; 990S-0136783.
 XX
 PA (APOP-) APOPTOSIS TECHNOLOGY INC.
 XX
 PI Zhou X;
 XX
 DR WPI: 2001-138734/14.
 XX
 PT New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,
 PT useful for screening for candidate compounds which induce or inhibit
 PT apoptosis, comprises amino acid substitutions at Ser118, Ser135 or
 PT Ser113 -
 XX
 PS Example 2; Fig 3a; 157pp; English.
 XX
 CC The present invention describes an isolated or synthetic polypeptide
 CC (I) comprising a less than full length amino acid sequence of a mutant
 CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its
 CC fragment, which contains amino acid substitutions at Ser118 of a human
 CC BAD, Ser135 of a murine BAD (longer murine BAD) or Ser113 of a murine
 CC BAD (shorter murine BAD). (ii) has immunostimulant, neuroprotective,
 CC nocitropic, antischismic, vulnery, cyrostatic, antiviral,
 CC antitumor, antitumor and immunosuppressive activities, and
 CC can be used as an apoptosis inducer or inhibitor. BAD polypeptides and
 CC polynucleotides can be used for screening candidate compounds and drugs
 CC for activity that promote cell survival or apoptosis. Other uses include
 CC inducing or inhibiting apoptosis in a cell. Candidate compounds
 CC identified and (mutant) BAD polypeptides are useful in treating
 CC immunodeficiency diseases, neurodegenerative diseases, ischaemic cell
 CC death, reperfusion cell death, wound healing, cancer, viral infections,
 CC lymphoproliferative conditions, arthritis, infertility, inflammation and
 CC autoimmune diseases. The present sequence represents a Bcl-family member
 CC BH3 domain consensus sequence which is used in an example from the
 CC present invention.
 XX
 SO Sequence 26 AA;

Query Match 100.0%; Score 83; DB 22; Length 26;
 Best Local Similarity 100.0%; Pred. No. 1.6e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ORRGRLRRMSDEPVD 16
 |||||
 Db 3 qrygrellrmsdeivd 18

RESULT 5

AAW32476
 ID AAW32476 standard; Protein; 166 AA.
 XX
 AC AAW32476;
 XX
 DT 15-JAN-1998 (first entry)
 XX
 DE BHC6 protein for regulating cell death.
 XX
 KW BHC6 gene; cell death; cell cycle; Bcl2; human.
 XX
 OS Homo sapiens.
 XX
 PA US563316-A.
 XX
 PD 02-SEP-1997.
 XX
 PF 18-JUN-1996; 96US-0665617.
 XX
 PR 18-JUN-1996; 96US-0665617.
 XX
 PA (CLON-) CLONTECH LAB INC.
 XX
 PI Xudong Y;
 XX
 DR WPI: 1997-447980/41.
 XX
 DR N-PSDB; AAT91561.
 XX
 PT Isolated BHC6 gene - encodes a protein that regulates cell death
 PT through interaction with Bcl-2
 XX
 PS Claim 1; Column 11-12; 7pp; English.
 XX
 CC The present sequence represents a protein of 166 amino acids. The
 CC sequence is disclosed as being a protein called BHC6 which regulates
 CC cell death through interaction with Bcl-2. The DNA may be used for the
 CC production of the recombinant protein, which can be used in unspecified
 CC therapeutic or diagnostic procedures, as a molecular weight marker, and
 CC to raise antibodies that can be used in unspecified diagnostic or
 CC therapeutic applications and to reduce or eliminate the biological
 CC activity of the BHC6 protein in vivo.
 XX
 SO Sequence 166 AA;

Query Match 100.0%; Score 83; DB 18; Length 166;
 Best Local Similarity 100.0%; Pred. No. 1.2e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ORRGRLRRMSDEPVD 16
 |||||
 Db 106 qrygrellrmsdeivd 121

RESULT 6

AAW5779
 ID AAW5779 standard; Protein; 168 AA.
 XX
 AC AAW5779;
 XX
 DT 17-JUL-1998 (first entry)

DE		Human Bcl-xL/Bcl-2 associated death promoting polypeptide.
XX		
KW	Human: Bcl-xL/Bcl-2 associated death promoting polypeptide; Bad;	
XV	programmed cell death; apoptosis.	
OS	Homo sapiens.	
XX		
PN	WO9812328-A2.	
XX		
PD	26-MAR-1998.	
XX		
PF	18-SEP-1997; 97MO-US16991.	
XX		
PR	20-SEP-1996; 96US-0717123.	
PA	(IDUN-) IDUN PHARM INC.	
XX		
P1	Horne MA, Oltersdorf T;	
DR	WPL; 1998-217267/19.	
N-PDB:	AAV23577.	
PT	Bad gene mediating apoptosis - used to develop products for treating	
PS	e.g. neurodegenerative disease, cancers or autoimmune disease	
ClaIn 8:	Fig 1; 41pp; English.	
XX		
CC	The present sequence is the human Bcl-xL/Bcl-2 associated	
CC	death promoting polypeptide, Bad, the binding of which to Bcl-Xl	
CC	results in the induction of programmed cell death, i.e. apoptosis.	
CC	Bad can be used in screening assays for compounds to treat or	
CC	prevent diseases characterised by apoptotic cell death, such as	
CC	neurodegenerative disorders, e.g. Alzheimer's and Parkinson's	
CC	disease, amyotrophic lateral sclerosis, retinitis pigmentosa and	
CC	aplastic anaemia and ischemic injury including myocardial	
CC	infarction, stroke and reperfusion injury. Assays can also be	
CC	used to obtain apoptosis enhancing compounds to treat or prevent as	
CC	cancers characterised by the loss of apoptotic cell death, such as	
CC	cancers, e.g. lymphoma and hormone dependent tumours, autoimmune	
CC	glomerulonephritis and viral infections, e.g. herpesvirus,	
CC	poxvirus or adenovirus infection. Bad can also be used for	
CC	detection and diagnosis.	
SQ	Sequence 168 AA:	
Query Match	100.0%;	Score 83; DB 19; Length 168;
Best Local Similarity	100.0%;	Pred. No. 1.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 QRYGRLRMSDEPVD 16	
Dd	iiiiiiiii	
	108 qrygrrlrmsdefvd 123	
RESULT 7		
ID	AAAB13512 standard; protein; 168 AA.	
AC	AAAB13512;	
DT	02-NOV-2000 (first entry)	
DE	Human cell proliferation protein Apop-1.	
KM	Human; cell proliferation; Apop-1; cancer; inflammation; infection;	
KM	trauma; neurodegenerative disease; ischemic injury; wasting disease.	
SS	Homo sapiens.	

XX	US6080847-A.
PN	27-JUN-2000.
PD	04-DEC-1997; 97US-0985335.
PF	04-DEC-1997; 97US-0985335.
PR	04-DEC-1997; 97US-0985335.
PP	(INCYTE) INCYTE PHARM INC.
PA	Corley NC, Hillman JL, Yue H, Lal P, Shah P:
PB	WPI: 2000-451230/39.
PC	N-PDB: AAA63332.
PE	Newel polynucleotide and polypeptide sequences of proteins associated
PF	with cell proliferation for diagnosis, prevention and treatment of e.g.
PG	cancer, acquired immunodeficiency syndrome, and Parkinson's disease -
PH	Example 8; Fig 1; 58pp; English.
PI	The present sequence is the human APOE-1 protein. This protein, which
PJ	shares structural and chemical homology with Bcl-2, is involved in cell
PK	proliferation. Its coding sequence was isolated by screening a synovial
PL	tissue cDNA library using a computer search for amino acid sequence
PM	alignments. The gene and protein can be used in the treatment of various
PN	cancers, disorders with associated inflammation such as Addison's
PO	disease, adult respiratory distress syndrome, allergies, anaemia, asthma,
PP	atherosclerosis, Crohn's disease, ulcerative colitis, diabetes mellitus,
PQ	emphysema, glomerulonephritis, gout, Graves' disease, irritable bowel
PR	sndrome, lupus erythematosus, multiple sclerosis, myasthenia gravis,
PS	myocardial or pericardial inflammation, osteoporosis, rheumatoid
PT	arthritis, Sjogren's syndrome and autoimmune thyroiditis, complications
PV	of cancer, haemodialysis and extracorporeal circulation, infections,
PW	trauma, disorders with associated apoptosis including AIDS and other
PX	infectious and genetic immunodeficiencies, neurodegenerative diseases
PY	such as Alzheimer's disease and Parkinson's disease, ischaemic injuries
PZ	such as myocardial infarction, and wasting diseases including cachexia.
QA	Sequence 168 AA:
QB	Query Match 100.0%; Score 83; DB 21; Length 168;
QC	Best Local Similarity 100.0%; Pred. NO. 1.2e-06;
QD	Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QE	1 QRTGRLRRMSDEVD 16
QF	
QG	108 qrtgrelrrmsdevd 123
QH	RESULT 8
QI	AAB70368
QJ	AAB70368 standard; protein: 168 AA.
QK	AAB70368:
QL	02-MAY-2001 (first entry)
QM	Human BAD mutant amino acid sequence SEQ ID NO:1.
QN	Bcl-XL/Bcl-2 associated cell death regulator; BAD: mutant; apoptosis;
QO	immunostimulant; neuroprotective; neurotrophic; antischismatic; vulnerary;
QP	cytotoxic; antiviral; antitubercular; antiinflammatory; wound healing;
QQ	immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;
QR	immunodeficiency disease; neurodegenerative disease; viral infection;
QS	ischaemic cell death; reperfusion cell death; arthritis; infertility;
QT	lymphoproliferative condition; inflammation; autoimmune disease.
QU	Homo sapiens.
QV	Synthetic.
QW	NC0200110888-A1.
QX	NC

XX 15-FEB-2001.
 PD 30-MAY-2000; 2000MO-US11864.
 XX 28-MAY-1999; 99US-0136783.
 XX (APOB-) APOPTOSIS TECHNOLOGY INC.
 PA Zhou X;
 PI WPI: 2001-138734/14.
 DR
 XX New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,
 PT useful for screening for candidate compounds which induce or inhibit
 PT apoptosis, comprises amino acid substitutions at Ser118, Ser155 or
 PT Ser113 -
 XX
 PS Claim 1, Page 147; 157pp; English.
 XX
 CC The present invention describes an isolated or synthetic polypeptide
 CC (1) comprising a less than full length amino acid sequence of a mutant
 CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its
 CC fragment, which contains amino acid substitutions at Ser118 of a human
 CC BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine
 CC BAD (shorter murine BAD). (1) has immunostimulant, neuroprotective,
 CC neurotropic, antischismatic, cytostatic, antiviral,
 CC antiarthritic, antiinflammatory and immunosuppressive activities, and
 CC can be used as an apoptosis inducer or inhibitor. BAD polypeptides and
 CC polynucleotides can be used for screening candidate compounds and drugs
 CC for activity that promote cell survival or apoptosis. Other uses include
 CC inducing or inhibiting apoptosis in a cell. Candidate compounds
 CC identified and (mutant) BAD polypeptides are useful in treating
 CC immunodeficiency diseases, neurodegenerative diseases, ischemic cell
 CC death, reperfusion cell death, wound healing, cancer, viral infections,
 CC lymphoproliferative conditions, arthritis, infertility, inflammation and
 CC autoimmune diseases. The present sequence represents a specifically
 CC claimed human BAD mutant amino acid sequence from the present invention.
 CC
 XX Sequence 168 AA:
 SQ
 Query Match 100.0%; Score 83; DB 22; Length 168;
 Best Local Similarity 100.0%; Pred. NO. 1.2e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 ORYGRELRMSDEPVD 16
 Db 108 qrygrellrmsdelvd 123
 XX
 RESULT 9
 AAB48287
 ID AAB48287 standard; protein: 168 AA.
 AC AAB48287;
 XX
 DT 02-APR-2001 (first entry)
 DE Human Bad protein.
 XX
 DE S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; ZF;
 KW CUL-1; cullin; CDC53; P27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax;
 KW Bad; Bcl-2; tumour; cytosolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200075184-A1.
 XX
 PD 14-DEC-2000.
 XX
 PF 05-JUN-2000; 2000MO-US15449.
 XX

PR 04-JUN-1999; 99US-0137494.
 XX
 PA (UYVA) UNIV YALE.
 XX
 PI Zhang H, Tsvetkov LM, Kondo T;
 XX
 DR WPI: 2001-061703/07.
 DR N-PSDB; AAC84599.
 PT Modulating polypeptide levels in a cell, diagnosing and treating tumor,
 PT involves altering levels of proteins such as S-phase kinase associated
 PT proteins 1, 2 and cullin/CDC53 proteins -
 XX
 PS Claim 5; Page 102-103; 162pp; English.
 XX
 CC The invention relates to methods of altering the polypeptide levels in a
 CC cell, using proteins selected from S-phase kinase associated proteins 1
 CC and 2 (SKP1, SKP2), SKP2-like proteins (ZF) and CUL-1 (a member of the
 CC cullin/CDC53 family of proteins). The method is useful for altering the
 CC level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2
 CC polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for
 CC detecting tumours, and in monitoring tumor treatment in a mammal. Agents
 CC that modulate interactions between SKP and target proteins are useful for
 CC treating tumours.
 CC
 XX Sequence 168 AA:
 SQ
 Query Match 100.0%; Score 83; DB 22; Length 168;
 Best Local Similarity 100.0%; Pred. NO. 1.2e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 ORYGRELRMSDEPVD 16
 Db 108 qrygrellrmsdelvd 123
 XX
 RESULT 10
 AAG67688
 ID AAG67688 standard; protein: 168 AA.
 AC AAG67688;
 XX
 DT 26-NOV-2001 (first entry)
 DE Amino acid sequence of protein associated with cell proliferation-1.
 XX
 KW Human; cell proliferation; APOB-1; APOB-2; APOB-3; apoptosis; cancer;
 KW brain cancer; breast cancer; Alzheimer's disease; Parkinson's disease;
 KW inflammation; allergy; gout; osteoarthritis; bronchitis.
 XX
 OS Homo sapiens.
 XX
 FH Location/Qualifiers
 FT 10..13 "potential casein kinase II phosphorylation site"
 FT /note="potential casein kinase II phosphorylation site"
 FT 16..19 "potential casein kinase II phosphorylation site"
 FT /note="potential casein kinase II phosphorylation site"
 FT 34..36 "potential casein kinase II phosphorylation site"
 FT /note="potential casein kinase II phosphorylation site"
 FT 80..83 "potential casein kinase II phosphorylation site"
 FT /note="potential casein kinase II phosphorylation site"
 FT 115..118 "potential casein kinase II phosphorylation site"
 FT /note="potential casein kinase II phosphorylation site"
 FT 124..126 "potential casein kinase II phosphorylation site"
 FT /note="potential casein kinase II phosphorylation site"
 FT 153..156 "potential casein kinase II phosphorylation site"
 FT /note="potential casein kinase II phosphorylation site"
 XX
 PN US6281334-B1.
 XX
 PD 28-AUG-2001.
 XX

XX 30-SEP-1999: 99US-0410372.
 PF 04-DEC-1997: 97US-0985335.
 PR (INCY-) INCYTE GENOMICS INC.
 PX
 PI Hillman JL, Yue H, Lal P, Shah P, Corley NC;
 XX WPI; 2001-569661/64.
 DR N-PSDB: AAH78430.
 XX
 PT New polypeptides associated with cell proliferation, useful for
 PT preventing or treating cancer (e.g. brain cancer), a disorder
 PT associated with an increase in apoptosis (e.g. Alzheimer's disease) or
 PT inflammation (e.g. gout) -
 PS Example: Fig 1A-C; 59pp; English.
 CC The present sequence represents a human protein which is associated
 CC with cell proliferation, designated Apop-1. The specification also
 CC describes Apop-2 and Apop-3. The Apop polypeptides are useful for
 CC diagnosing, preventing or treating disorders associated with abnormal
 CC cell proliferation and apoptosis. The polypeptides and composition are
 CC particularly useful for treating or preventing cancer (e.g. brain or
 CC breast cancer), a disorder associated with an increase in apoptosis
 CC (e.g. Alzheimer's disease or Parkinson's disease) or inflammation
 CC (e.g. allergies, gout, osteoarthritis or bronchitis).
 CC
 SO Sequence 168 AA:

Query Match 100.0%; Score 83; DB 22; Length 168;
 Best Local Similarity 100.0%; Pred. No. 1.2e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ORYGRELRMSDEFVD 16
 Db 108 gyygrellrmsdefvd 123
 |||

RESULT 11
 AAB70379
 ID AAB70379 standard; Peptide: 18 AA.
 AC AAB70379;
 XX
 DT 02-MAY-2001 (first entry)
 DE BAD BH3 domain region phosphopeptide SEQ ID NO:17.
 XX
 KW Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;
 KW immunostimulant; neuroprotective; neurotropic; antischlemic; vulnary;
 KW cytosolic; antiviral; antitumor; antineoplastic; wound healing;
 KW immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;
 KW immunodeficiency disease; neurodegenerative disease; viral infection;
 KW ischemic cell death; reperfusion cell death; arthritis; infertility;
 KW lymphoproliferative condition; inflammation; autoimmune disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200110888-A1.
 PD 15-FEB-2001.
 XX
 PF 30-MAY-2000; 2000WO-US11864.
 XX
 PR 28-MAY-1999; 99US-0136783.
 XX
 PA (APOP-) APOPTOSIS TECHNOLOGY INC.
 XX
 PI Zhou X;
 XX

DR WPI; 2001-138734/14.
 XX
 PT New mutant Bcl-XL/Bcl-2 associated cell death regulator polypeptide,
 PT useful for screening for candidate compounds which induce or inhibit
 PT apoptosis, comprises amino acid substitutions at Ser118, Ser15 or
 PT Ser113 -
 PS Example 9; Page 92; 157pp; English.
 CC
 CC The present invention describes an isolated or synthetic polypeptide
 CC (I) comprising a less than full length amino acid sequence of a mutant
 CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its
 CC fragment, which contains amino acid substitutions at Ser118 of a human
 CC BAD, Ser15 of a murine BAD (longer murine BAD) or Ser113 of a murine
 CC BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective,
 CC neurotropic, antischlemic, vulnary, cytosolic, antiviral,
 CC antitumor, antineoplastic, antineoplastic and immunosuppressive activities, and
 CC can be used as an apoptosis inducer or inhibitor. BAD polypeptides and
 CC polynucleotides can be used for screening candidate compounds and drugs
 CC for activity that promote cell survival or apoptosis. Other uses include
 CC inducing or inhibiting apoptosis in a cell. Candidate compounds
 CC identified and (mutant) BAD polypeptides are useful in treating
 CC immunodeficiency diseases, neurodegenerative diseases, ischemic cell
 CC death, reperfusion cell death, wound healing, cancer, viral infections, and
 CC lymphoproliferative conditions, arthritis, infertility, inflammation, and
 CC autoimmune diseases. The present sequence represents a BAD BH3 domain
 CC region phosphopeptide which is used in an example from the present
 CC invention.
 CC
 SO Sequence 18 AA:

Query Match 90.4%; Score 75; DB 22; Length 18;
 Best Local Similarity 93.8%; Pred. No. 2.6e-06;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ORYGRELRMSDEFVD 16
 Db 1 gyygrellrmsdefvd 16
 |||

RESULT 12
 AAB70380
 ID AAB70380 standard; Peptide: 20 AA.
 AC AAB70380;
 XX
 DT 02-MAY-2001 (first entry)
 DE BAD BH3 domain region related phosphopeptide SEQ ID NO:18.
 XX
 KW Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;
 KW immunostimulant; neuroprotective; neurotropic; antischlemic; vulnary;
 KW cytosolic; antiviral; antitumor; antineoplastic; wound healing;
 KW immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;
 KW immunodeficiency disease; neurodegenerative disease; viral infection;
 KW ischemic cell death; reperfusion cell death; arthritis; infertility;
 KW lymphoproliferative condition; inflammation; autoimmune disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200110888-A1.
 PD 15-FEB-2001.
 XX
 PF 30-MAY-2000; 2000WO-US11864.
 XX
 PR 28-MAY-1999; 99US-0136783.
 XX
 PA (APOP-) APOPTOSIS TECHNOLOGY INC.
 XX
 PI Zhou X;
 XX

DR WPI; 2001-138734/14.

XX New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,
PT useful for screening for candidate compounds which induce or inhibit
PT apoptosis, comprises amino acid substitutions at Ser118, Ser155 or
PT Ser113 -

XX Example 9; Page 92; 157pp; English.

XX The present invention describes an isolated or synthetic polypeptide
CC (1) comprising a less than full length amino acid sequence of a mutant
CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its
CC fragment, which contains amino acid substitutions at Ser118 of a human
CC BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine
CC BAD (shorter murine BAD). (1) has immunostimulant, neuroprotective,
CC neurotropic, antisclerotic, vulnary, cytoskeletal, antiviral,
CC antitumor, antiinflammatory and immunosuppressive activities, and
CC can be used as an apoptosis inducer or inhibitor. BAD polypeptides and
CC polynucleotides can be used for screening candidate compounds and drugs
CC for activity that promote cell survival or apoptosis. Other uses include
CC inducing or inhibiting apoptosis in a cell. Candidate compounds
CC identified and (mutant) BAD polypeptides are useful in treating
CC immunodeficiency diseases, neurodegenerative diseases, ischaemic cell
CC death, reperfusion cell death, wound healing, cancer, viral infections,
CC lymphoproliferative conditions, arthritis, infertility, inflammation and
CC autoimmune diseases. The present sequence represents a BAD BH3 domain
CC region related phosphopeptide which is used in an example from the
CC present invention.

XX Sequence 20 AA;

Query Match 90.4%; Score 75; DB 22; Length 20;
Best Local Similarity 93.8%; Pred. No. 2, 9e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 QRYGRELPRMSDEPD 16
Db 3 qrygrellrmsdesvd 18

RESULT 13

AA05422
ID AAY05422 standard; peptide: 16 AA.

XX AAY05422;

XX 02-JUL-1999 (first entry)

XX Mouse BAD BH3 domain.

XX BH3 domain; cell death agonist; bcl homology domain; BCL-2 family;
KW apoptosis promoter; cancer cell; virus infected cell; inflammation;
KW autoantibody producing cell; cancer; lymphoproliferative condition;
KW arthritis; autoimmune disease; therapy.

XX Mus sp.

XX W09916787-A1.

XX 08-APR-1999.

XX 22-SEP-1998; 98WO-US19765.

XX 07-OCT-1997; 97US-0946039.

XX 26-SEP-1997; 97US-0060133.

XX (UNIV) UNIV WASHINGTON.

XX Kortsmeier SJ;

XX WPI; 1999-255058/21.

PT Bcl homology domain 3 polypeptide

XX Example 1; Fig 4; 104pp; English.

XX This sequence represents the BH3 domain of mouse BAD.
CC The invention relates to a bcl homology domain 3 (BH3 domain),
CC derived from a proapoptotic member of the BCL-2 family. The
CC BH3 polypeptide can be used in a method for promoting apoptosis in a
CC target cell, especially where the cell is a cancer cell, a virus infected
CC cell or an autoantibody producing cell. The BH3 polypeptide can be used
CC in therapeutic compositions for treating disease including cancer, other
CC lymphoproliferative conditions, arthritis, inflammation, and autoimmune
CC diseases, which may result from the down regulation of cell death
CC regulation.

XX Sequence 16 AA;

Query Match 88.0%; Score 73; DB 20; Length 16;
Best Local Similarity 100.0%; Pred. No. 5, 1e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QRYGRELPRMSDEF 14
Db 1 qrygrellrmsdef 14

RESULT 14

AAB37028
ID AAB37028 standard; peptide: 16 AA.

XX AAB37028;

XX 28-FEB-2001 (first entry)

XX Bcl2 polypeptide BH3 domain peptide #28.

XX Cytostatic; neuroprotective; anti-HIV; virocid; cerebroprotective;
KW cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;
KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;
KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;
KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
KW stroke; myocardial infarction.

XX Homo sapiens.

XX W0200059526-A1.

XX 12-OCT-2000.

XX 06-APR-2000; 2000WO-US09352.

XX 07-APR-1999; 99US-0128202.

XX (UNIV-) UNIV JEFFERSON THOMAS.

XX Huang Z, Zhang J, Shan S, Lu Z;

XX WPI; 2000-679325/66.

XX New peptide conjugates for modulating apoptosis or for inhibiting B
PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for
PT treating neurodegenerative disorders, stroke, or cancer -
XX Claim 18; Page 18; 74pp; English.

XX The invention relates to a peptide conjugate having the formula:
CC (R-X)n-peptide where n = 1-10; X = C=O, when the R-X group is attached
CC to the N-terminus of the peptide, or a side chain of the peptide where
CC the functional group of the side chain is NH2 or OH; or X = O or NH,
CC when the R-X group is attached to the C-terminus of the peptide, or a
CC side chain of the peptide, where the side chain functional group is COOH
CC or CONH2; and R = 2-Iso alkyl or alkoxy, 2-Iso alkyl containing one

CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain
 CC alkyl group, or benzyl. The peptides AAR37001-B37058 represent examples
 CC of the peptide portion of the conjugate. The peptides represent analogues
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of
 CC the Bcl-2 domain of the cell death agonist Bad. The peptide conjugate is
 CC useful for modulating apoptosis in the cells of a subject, or for
 CC reversing B cell lymphoma/leukemia 2 (bcl-2)-mediated blockage of
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2
 CC function. In particular, the peptide conjugate is useful for treating a
 CC subject afflicted with a cancer characterized by cancer cells that
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric,
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
 CC conjugate is also useful for treating disorders characterized by
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
 CC
 XX

Sequence 16 AA:

Query Match 88.0%; Score 73; DB 21; Length 16;

Best Local Similarity 100.0%; Pred. No. 5, 1e-06; Mismatches 0; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QRYGRELRRMSDEF 14

DB 1 qrygrellrmsdef 14

RESULT 15

AAR35166 standard; peptide: 23 AA.

AAR35166;

03-JAN-1997 (first entry)

bcl-x(L)/bcl-2 associated death promoter epitope, residues 138-160.

Epitope; murine; bcl-x(L)/bcl-2 associated death promoter; Bad; stroke;

polypeptide; bcl-x; cell death; regulate; BH1; BH2; Apoptotic cell death;

cytokine deprivation; IL-3 dependent cell line; Immunodeficiency; AIDS;

neurodegenerative disease; senescence; ischaemia; neoplasia.

Mus musculus.

WO9613614-A1.

09-MAY-1996.

31-OCT-1995; 95WO-US14246.

31-OCT-1994; 94US-0333565.

(UNIT) UNIV WASHINGTON.

Korsmeyer SJ;

WPI: 1996-251465/25.

Polynucleotide encoding bcl-x(L)/bcl-2 associated death promoter -

useful to treat neoplasia and apoptosis and to identify agents

inhibiting its binding to bcl-2 or bcl-x(L) to form heteromultimers

Claim 2: Page 103: 130pp; English.

The sequences given in AAR35155-67 represent epitopes derived from the
 murine bcl-x(L)/bcl-2 associated death promoter (Bad) polypeptide (see
 also AAR35168). Bad is a 22.1 kD protein which interacts with bcl-2 and
 bcl-x proteins and regulates cell death. It has homology to the Bcl-2-
 related family clustered in the BH1 and BH2 domain. Bad has been found

CC to hybridise to bcl-x(L) and bcl-2 in yeast two-hybrid assays and in
 CC vivo in mammalian cells. Overexpressed Bad counters the death
 CC inhibitory activity of bcl-x(L) but is much less effective at countering
 CC the death inhibitory activity of bcl-2. Bad expression can accelerate
 CC apoptotic cell death induced by cytokine deprivation in an IL-3 dependent
 CC cell line expressing bcl-x(L), and it also counters the death repressor
 CC activity of bcl-x(L). Bad competes with Bax for binding to bcl-x(L).
 CC Bad may be used to identify agents which inhibit its binding to bcl-2
 CC or bcl-x(L) to form heterodimers. Such agents may be used to treat
 CC neurodegenerative diseases, immunodeficiency diseases, e.g. AIDS,
 CC senescence or ischaemia.
 CC
 XX

Sequence 23 AA:

Query Match 88.0%; Score 73; DB 17; Length 23;

Best Local Similarity 100.0%; Pred. No. 7, 6e-06; Mismatches 0; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QRYGRELRRMSDEF 14

DB 8 qrygrellrmsdef 21

Search completed: September 20, 2002, 10:35:58
 Job time: 426 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 20, 2002, 10:37:20 ; Search time 75.64 Seconds
(without alignments)
5.167 Million cell updates/sec

Title: US-09-544-664-29

Perfect score: 83

Sequence: 1 QRYGRLRRMSDFVD 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA: *
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3: /cgn2.6/prodata/2/iaa/6A_COMB.pep: *
4: /cgn2.6/prodata/2/iaa/6B_COMB.pep: *
5: /cgn2.6/prodata/2/iaa/PCUTS_COMB.pep: *
6: /cgn2.6/prodata/2/iaa/backfilest1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	83	100.0	166	1 US-08-665-617-2	Sequence 2, Appl1
2	83	100.0	168	2 US-08-717-123-2	Sequence 2, Appl1
3	83	100.0	168	3 US-08-985-335-1	Sequence 1, Appl1
4	83	100.0	168	4 US-08-985-335-7	Sequence 7, Appl1
5	83	100.0	168	5 US-09-410-372-1	Sequence 1, Appl1
6	83	100.0	168	6 US-09-410-372-7	Sequence 7, Appl1
7	73	88.0	23	1 US-08-333-565-10	Sequence 10, Appl1
8	73	88.0	23	2 US-08-661-479-10	Sequence 10, Appl1
9	73	88.0	59	2 US-08-733-505A-55	Sequence 55, Appl1
10	73	88.0	59	2 US-08-733-505A-56	Sequence 56, Appl1
11	73	88.0	59	2 US-08-733-505A-57	Sequence 57, Appl1
12	73	88.0	59	2 US-08-733-505A-58	Sequence 58, Appl1
13	73	88.0	204	1 US-08-333-565-2	Sequence 2, Appl1
14	73	88.0	204	1 US-08-661-479-2	Sequence 2, Appl1
15	73	88.0	204	2 US-08-733-505A-1	Sequence 1, Appl1
16	73	88.0	204	2 US-08-733-505A-12	Sequence 13, Appl1
17	73	88.0	204	2 US-08-733-505A-13	Sequence 13, Appl1
18	73	88.0	204	2 US-08-733-505A-14	Sequence 14, Appl1
19	70	84.3	204	2 US-08-717-123-3	Sequence 3, Appl1
20	67	80.7	16	1 US-08-333-565-26	Sequence 26, Appl1
21	67	80.7	16	2 US-08-661-479-26	Sequence 26, Appl1
22	42	50.6	11	2 US-08-733-505A-34	Sequence 34, Appl1
23	42	50.6	11	2 US-08-706-741B-69	Sequence 69, Appl1
24	42	50.6	11	2 US-08-924-695A-69	Sequence 69, Appl1
25	42	50.6	876	1 US-08-785-429-2	Sequence 2, Appl1
26	42	50.6	876	1 US-08-966-621-2	Sequence 2, Appl1
27	38	45.8	432	3 US-09-075-087-2	Sequence 2, Appl1

28	38	45.8	432	4 US-09-472-971-1	Sequence 1, Appl1
29	38	45.8	575	3 US-08-913-805A-2	Sequence 2, Appl1
30	38	45.8	575	3 US-08-913-805A-10	Sequence 10, Appl1
31	38	45.8	575	4 US-09-442-629-2	Sequence 2, Appl1
32	38	45.8	575	4 US-09-442-629-10	Sequence 10, Appl1
33	36	43.4	173	3 US-08-669-408B-8	Sequence 8, Appl1
34	36	43.4	1093	5 PCT-US93-03077-1	Sequence 1, Appl1
35	35	42.2	108	2 US-08-160-524A-10	Sequence 10, Appl1
36	35	42.2	380	4 US-08-857-076-110	Sequence 12, Appl1
37	35	42.2	1724	4 US-08-857-076-12	Sequence 12, Appl1
38	34	41.0	66	2 US-08-867-087B-40	Sequence 40, Appl1
39	34	41.0	168	4 US-09-199-637A-425	Sequence 425, App
40	34	41.0	339	3 US-08-758-280-1	Sequence 1, Appl1
41	34	41.0	339	3 US-08-758-280-2	Sequence 2, Appl1
42	34	41.0	339	3 US-08-964-614A-1	Sequence 1, Appl1
43	34	41.0	339	3 US-08-964-614A-2	Sequence 2, Appl1
44	34	41.0	355	4 US-09-194-905-10	Sequence 10, Appl1
45	34	41.0	476	1 US-08-216-276A-33	Sequence 33, Appl1

ALIGNMENTS

RESULT 1
US-08-665-617-2
; Sequence 2, Application US/08665617
; Patent No. 5663316
; GENERAL INFORMATION:
; APPLICANT: Xudong, Yin
; TITLE OF INVENTION: Gene and Protein for Regulation of Cell Death
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,617
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: CL-8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-665-617-2

Query Match 100.0%; Score 83; DB 1; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRYGRLRRMSDFVD 16
DB 106 QRYGRLRRMSDFVD 121

```
RESULT 2
US-08-717-123-2
; Sequence 2, Application US/08717123
; Patent No. 5965703
; GENERAL INFORMATION:
; APPLICANT: Horne, William A.
; APPLICANT: Oltersdorf, Tilmann
; TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
; TITLE OF INVENTION: Acids and Methods of Use
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/717,123
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 1929
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 168 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-717-123-2

Query Match          100.0%; Score 83; DB 2; Length 168;
Best Local Similarity 100.0%; Pred. NO. 1.5e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ORYGRELRRMSDEYD 16
|||||
DB 108 ORYGRELRRMSDEYD 123

RESULT 3
US-08-985-335-1
; Sequence 1, Application US/08985335
; Patent No. 6080847
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; TITLE OF INVENTION: PROLIFERATION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
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```
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,335
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SYNORAB01
CLONE: 358673
US-08-985-335-1

Query Match          100.0%; Score 83; DB 3; Length 168;
Best Local Similarity 100.0%; Pred. NO. 1.5e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ORYGRELRRMSDEYD 16
|||||
DB 108 ORYGRELRRMSDEYD 123

RESULT 4
US-08-985-335-7
; Sequence 7, Application US/08985335
; Patent No. 6080847
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; TITLE OF INVENTION: PROLIFERATION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,335
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0421 US
; TELECOMMUNICATION INFORMATION:
```

TELEPHONE: 650-855-0555
 TELEFAX: 650-845-4166
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 168 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 1683637
 US-08-965-335-7

Query Match 100.0%; Score 83; DB 3; Length 168;
 Best Local Similarity 100.0%; Pred. No. 1.5e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ORYGRELRMSDFVD 16
 |||||||
 DB 108 ORYGRELRMSDFVD 123

RESULT 5
 US-09-410-372-1
 Sequence 1 Application US/09410372
 Patent No. 6281334
 GENERAL INFORMATION:
 APPLICANT: Hillman, Jennifer L.
 APPLICANT: Yue, Henry
 APPLICANT: Lal, Preeti
 APPLICANT: Shah, Purvi
 APPLICANT: Corley, Neil C.
 TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
 NUMBER OF INVENTION: PROLIFERATION
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Dr.
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: PASTISO for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/410,372
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/965,335
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0421 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-855-0555
 TELEFAX: 650-845-4166
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 168 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: SYNORAB01
 CLONE: 358673
 US-09-410-372-1

Query Match 100.0%; Score 83; DB 4; Length 168;
 Best Local Similarity 100.0%; Pred. No. 1.5e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ORYGRELRMSDFVD 16
 |||||||
 DB 108 ORYGRELRMSDFVD 123

RESULT 6
 US-09-410-372-7
 Sequence 7 Application US/09410372
 Patent No. 6281334
 GENERAL INFORMATION:
 APPLICANT: Hillman, Jennifer L.
 APPLICANT: Yue, Henry
 APPLICANT: Lal, Preeti
 APPLICANT: Shah, Purvi
 APPLICANT: Corley, Neil C.
 TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
 NUMBER OF INVENTION: PROLIFERATION
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Dr.
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: PASTISO for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/410,372
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/965,335
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0421 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-855-0555
 TELEFAX: 650-845-4166
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 168 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 1683637
 US-09-410-372-7

Query Match 100.0%; Score 83; DB 4; Length 168;
 Best Local Similarity 100.0%; Pred. No. 1.5e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ORYGRELRMSDFVD 16
 |||||||
 DB 108 ORYGRELRMSDFVD 123

RESULT 7
 US-08-333-565-10
 Sequence 10 Application US/08333565
 Patent No. 5622852
 GENERAL INFORMATION:

APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: BCL-X/BCL-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,565
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000700
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-333-565-10

Query Match 88.0%; Score 73; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ORYGRELRMSDEF 14
DB 8 ORYGRELRMSDEF 21

RESULT 8
US-08-661-479-10
Sequence 10, Application US/08661479
Patent No. 5634209
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: BCL-X/BCL-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,479
FILING DATE: 11-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/333,565

FILING DATE: 31-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-661-479-10

Query Match 88.0%; Score 73; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ORYGRELRMSDEF 14
DB 8 ORYGRELRMSDEF 21

RESULT 9
US-08-733-505A-55
Sequence 55, Application US/08733505A
Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
NUMBER OF SEQUENCES: 60
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-6092
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 59 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-733-505A-55

Query Match 88.0%; Score 73; DB 2; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QRYGRELIRMSDEF 14
 DB 46 QRYGRELIRMSDEF 59

RESULT 10

US-08-733-505A-56

; Sequence 56, Application US/08733505A

; Patent No. 5856445

; GENERAL INFORMATION:

; APPLICANT: KORSMEYER, STANLEY J.

; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF

; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR

; NUMBER OF SEQUENCES: 60

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: HOMEIL & HAFERKAMP, L.C.

; STREET: 7733 FORSYTH BLVD., SUITE 1400

; CITY: ST. LOUIS

; STATE: MISSOURI

; COUNTRY: USA

; ZIP: 63105

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/733,505A

; FILING DATE:

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: HOLLAND, DONALD R.

; REGISTRATION NUMBER: 35,197

; REFERENCE/DOCKET NUMBER: 965458

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (314) 727-5188

; TELEFAX: (314) 727-6092

; INFORMATION FOR SEQ ID NO: 56:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 59 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-733-505A-56

Query Match 88.0%; Score 73; DB 2; length 59;
 Best Local Similarity 100.0%; Pred. No. 2,9e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QRYGRELIRMSDEF 14
 DB 46 QRYGRELIRMSDEF 59

RESULT 11

US-08-733-505A-57

; Sequence 57, Application US/08733505A

; Patent No. 5856445

; GENERAL INFORMATION:

; APPLICANT: KORSMEYER, STANLEY J.

; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF

; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR

; NUMBER OF SEQUENCES: 60

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: HOMEIL & HAFERKAMP, L.C.

; STREET: 7733 FORSYTH BLVD., SUITE 1400

; CITY: ST. LOUIS

; STATE: MISSOURI

; COUNTRY: USA

; ZIP: 63105

; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/733,505A
 FILING DATE:
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: HOLLAND, DONALD R.
 REGISTRATION NUMBER: 35,197
 REFERENCE/DOCKET NUMBER: 965458
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (314) 727-5188
 TELEFAX: (314) 727-6092
 INFORMATION FOR SEQ ID NO: 57:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 59 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-733-505A-57

Query Match 88.0%; Score 73; DB 2; length 59;
 Best Local Similarity 100.0%; Pred. No. 2,9e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QRYGRELIRMSDEF 14
 DB 46 QRYGRELIRMSDEF 59

RESULT 12

US-08-733-505A-58

; Sequence 58, Application US/08733505A

; Patent No. 5856445

; GENERAL INFORMATION:

; APPLICANT: KORSMEYER, STANLEY J.

; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF

; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR

; NUMBER OF SEQUENCES: 60

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: HOMEIL & HAFERKAMP, L.C.

; STREET: 7733 FORSYTH BLVD., SUITE 1400

; CITY: ST. LOUIS

; STATE: MISSOURI

; COUNTRY: USA

; ZIP: 63105

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/733,505A

; FILING DATE:

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: HOLLAND, DONALD R.

; REGISTRATION NUMBER: 35,197

; REFERENCE/DOCKET NUMBER: 965458

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (314) 727-5188

; TELEFAX: (314) 727-6092

; INFORMATION FOR SEQ ID NO: 58:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 59 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-733-505A-58

Query Match

88.0%; Score 73; DB 2; Length 59;

Best Local Similarity 100.0%; Pred. No. 2.9e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ORYGRELRMSDEF 14

DB 46 ORYGRELRMSDEF 59

RESULT 13

US-08-333-565-2

Sequence 2, Application US/08333565

Patent No. 5622852

GENERAL INFORMATION:

APPLICANT: KORSMEYER, Stanley J.

TITLE OF INVENTION: BCL-X/BCL-2 ASSOCIATED CELL DEATH

TITLE OF INVENTION: REGULATOR

NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

STREET: 379 Lytton Avenue and Townsend Khourie and Crew

CITY: Palo Alto

STATE: California

COUNTRY: US

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/333,565

FILING DATE: 31-OCT-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M

REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 15726A-000700

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400

TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 204 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: Protein

LOCATION: 1..204

OTHER INFORMATION:

OTHER INFORMATION: of mouse BAD.*

US-08-333-565-2

QY 1 ORYGRELRMSDEF 14

DB 145 ORYGRELRMSDEF 158

RESULT 14

US-08-661-479-2

Sequence 2, Application US/08661479

Patent No. 5834209

GENERAL INFORMATION:

88.0%; Score 73; DB 1; Length 204;

Best Local Similarity 100.0%; Pred. No. 1.1e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: BCL-X/BCL-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,479
FILING DATE: 11-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/333,565
FILING DATE: 31-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2422
TELEFAX: (415) 326-2400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..204
OTHER INFORMATION:
OTHER INFORMATION: of mouse BAD.*

US-08-661-479-2

Query Match 88.0%; Score 73; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ORYGRELRMSDEF 14

DB 145 ORYGRELRMSDEF 158

RESULT 15

US-08-733-505A-1

Sequence 1, Application US/08733505A

Patent No. 5856445

GENERAL INFORMATION:

APPLICANT: KORSMEYER, Stanley J.

TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF

TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESS: HOWELL & HAPERKAMP, L.C.

STREET: 7733 FORSYTH BLVD., SUITE 1400

CITY: ST. LOUIS

STATE: MISSOURI

COUNTRY: USA

ZIP: 63105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-733-505A-1

Query Match 88.0%; Score 73; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ORYGRELRRMSDEF 14
|||||
DB 145 ORYGRELRRMSDEF 158

Search completed: September 20, 2002, 10:37:20
Job time: 408 sec

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OM protein - protein search, using sw model

Run on: September 20, 2002, 10:39:07 ; Search time 95.59 Seconds
(without alignments)
16.084 Million cell updates/sec

File: US-09-544-664-29

Perfect score: 83

Sequence: 1 QRYGRLRMSDFVD 16

Scoring table: BLASTM62

Gapop 10.0 , Gapext 0.5

Searched: 28138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 28138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	73	88.0	204	2 A55671	bad protein - mouse
2	45	54.2	564	2 H75403	glycosyl hydrolase
3	44	53.0	1248	2 G83278	cobalamin biosynth
4	42	50.6	876	2 E89949	valine-tRNA ligase
5	41.5	50.0	191	2 AD3414	hypothetical cytos
6	41	49.4	447	2 F85356	hypothetical prote
7	41	49.4	577	2 T40297	membrane transport
8	41	49.4	858	2 A44919	CCR3 protein - yea
9	40	48.2	109	2 F84388	hypothetical prote
10	40	48.2	113	2 B95043	conserved hypothet
11	40	48.2	113	2 D97913	hypothetical prote
12	40	48.2	219	2 A75088	hypothetical prote
13	40	48.2	275	2 E91102	probable enzyme [i
14	40	48.2	275	2 F65076	hypothetical prote
15	40	48.2	275	2 A85948	probable enzyme y
16	40	48.2	335	2 T52577	gibberellin 2beta-
17	40	48.2	360	2 B83211	transcriptional regu
18	40	48.2	411	2 E87644	transcriptional regu
19	40	48.2	429	2 OC4966	site-specific DNA
20	40	48.2	445	2 G97123	probable Fe-S oxid
21	40	48.2	631	2 G70188	transcriptional init
22	40	48.2	5138	2 B96695	hypothetical prote
23	39.5	47.6	198	2 E87441	conserved hypothet
24	39.5	47.6	414	2 B84275	hypothetical prote
25	39	47.0	73	2 AC3365	hypothetical prote
26	39	47.0	172	2 B71339	probable cationic
27	39	47.0	207	2 B95348	hypothetical prote
28	39	47.0	220	2 F72289	oxidoreductase, so
29	39	47.0	275	2 C69808	transporter homo

30	39	47.0	331	2 E90121	DNA repair protein
31	39	47.0	360	2 D86200	protein F12K11.20
32	39	47.0	365	2 S42107	RAD51 protein homo
33	39	47.0	380	2 T32163	hypothetical prote
34	39	47.0	383	2 T31738	hypothetical prote
35	39	47.0	418	1 FOXRL2	sigma 2 protein -
36	39	47.0	418	1 FOXRL2	sigma 2 protein -
37	39	47.0	432	2 AB0558	trigger factor (im
38	39	47.0	503	1 CTBPR	site-specific DNA-
39	39	47.0	536	2 F90299	acylaminoacyl-pept
40	39	47.0	689	2 T29772	hypothetical prote
41	39	47.0	880	1 SYBSVS	valine-tRNA ligas
42	39	47.0	959	1 B71405	probable kinesin -
43	39	47.0	965	2 AE2452	two-component hybr
44	39	47.0	1805	2 T02712	similar to late em
45	39	47.0	1967	2 S64604	hypothetical prote

ALIGNMENTS

RESULT 1
A55671
bad protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 05-Nov-1999
C:Accession: A55671
R:Yang, E.; Zha, J.; Jockel, J.; Boise, L.H.; Thompson, C.B.; Korsmeyer, S.J.
Cell 80, 285-291, 1995
A:Title: Bad, a heterodimeric partner for Bcl-x-L and Bcl-2, displaces Bax and promot
A:Reference number: A55671; MUID:95136361
A:Accession: A55671
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-204 <YAN>
A:Cross-references: GB:137296; NID:9639778; PIDN:AAA64465.1; PID:9639779
C:Keywords: heterodimer

Query Match 88.0%; Score 73; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRYGRLRMSDFE 14
DB 145 QRYGRLRMSDFE 158

RESULT 2
H75403
glycosyl hydrolase, family 13 - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: H75403
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
M.; Shen, M.; Vamthavan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1
A:Reference number: A75250; MUID:20036896
A:Accession: H75403
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-564 <NHT>
A:Cross-references: GB:AE001983; GB:AE000513; NID:96459123; PIDN:AAF10944.1; PID:9645
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR1375
A:Map position: 1
C:Superfamily: alpha-glucosidase; alpha-amyrase core homology

Query Match 54.2%; Score 45; DB 2; Length 564;

A:Experimental source: strain 97zh-; cosmid c36
 C:Genetics:
 A:Gene: SPB:SPB36.02c
 A:Map position: 2
 C:Superfamily: benomyl/methotrexate resistance protein

Query Match 49.4%; Score 41; DB 2; Length 577;
 Best Local Similarity 57.1%; Pred. No. 67;
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 3 YGRELRRMSDEVD 16
 :||:|||||
 Db 563 FGKIRKSMKMYD 576

RESULT 8
 A4919
 GCR3 protein - yeast (Saccharomyces cerevisiae)
 N:Alternate names: protein YM8564.07; protein YM9553.01; protein YMR125W
 C:Species: Saccharomyces cerevisiae
 C:Date: 30-Sep-1993 #sequence,revision 30-Sep-1993 #text_change 29-Oct-1999
 C:Accession: A44919; S53055; S54494
 R:Uemura, H.; Jigami, Y.
 J:Biochem Biophys Res Commun 174, 5526-5532, 1992
 A:Title: GCR3 encodes an acidic protein that is required for expression of glycolytic ge
 A:Reference number: A44919; M01D:92380925
 A:Accession: A44919
 A:Molecule type: DNA
 A:Residues: 1-858 <UJM>
 A:Cross-references: GB:D10224; NID:9464221; PIDN:BA01076.1; PID:di001545; PID:9464222
 A:Note: sequence extracted from NCBI backbone (NCBIN:112104, NCBIPI:112106)
 R:Badcock, K.; Churcher, C.
 Submitted to the EMBL Data Library, March 1995
 A:Reference number: S53055
 A:Accession: S53055
 A:Molecule type: DNA
 A:Residues: 339-858 <BAD>
 A:Cross-references: EMBL:Z48622; NID:g728663; PIDN:CA88550.1; PID:9728664; MIPS:YMR125W
 R:Lyde, G.; Churcher, C.M.
 submitted to the EMBL Data Library, May 1995
 A:Reference number: S54014
 A:Accession: S54494
 A:Molecule type: DNA
 A:Residues: 'MNRKRC', 6-489 <LYE>
 A:Cross-references: EMBL:Z49273; NID:g809577; PIDN:CA89274.1; PID:9809584; MIPS:YMR125W
 C:Genetics:
 A:Gene: SGD:STO1; GCR3
 A:Cross-references: MIPS:YMR125W; SGD:S0004732
 A:Map position: 13R
 C:Keywords: DNA binding; nucleus

Query Match 49.4%; Score 41; DB 2; Length 856;
 Best Local Similarity 40.0%; Pred. No. 1e+02;
 Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

OY 1 QYRGRELRRMSDEVD 15
 :||:|||||
 Db 818 RRTSHEVRELADKFI 832

RESULT 9
 F84388
 Hypothetical protein Yng2379h [imported] - Halobacterium sp. NRC-1
 C:Species: Halobacterium sp. NRC-1
 C:Date: 02-Feb-2001 #sequence,revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: F84388
 R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.
 ; Leihhauser, B.; Keller, K.; Cruz, R.; Danoson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo
 Jung, K.H.; Alam, M.; Freitas, T.
 Proc Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
 A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.F.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li

A:Title: Genome sequence of Halobacterium species NRC-1.
 A:Reference number: A84160; M01D:20504483
 A:Accession: F84388
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-84 <STO>
 A:Cross-references: GB:AE004437; NID:q10581786; PIDN:AA620474.1; GSPDB:GN00138
 C:Genetics:
 A:Gene: YNG2379H

Query Match 48.2%; Score 40; DB 2; Length 84;
 Best Local Similarity 66.7%; Pred. No. 14;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 YRGRELRRMSDE 13
 :||:|||||
 Db 66 YRGTEASRMDE 77

RESULT 10
 B95043
 conserved hypothetical protein SP0372 [imported] - Streptococcus pneumoniae (strain T
 C:Species: Streptococcus pneumoniae
 C:Date: 03-Aug-2001 #sequence,revision 03-Aug-2001 #text_change 03-Aug-2001
 C:Accession: B95043
 R:Teitelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; H
 on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapf
 son, T.; Hickey, E.K.; Holt, I.E.
 Science 293, 498-506, 2001
 A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morris
 A:Title: Complete Genome Sequence of a Virulent Isolate of Streptococcus pneumoniae.
 A:Reference number: A95000; M01D:21357209; PMID:11463916
 A:Accession: B95043
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-109 <KUR>
 A:Cross-references: GB:AE005672; PIDN:AAK74539.1; PID:q14971841; GSPDB:GN00164; TIGR:
 A:Experimental source: strain TIGR4
 C:Genetics:
 A:Gene: SP0372

Query Match 48.2%; Score 40; DB 2; Length 109;
 Best Local Similarity 45.0%; Pred. No. 18;
 Matches 9; Conservative 4; Mismatches 3; Indels 4; Gaps 1;

OY 1 QYRGRELRRMS---DEVD 16
 :||:|||||
 Db 14 QYRGREYRGYKRVDEFLD 33

RESULT 11
 D97913
 conserved hypothetical protein SP0332 [imported] - Streptococcus pneumoniae (strain
 C:Species: Streptococcus pneumoniae
 C:Date: 22-Oct-2001 #sequence,revision 22-Oct-2001 #text_change 22-Oct-2001
 C:Accession: D97913
 R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burett, S.; Dehoff, B.S.
 e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; Mehren, S.
 y, P.; Sun, P.M.; Winkler, M.E.
 J. Bacteriol. 183, 5709-5717, 2001
 A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Balcz, R.H.; Jaskunas, S.
 A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
 A:Reference number: A97872; M01D:21429245; PMID:11544234
 A:Accession: D97913
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-113 <KUR>
 A:Cross-references: GB:AE007317; PIDN:AAK99136.1; PID:q15457889; GSPDB:GN00174
 C:Genetics:
 A:Gene: SP0332

Query Match 48.2% Score 40; DB 2; Length 113;
 Best Local Similarity 45.0%; Pred. No. 19;
 Matches 9; Conservative 4; Mismatches 3; Indels 4; Gaps 1;
 QY 1 YGRELRLRMS---DEPVD 16
 1 : 111 : 1 : 111 : 1
 DB 18 QEGREVRGYNKVEDEFLD 37

RESULT 12
 A75088
 hypothetical protein PAB1640 - Pyrococcus abyssi (strain Orsay)
 C:Species: Pyrococcus abyssi
 C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
 C:Accession: A75088
 R:anonymous, Genoscope
 submitted to the EMBL Data Library, July 1999
 A:Description: Pyrococcus abyssi genome sequence: Insights into archaeal chromosome stru
 A:Reference number: A75001
 A:Accession: A75088
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-219 <KAP>
 A:Cross-references: GB:A0748286; GB:A1096836; NID:95458366; PIDN:CAB50006.1; PID:el51590
 A:Experimental source: strain Orsay
 C:Genetics:
 A:Gene: PAB1640

Query Match 48.2% Score 40; DB 2; Length 219;
 Best Local Similarity 47.1%; Pred. No. 37;
 Matches 8; Conservative 4; Mismatches 3; Indels 2; Gaps 1;
 QY 2 RYGRRLRMS--DEPVD 16
 1111 : 111 : 111 :
 DB 104 RYGRFQRYSPQENFLD 120

RESULT 13
 E91102
 Probable enzyme [Imported] - Escherichia coli (strain O157:H7, substrain RMD 0509952)
 C:Species: Escherichia coli
 C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
 C:Accession: E91102
 R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
 Geraswara, N.; Yasunaga, T.; Kuhara, S.; Shibata, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
 A:Reference number: A99629; MUID:21156231; PMID:11258796
 A:Accession: E91102
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-275 <HAY>
 A:Cross-references: GB:BA000007; PIDN:BA837212.1; PID:q1336361; GSPDB:GNO0454
 A:Experimental source: strain O157:H7, substrain RMD 0509952
 C:Genetics:
 A:Gene: EC53789
 C:Superfamily: naphthoate synthase; enoyl-CoA hydratase homology

Query Match 48.2% Score 40; DB 2; Length 275;
 Best Local Similarity 50.0%; Pred. No. 46;
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 3 YGRELRLRMSDEPVD 16
 1111 : 111 : 111 :
 DB 35 YGRKLMLSKVFID 48

RESULT 14
 F65076
 hypothetical protein b2919 - Escherichia coli (strain K-12)

C:Species: Escherichia coli
 C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 08-Oct-1999
 C:Accession: F65076
 R:Balterer, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
 A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A:Title: The complete genome sequence of Escherichia coli K-12.
 A:Reference number: A64720; MUID:97426617
 A:Accession: F65076
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-275 <BAT>
 A:Cross-references: GB:AE000375; GB:U00096; NID:91789282; PIDN:AMC75956.1; PID:q17892
 A:Experimental source: strain K-12, substrain MG1655
 C:Superfamily: naphthoate synthase; enoyl-CoA hydratase homology
 F:40-192/Domain: enoyl-CoA hydratase homology <ECH>

Query Match 48.2% Score 40; DB 2; Length 275;
 Best Local Similarity 50.0%; Pred. No. 46;
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 3 YGRELRLRMSDEPVD 16
 1111 : 111 : 111 :
 DB 35 YGRKLMLSKVFID 48

RESULT 15
 A85948
 Probable enzyme ygfG [Imported] - Escherichia coli (strain O157:H7, substrain EDL933)
 C:Species: Escherichia coli
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
 C:Accession: A85948
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
 Miller, L.; Grobeck, E.J.; Davis, N.W.; Liao, A.; Diallantha, E.; Potamoudis, K.; Apoda
 Nature 409, 528-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206331
 A:Accession: A85948
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-275 <STO>
 A:Cross-references: GB:AE005174; NID:q12517451; PIDN:AGS8045.1; GSPDB:GNO0145; UMGF:
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: ygfG
 C:Superfamily: naphthoate synthase; enoyl-CoA hydratase homology

Query Match 48.2% Score 40; DB 2; Length 275;
 Best Local Similarity 50.0%; Pred. No. 46;
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 3 YGRELRLRMSDEPVD 16
 1111 : 111 : 111 :
 DB 35 YGRKLMLSKVFID 48

Search completed: September 20, 2002, 10:39:09
 Job time: 481 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 20, 2002, 11:04:31 ; Search time 44.99 Seconds

(without alignments)
13.770 Million cell updates/sec

Title: US-09-544-664-29

Sequence: 1 QRYGRLRRMSDFVD 16

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	100.0	168	1	BAD_HUMAN
2	73	88.0	204	1	BAD_MOUSE
3	73	88.0	205	1	BAD_RAT
4	42	50.6	196	1	BIM_MOUSE
5	42	50.6	196	1	BIM_RAT
6	42	50.6	653	1	HT2A_HUMAN
7	41	49.4	370	1	AROG_CANAL
8	41	49.4	861	1	YGRG_YEAST
9	40	48.2	261	1	PHGC_TRYCR
10	40	48.2	380	1	PHGC_TRYCR
11	40	48.2	429	1	MTRAL_ACEPA
12	40	48.2	631	1	PRSD_BORU
13	39	47.0	220	1	6PQL_THEMA
14	39	47.0	365	1	RA51_SCHPO
15	39	47.0	418	1	VS12_REOVD
16	39	47.0	418	1	VS12_REOVL
17	39	47.0	503	1	MTBR_BPRU1
18	39	47.0	880	1	STV_BACST
19	39	47.0	1967	1	Y550_YEAST
20	38.5	46.4	468	1	SELA_PSEAE
21	38	45.8	87	1	Y152_UREPA
22	38	45.8	185	1	RRE_THEMA
23	38	45.8	198	1	BIM_HUMAN
24	38	45.8	251	1	KDKA_VIBCH
25	38	45.8	384	1	ODP2_MYCPN
26	38	45.8	432	1	ODP2_MYCPN
27	38	45.8	432	1	TIG_ECOLI
28	38	45.8	1521	1	EMBS_CAEEL
29	38	45.8	1557	1	LM11_CAEEL
30	37	44.6	375	1	DP3B_MYCCA
31	37	44.6	391	1	UBIF_ECOLI
32	37	44.6	398	1	PR51_ARCFU
33	37	44.6	481	1	Y335_SYNV3

ALIGNMENTS

RESULT	ID	Sequence	Score	Query Match	Length	DB ID	Description
1	BAD_HUMAN	092934: 014803;	777	1	168 AA.	1	BAD_HUMAN
2	BAD_HUMAN	092934: 014803;	787	1	168 AA.	1	BAD_HUMAN
3	BAD_HUMAN	092934: 014803;	787	1	168 AA.	1	BAD_HUMAN
4	BAD_HUMAN	092934: 014803;	787	1	168 AA.	1	BAD_HUMAN
5	BAD_HUMAN	092934: 014803;	787	1	168 AA.	1	BAD_HUMAN
6	BAD_HUMAN	092934: 014803;	787	1	168 AA.	1	BAD_HUMAN
7	BAD_HUMAN	092934: 014803;	787	1	168 AA.	1	BAD_HUMAN
8	BAD_HUMAN	092934: 014803;	787	1	168 AA.	1	BAD_HUMAN
9	BAD_HUMAN	092934: 014803;	787	1	168 AA.	1	BAD_HUMAN
10	BAD_HUMAN	092934: 014803;	787	1	168 AA.	1	BAD_HUMAN
11	BAD_HUMAN	092934: 014803;	787	1	168 AA.	1	BAD_HUMAN
12	BAD_HUMAN	092934: 014803;	787	1	168 AA.	1	BAD_HUMAN
13	BAD_HUMAN	092934: 014803;	787	1	168 AA.	1	BAD_HUMAN
14	BAD_HUMAN	092934: 014803;	787	1	168 AA.	1	BAD_HUMAN
15	BAD_HUMAN	092934: 014803;	787	1	168 AA.	1	BAD_HUMAN
16	BAD_HUMAN	092934: 014803;	787	1	168 AA.	1	BAD_HUMAN
17	BAD_HUMAN	092934: 014803;	787	1	168 AA.	1	BAD_HUMAN
18	BAD_HUMAN	092934: 014803;	787	1	168 AA.	1	BAD_HUMAN
19	BAD_HUMAN	092934: 014803;	787	1	168 AA.	1	BAD_HUMAN
20	BAD_HUMAN	092934: 014803;	787	1	168 AA.	1	BAD_HUMAN
21	BAD_HUMAN	092934: 014803;	787	1	168 AA.	1	BAD_HUMAN
22	BAD_HUMAN	092934: 014803;	787	1	168 AA.	1	BAD_HUMAN
23	BAD_HUMAN	092934: 014803;	787	1	168 AA.	1	BAD_HUMAN
24	BAD_HUMAN	092934: 014803;	787	1	168 AA.	1	BAD_HUMAN
25	BAD_HUMAN	092934: 014803;	787	1	168 AA.	1	BAD_HUMAN
26	BAD_HUMAN	092934: 014803;	787	1	168 AA.	1	BAD_HUMAN
27	BAD_HUMAN	092934: 014803;	787	1	168 AA.	1	BAD_HUMAN
28	BAD_HUMAN	092934: 014803;	787	1	168 AA.	1	BAD_HUMAN
29	BAD_HUMAN	092934: 014803;	787	1	168 AA.	1	BAD_HUMAN
30	BAD_HUMAN	092934: 014803;	787	1	168 AA.	1	BAD_HUMAN
31	BAD_HUMAN	092934: 014803;	787	1	168 AA.	1	BAD_HUMAN
32	BAD_HUMAN	092934: 014803;	787	1	168 AA.	1	BAD_HUMAN
33	BAD_HUMAN	092934: 014803;	787	1	168 AA.	1	BAD_HUMAN
34	BAD_HUMAN	092934: 014803;	787	1	168 AA.	1	BAD_HUMAN
35	BAD_HUMAN	092934: 014803;	787	1	168 AA.	1	BAD_HUMAN
36	BAD_HUMAN	092934: 014803;	787	1	168 AA.	1	BAD_HUMAN
37	BAD_HUMAN	092934: 014803;	787	1	168 AA.	1	BAD_HUMAN
38	BAD_HUMAN	092934: 014803;	787	1	168 AA.	1	BAD_HUMAN
39	BAD_HUMAN	092934: 014803;	787	1	168 AA.	1	BAD_HUMAN
40	BAD_HUMAN	092934: 014803;	787	1	168 AA.	1	BAD_HUMAN
41	BAD_HUMAN	092934: 014803;	787	1	168 AA.	1	BAD_HUMAN
42	BAD_HUMAN	092934: 014803;	787	1	168 AA.	1	BAD_HUMAN
43	BAD_HUMAN	092934: 014803;	787	1	168 AA.	1	BAD_HUMAN
44	BAD_HUMAN	092934: 014803;	787	1	168 AA.	1	BAD_HUMAN
45	BAD_HUMAN	092934: 014803;	787	1	168 AA.	1	BAD_HUMAN

099728	homo sapien
046640	mycobacteri
003601	caenorhabdi
038198	saccharomyc
094295	pyrococcus
064206	mycobacteri
042103	halobacteri
097177	drosophila
074806	schizosacch
066496	aquifex aeo
09yaf1	aeropyrum p

```

CC similarity). Appears to act as a link between growth factor
CC receptor signaling and the apoptotic pathways.
CC -1 SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-
CC x(L), Bcl-2 and Bcl-w. Also binds protein S100A10 (By similarity).
CC The Ser-75/Ser-99 phosphorylated form binds 14-3-3 proteins (By
CC similarity).
CC -1 SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon
CC phosphorylation, localizes to the cytoplasm.
CC -1 TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
CC -1 DOMAIN: Interact BH3 domain is required by BIK, BID, BAK, BAD AND
CC BAX for their pro-apoptotic activity and for their interaction
CC with anti-apoptotic members of the Bcl-2 family.
CC -1 PTM: Phosphorylated on Ser-75 in response to survival stimuli.
CC Subsequent phosphorylation on Ser-99 promotes heterodimerization
CC with 14-3-3 proteins. This interaction then facilitates the
CC phosphorylation at Ser-118, a site within the BH3 domain, leading
CC to the release of Bcl-x(L) and the promotion of cell survival.
CC Ser-99 is the major site of AKT/PKB phosphorylation. Ser-118 the
CC major site of protein kinase A (CAPK) phosphorylation (by
CC similarity).
CC -1 SIMILARITY: CONTAINS 1 BCL-3 HOMOLOG DOMAIN 3 (BH3).
CC -1 SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL; U66879; AAB36516.1; -
CC DR EMBL; AF021792; AAB72092.1; -
CC DR EMBL; AF031523; AAB88124.1; -
CC DR EMBL; BC001901; AAH01901.1; -
CC PDB: 1G5J; 07-FEB-01.
CC MIM: 603167; -
CC DR InterPro; IPR000712; Bcl_2
CC PROSITE; PS01259; BH3; FALSE_NEG.
CC KW Apoptosis; Phosphorylation; 3D-structure.
CC FT DOMAIN 110 124
CC FT MOD_RES 75 75
CC FT MOD_RES 99 99
CC FT MOD_RES 118 118
CC FT MOD_RES 118 118
CC FT CONFLICT 64 91
CC FT SEQUENCE 168 AA; 18392 MW; 69FDB827DDEE3241 CRC64.
CC -----
CC Query Match 100.0%; Score 83; DB 1; Length 168;
CC Best Local Similarity 100.0%; Pred. No. 9.6e-07;
CC Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC -----
CC Oy 1 ORYGLRLRRMSDEPYD 16
CC | | | | | | | | | | | | | |
CC Db 108 ORYGLRLRRMSDEPYD 123
CC -----
CC RESULT 2
CC BAD_MOUSE STANDARD: PRT: 204 AA.
CC ID BAD_MOUSE
CC AC Q61337;
CC DT 01-NOV-1997 (Rel. 35, Created)
CC DT 01-NOV-1997 (Rel. 35, Last sequence update)
CC DT 01-MAR-2002 (Rel. 41, Last annotation update)
CC DE Bcl2-antagonist of cell death (BAD) (Bcl-2 binding component
CC 6) (Bcl-xL/Bcl-2 associated death promoter).
CC GN BAD OR BBC6.
CC OS Mus musculus (Mouse).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

CC Mammalia:Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Brain, and Thymus;
RX MEDLINE=95136361; PubMed=7834748;
RA Yang E., Zha J., Jockel J., Boise L.H., Thompson C.B., Korsmeyer S.J.;
RT "Bad, a heterodimeric partner for Bcl-XL and Bcl-2, displaces Bax and
RL Cell 80:285-291(1995).
RN [2]
RP PHOSPHORYLATION AND MUTAGENESIS OF SER-112 AND SER-136.
RX MEDLINE=96022383; PubMed=9381178;
RA Del Peso L., Gonzalez-garcia M., Page C., Herrera R., Nunez G.;
RT "Interleukin-3-induced phosphorylation of BAD through the protein
RL kinase Akt".
RN Science 278:687-689(1997).
RN [3]
RP MUTAGENESIS OF SERINE RESIDUES.
RX MEDLINE=20403302; PubMed=10945026;
RA Delta S.R., Katsov A., Hu L., Petros A., Pesik S.W., Yaffe M.B.,
RN Greenberg M.E.;
RT "14-3-3 proteins and survival kinases cooperate to inactivate BAD by
RL BH3 domain phosphorylation".
RN Mol. Cell 6:41-51(2000).
CC -I- FUNCTION: Promotes cell death. Successfully competes for the
CC binding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level
CC of heterodimerization of these proteins with BAX. Can reverse the
CC death repressor activity of Bcl-x(L), but not that of Bcl-2.
CC Appears to act as a link between growth factor receptor signaling
CC and the apoptotic pathways.
CC -I- SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-
CC x(L), Bcl-2 and Bcl-w. Also binds protein S100A10 (by similarity).
CC The Ser-112/Ser-136 phosphorylation form binds 14-3-3 proteins.
CC -I- SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon
CC phosphorylation, localizes to the cytoplasm.
CC -I- DOMAIN: Interact BH3 domain is required by BIK, BID, BAX, BAD AND
CC BAX for their pro-apoptotic activity and for their interaction
CC with anti-apoptotic members of the Bcl-2 family.
CC -I- PTM: Phosphorylated on Ser-112 in response to survival stimuli.
CC Subsequent phosphorylation on Ser-136 promotes heterodimerization
CC with 14-3-3 proteins. This interaction then facilitates the
CC phosphorylation at Ser-155, a site within the BH3 domain, leading
CC to the release of Bcl-x(L) and the promotion of cell survival.
CC Ser-136 is the major site of AKT/PKB phosphorylation. Ser-155 the
CC major site of protein kinase A (CAK) phosphorylation.
CC -I- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -I- SIMILARITY: COMAINS A BCL-3 HOMOLOG DOMAIN 3 (BH3).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L37296; AAA64465.1; -
CC MGD: MGI:1096330; Bad.
CC InterPro: IPR000712; Bcl-2.
DR PROSITE: PS01259; BH3; FALSE_NEG.
DR Apoptosis; Phosphorylation.
KW DOMAIN 147 161 BH3.
FT MOD_RES 112 112 PHOSPHORYLATION (BY CAK AND PKB).
FT MOD_RES 136 136 PHOSPHORYLATION (BY CAK AND PKB).
FT MOD_RES 155 155 PHOSPHORYLATION (BY CAK AND PKB).
FT MUTAGEN 112 112 S->A: NO PHOSPHORYLATION.
FT MUTAGEN 136 136 S->A: NO PHOSPHORYLATION.
FT MUTAGEN 155 155 S->A: NO PHOSPHORYLATION; INTERACTS WITH
FT BCL-X(L).
SQ SEQUENCE 204 AA: 22080 MW: 6625BA91020503F7 CRC64;

	Query Match	89.0%	Score 73:	DB 1:	Length 204:
	Best Local Similarity	100.0%	Pred. No. 5.1e-05:		
	Matches 14:	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
Ox	1 ORYZETRAPRIMIDE 14				
Dd	145 ORYZETRAPRIMIDE 158				
RESULT	3	STANDARD:	PRT:	205 AA.	
ID	BAD_RAT				
DC	C35147: 070256; Q9QHX1;				
DT	16-OCT-2001 (Rel. 40, Created)				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DT	01-MAR-2002 (Rel. 41, Last annotation update)				
Dc	Bcl2-antagonist of cell death (BAD) (Bcl-2 binding component				
Dd	6) (Bcl-xL/Bcl-2 associated death promoter).				
GN	BAD.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus,				
OX	NCR_TaxID=10116;				
RM	SEQUENCE FROM N.A., AND MUTAGENESIS OF SER-113 AND SER-137.				
RC	TISSUE-Ovary;				
KX	MEDLINE=98034386; PubMed=9369435;				
RA	Hsu S.Y., Kalpita A., Zhu L., Hansen A.J.M.;				
FT	Interference of BAD (Bcl-xL/Bcl-2-associated death promoter)-induced				
MT	apoptosis in mammalian cells by 14-3-3 isoforms and P11-?				
RL	Mol. Endocrinol. 11:1858-1867(1997).				
RM	SEQUENCE FROM N.A.				
RC	TISSUE-Brain;				
KX	MEDLINE=98194755; PubMed=9535132;				
RA	DiGiuseppe J., Musco S., Cavallaro S.;				
FT	"Cloning and expression of the programmed cell death regulator BMD in				
RT	the rat brain." Neurosci. Lett. 243:137-140(1998).				
RM	SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).				
RC	TISSUE-Brain;				
KX	MEDLINE=21109372; PubMed=11161472;				
RA	Hamer S., Arumae U., Yu L.-Y., Sun Y.-F., Saarala M., Lindholm D.;				
FT	"Functional characterization of two splice variants of rat BAD and				
RT	their interaction with Bcl-w in sympathetic neurons."				
RL	Mol. Cell. Neurosci. 17:97-106(2001).				
CC	- FUNCTION: Promotes cell death. Successfully competes for the				
CC	binding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level				
CC	of heterodimerization of these proteins with BAX. Can reverse the				
CC	death repressor activity of Bcl-x(L), but not that of Bcl-2 (By				
CC	similarity). Appears to act as a link between growth factor				
CC	receptor signaling and the apoptotic pathways.				
CC	- SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-				
CC	x(L), Bcl-2 and Bcl-w. Also binds protein S100A10. The ser-				
CC	113/Ser-137 phosphorylated form binds 14-3-3 proteins.				
CC	- SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon				
CC	phosphorylation, localizes to the cytoplasm (By similarity).				
CC	- ALTERNATIVE PRODUCTS: 2 isoforms; alpha (shown here) and beta; are				
CC	produced by alternative splicing. They differ only in their C-				
CC	terminal regions.				
CC	- TISSUE SPECIFICITY: Expressed in all tissues tested, including				
CC	brain, liver, spleen and heart. In the brain, restricted to				
CC	epithelial cells of the choroid plexus. Isoform alpha is the more				
CC	abundant form.				
CC	- DOMAIN: Inact. BH3 domain is required by BIK, BID, BAK, BAD AND				
CC	BAX for their pro-apoptotic activity and for their interaction				
CC	with anti-apoptotic members of the Bcl-2 family.				
CC	- PMW: Phosphorylated on Ser-113 in response to survival stimuli.				
CC	- Subsequent phosphorylation on Ser-137 promotes heterodimerization				
CC	with 14-3-3 proteins. This interaction then facilitates the				
CC	phosphorylation at Ser-136, a site within the BH3 domain, leading				
CC	to the release of Bcl-x(L) and the promotion of cell survival.				

CC		Sec737 is the major site of AKT/PKB phosphorylation, Sec356 the
CC		major site of protein kinase A (CAK) phosphorylation (by
CC		similarity).
CC	-1-	SIMILARITY: CONTAINS A BCL-3 HOMOLOGY DOMAIN 3 (BH3).
CC	-1-	SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC	-1-	SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC		This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC		entities requires a license agreement (See http://www.isb.slb.ch/announce/
CC		or send an email to license@isb-slb.ch).
CC		
DR	EMBL:	AEO35323; AAC53374.1; -
DR	EMBL:	AEO35323; AAC53374.1; -
DR	EMBL:	AF279910; AAP91428.1; -
DR	EMBL:	AF279911; AAP91428.1; -
DR	InterPro:	IPIR000712; BCL_2
DR	PROSITE:	PS01259; BH3; FALSE_NEG.
KM	Apoptosis:	Phosphorylation; Alternative splicing.
FT	DOMAIN:	146 162
FT	MOD_RES:	113 113
FT	MOD_RES:	137 137
FT	MOD_RES:	156 156
FT	VARSPPLIC:	166 205
FT	MUTAGEN:	113 113
FT	MUTAGEN:	137 137
FT	MUTAGEN:	137 137
FT	CONFLICT:	29 34
SO	SEQUENCE:	205 AA; 22328 MW; 7AA7A7DABE9CFA481 CRC64;
OY		1 ORYGRELIRMSDF 14
DB		146 ORYGRELIRMSDF 159
RESULT		
BIM_MOUSE		
ID	BIM_MOUSE	STANDARD: PRT: 196 AA.
AC	O54918; O54919; O54920;	
DT	16-OCT-2001 (Rel. 40, Created)	
DT	16-OCT-2001 (Rel. 40, Last sequence update)	
DT	01-MAR-2002 (Rel. 41, Last annotation update)	
DE	BCL2-like protein 11 (BCL2 interacting mediator of cell death).	
GN	BCL2L1 OR BIM.	
NS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.	
OX	NCBITaxID=10090;	
RN	NCBI	
RP	SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, TISSUE	
RE	SPECIFICITY, AND ALTERNATIVE SPLICING.	
RX	MEDLINE=98094360; PUBMED=9430630;	
RA	O'Connor L., Strasser A., O'Reilly L.A., Hausmann G., Adams J.M.,	
RA	Cory S., Huang D.C.S.;	
RL	Bim: a novel member of the bcl-2 family that promotes apoptosis.*	
RL	Embo J. 17:384-393(1998).	
CC	FUNCTIO: INDUCES APOPTOSIS. THE ISOFORMS VARY IN CYTOCHROMICITY	
CC	WITH ISOFORM BIMS BEING THE MOST POTENT AND ISOFORM BIME1 BEING	
CC	THE LEAST POTENT.	

CC	-1	SUBUNIT: FORMS HETERODIMERS WITH A NUMBER OF ANTIAPOPTOTIC BCL-2 PROTEINS INCLUDING BCL-1, BCL-2, BCL-XL, BFL-1, AND BHRF-1. DOES NOT HETEROHOMERIZE WITH PROAPOPTOTIC PROTEINS SUCH AS BAD, BOK, BAX OR BAK (BY SIMILARITY).
CC	-1	SUBCELLULAR LOCATION: ASSOCIATED WITH INTRACYTOSOLIC MEMBRANES.
CC	-1	ALTERNATIVE PRODUCTS: 3 ISOFORMS: BIMEL (SHOWN HERE), BIML AND BIMs; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC	-1	TISSUE SPECIFICITY: EXPRESSED IN A NUMBER OF B-AND T-LYMPHOID CELL LINES.
CC	-1	DOMAIN: THE BH3 DOMAIN IS REQUIRED FOR BCL-2 BINDING AND CYTOTOXICITY.
CC	-1	SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
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CC	EMBL; AF032459; AAC0098.1; -	
DR	EMBL; AF032460; AAC0030.1; -	
DR	EMBL; AF032461; AAC0031.1; -	
DR	MOD; M01119; M01119.2; BCL2.11.2	
DR	InterPro; IP0020712; BCL2	
DR	PROSITE; PS01259; BH: FALSE_NG.	
DR	KO; K00001s; Alternative splicing.	
DR	NCBI; P0001s; Alternative splicing.	
FT	VARIABLE 145 156 97	
FT	VARSPPLIC 42 127 MISSING (IN ISOFORM BIML).	
SO	SEQUENCE 196 AA: 22066 MW: 51317655FPAC9AA CRC64:	
Query Match	50.68; Score 42; DB 1; Length 196;	
Best Local Similarity	61.55; Pred. No. 6;	
Matches	8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;	
OY	2 RYCGRLRMSDF 14	
DB	145 RIAGELRIRIDGF 157	
RESULT	5	
BIM_RAT	STANDARD: PRT: 166 AA.	
ID	C088498; CPMUR8; C088497;	
RA	16-OCT-2001 (Rel. 40, Created)	
RT	15-OCT-2001 (Rel. 40, Last sequence update)	
RT	01-MAR-2002 (Rel. 41, Last annotation update)	
DE	BCL2-like protein 11 (BCL2 interacting mediator of cell death)	
DE	(BCL2-2 related ovarian death protein).	
GN	BCL2L1 OR BIM OR BOD.	
OS	Rattus norvegicus (Rat).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	
OC	NCBI_TaxId=10116;	
OC	11	
CC	SEQUENCE FROM N.A., FUNCTION, SUBUNIT, AND TISSUE SPECIFICITY (ISOFORMS BOD-L; BOD-M AND BOD-S).	
CC	TISSUE=Ovary;	
CC	MEDLINE=98400436; PubMed=9731710;	
CC	Hsu S.Y., Lin P., Hsueh A.J.W.:	
CC	"BOD (bcl-2-related ovarian death gene) is an ovarian BH3 domain-	
CC	containing proapoptotic bcl-2 protein capable of dimerization with	
CC	diverse antiapoptotic Bcl-2 members".	
CC	MOL. Endocrinol. 12:1432-1440(1998).	
CC	12	
CC	SEQUENCE FROM N.A. (ISOFORM BIML).	
CC	Chen D., Simon P., Chen J.:	
CC	"Cloning of rat bImel and bImL, and their differential expression in	
CC	ischemic and normal rat brain".	
CC	Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.	

CC -1- FUNCTION: INDUCES APOPTOSIS.
CC -1- SUBUNIT: FORMS HETERODIMERS WITH A NUMBER OF ANTIAPOPTOTIC BCL-2
CC PROTEINS INCLUDING MCL-1, BCL-2, BCL-XL, BFL-1, AND BHRP-1. DOES
CC NOT HETERODIMERIZE WITH PROAPOPTOTIC PROTEINS SUCH AS BAD, BOK,
CC BAX OR BAK.
CC -1- SUBCELLULAR LOCATION: ASSOCIATED WITH INTRACYTOSOLIC MEMBRANES
CC (BY SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: BOD-L (SHOWN HERE) AND BOD-S;
CC ARE PRODUCED BY THE USE OF ALTERNATIVE INITIATION SITES. TWO
CC FURTHER ISOFORMS: BIML AND BOD-M, ARE PRODUCED BY ALTERNATIVE
CC SPLICING OF BOD-L.
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED.
CC -1- DOMAIN: THE BH3 DOMAIN IS REQUIRED FOR BCL-2 BINDING AND
CC CYTOTOXICITY.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC
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CC
CC EMBL: AF065433; AAC23595.1; -
CC EMBL: AF065431; AAC23593.1; -
CC EMBL: AF065432; AAC23594.1; -
CC EMBL: AF135927; AAC26594.1; -
CC InterPro: IPR000712; BCL2.1
CC DR PROSITE: PS01259; BH3; FALSE_NG.
CC KW Apoptosis; Alternative splicing; Membrane; Alternative Initiation.
CC FT CHAIN 1 196 BCL2-LIKE PROTEIN 11, ISOFORM BOD-L.
FT INIT MET 104 104 FOR ISOFORM BOD-S.
FT DOMAIN 146 160 BH3.
FT VARSLIC 42 97 MISSING (IN ISOFORM BIML).
FT VARSLIC 42 127 MISSING (IN ISOFORM BOD-M).
FT CONFLICT 136 136 E -> D (IN REF. 1; AAC23594).
FT SEQUENCE 196 AA; 22055 MW; BAD2146F9C0B37AD CRC64;
SO

Query Match 50.6%; Score 42; DB 1; Length 196;
Best local similarity 61.5%; Pct. No. 6;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 RYGRRLRMSDEP 14
1 :||||: |||
DB 145 RIAGELRIKDEP 157

RESULT 6
HT2A_HUMAN STANDARD; PRT; 653 AA.
ID HT2A_HUMAN
AC 013049;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE zinc-finger protein HT2A (72 kDa Tat-interacting protein) ("particle
DE motif-containing protein 32").
OS TRIM32 OR HT2A.
GN Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RX 11)
RP MEDLINE=9529135; PubMed=7778269;
FA Fiddell R.A., Harding L.S., Bogerd H.P., Cullen B.R.;
RT Identification of a novel human zinc finger protein that
RT specifically interacts with the activation domain of lentiviral "tat
RT proteins".
RL Virology 209:347-357(1995).
CC -1- FUNCTION: MAY PLAY A SIGNIFICANT ROLE IN MEDITATING THE BIOLOGICAL


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RC STRAIN=5288C / AB9722;
RA Badcock K., Chuchner C., Barrell B.C., Rajandream M.A., Walsh S.V.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: REQUIRED FOR EXPRESSION OF GLYCOTIC GENES. HAS
CC CERTAIN CHARACTERISTICS OF A TRANSCRIPTIONAL ACTIVATOR.
CC -1- SUBCELLULAR LOCATION: Nuclear (probable).
CC -1- SIMILARITY: SOME TO HUMAN CBP80.
CC -1- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 708
CC ONWARD AND IS SHORTER (725 AA) DUE TO A FRAMESHIFT.
CC -----
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CC -----
DR EMBL: D10224; BAO1076.1; ALT_SEQ.
DR EMBL: L07650; NOT_ANNOTATED_CDS.
DR EMBL: L27744; NOT_ANNOTATED_CDS.
DR EMBL: Z49273; CA89274.1; -.
DR EMBL: Z48622; CA88350.1; -.
DR PIR: A44919; A44919.
DR SCD: S0004732; STOI.
DR InterPro: IPR003890; ERF4G-cent.
DR Pfam: PF02854; MIF4G.1.
DR SMART: SM00543; MIF4G.1.
DR DNA-binding: Nuclear protein.
KW DOMAIN 22 30 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 774 801 ASP/GLU-RICH (ACIDIC).
FT DOMAIN 802 825 ARG/LYS-RICH (BASIC).
FT CONFLICT 164 164 D -> V (IN REF. 3).
FT CONFLICT 633 633 R -> I (IN REF. 3).
FT CONFLICT 704 704 A -> R (IN REF. 3).
SQ SEQUENCE 861 AA; 100017 MW; BDD04907BDC9207D CAC64;

Query Match 49.4%; Score 41; DB 1; Length 861;
Best Local Similarity 40.0%; Pred. No. 43;
Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

OY 1 OYRGELRRMSDEFV 15
DB 821 RRYSHREYRELADKFI 835

RESULT 9
YGRG_ECOLI STANDARD; PRT; 261 AA.
ID YGRG_ECOLI
AC P52045; P76643;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein ygrG.
GN ygrG OR B2919.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blatter F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
CC -1- SIMILARITY: BELONGS TO THE ENOYL-COA HYDRASTASE/FISOMERASE FAMILY.
CC -----
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CC -----
DR EMBL: U28377; AA69086.1; ALT_INIT.
DR EMBL: AE000375; AAC75956.1; ALT_INIT.
DR HSSP: P14604; 2DUB.
DR Ecocyc: EC19272; YgrG.
DR InterPro: IPR001753; Enoyl-CoA_hydrtase.
DR Pfam: PF00378; ECH.1.
DR PROSITE: PS00166; ENOYL_COA_HYDRASTASE.1.
KW Hypothetical protein; Lyase; Complete Proteome.
SQ SEQUENCE 261 AA; 29172 MW; BDA8A13BC2C2EBE0 CAC64;

Query Match 48.2%; Score 40; DB 1; Length 261;
Best Local Similarity 50.0%; Pred. No. 17;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 3 YGRGLRRMSDEFVD 16
DB 21 YGRKLNLAKVFTD 34

RESULT 10
PHLC_TRYCR STANDARD; PRT; 380 AA.
ID PHLC_TRYCR
AC O15886;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Variant-surface-glycoprotein phospholipase C (EC 3.1.4.47) (VSG
DE lipase) (glycosylphosphatidylinositol-specific phospholipase C)
DE (GPI-PLC).
OS Trypanosoma cruzi.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5693;
RN [1]
RP SEQUENCE FROM N.A.
RA Redpath M., Carnali N., Webb H., Courel M., Amorim A.,
RA Cardosodalmela M.L., Carrington M.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: BY HYDROLYSIS OF THE ATTACHED GLYCOPHOSPHOLIPID, RELEASES
CC SOLUBLE VARIANT SURFACE GLYCOPROTEIN CONTAINING PHOSPHOTINOSITOL
CC FROM THE CELL WALL OF T. BRUCEI AFTER CELL LYSIS. IT ALSO CLEAVES
CC SIMILAR MEMBRANE ANCHORS ON SOME MAMMALIAN PROTEINS. VSG LIPASE
CC MAY PLAY A ROLE IN PROCESSES SUCH AS PARASITE DIFFERENTIATION OR
CC ANTIGENIC VARIATION (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Variant-surface-glycoprotein 1,2-didecanoyl-
CC sn-phosphatidylinositol + H(2)O -> 1,2-didecanoylglycerol + soluble
CC variant-surface-glycoprotein.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Membrane-associated.
CC -1- SIMILARITY: DOMAIN X IS CONSERVED IN DIFFERENT FORMS OF PLC AND IS
CC ESSENTIAL FOR CATALYTIC ACTIVITY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: AJ000079; CA03904.1; -.
DR InterPro: IPR000909; PI-PLC_X.
DR InterPro: IPR002633; Varsurfglyc_PPIC.
DR Pfam: PF00386; PI-PLC-X; 1.
DR PRODOM: PD041675; Varsurfglyc_PPIC; 1.
DR SMART: SM00148; PLCXG; 1.

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DR PROSITE: PS50007; PIPIC_X_DOMAIN: 1.
 KM Hydrolase; Membrane.
 FT DOMAIN 31
 SO SEQUENCE 380 AA; 42736 MW; 273CD402B52068C5 CRC64;

Query Match 48.2%; Score 40; DB 1; Length 380;
 Best Local Similarity 50.0%; Pred. No. 26;
 Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 2 RYGRRLRMSDEFV 15
 DB 165 KFERELDRSLDRPI 178

RESULT 11
 ID MTAL_ACEPA STANDARD; PRT: 429 AA.
 AC 052702;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Modification methylase Apali (EC 2.1.1.73) (Cytosine-specific
 methyltransferase Apali) (M.Apali).
 GN APALIM
 OS Acetobacter pasteurianus (Acetobacter turbidans).
 OC Bacteria; Proteobacteria; alpha subdivision; Acetobacteraceae;
 OC Acetobacter.
 OX NCBI_TaxID=438;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 12875;
 RX MEDLINE=99077292; PubMed=9862476;
 RA Xu S.-Y., Xiao J.-P., Ettwiller L., Holden M., Aliotta J., Poh C.L.,
 RA Dalton M., Robinson D.P., Petronzio T.R., Moran L., Ganatta M.,
 RA Ware J., Slanko B., Benner J. II;
 RT Cloning and expression of the Apali, NSPI, NSPII, SactI, SactI, and
 RT SactI restriction-modification systems in *Escherichia coli*.
 RL Mol. Genet. 260:226-231(1998).
 CC -1- FUNCTION: THIS METHYLASE RECOGNIZES THE DOUBLE-STRANDED SEQUENCE
 CC GTGCAC, CAUSES SPECIFIC METHYLATION ON C-? ON BOTH STRANDS, AND
 CC PROTECTS THE DNA FROM CLEAVAGE BY THE APALI ENDONUCLEASE.
 CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + DNA cytosine = S-
 CC adenosyl-L-homocysteine + DNA 5-methylcytosine.
 CC -1- SIMILARITY: BELONGS TO THE C5-METHYLTRANSFERASE FAMILY.
 CC -----
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 CC -----
 CC EMBL: AF04847; AAC97180.1;
 DR REBASE: 3281; M.Apali.
 DR InterPro: IPR001525; C5_DNA_meth.
 DR Pfam: PF00145; DNA_methylase. 2.
 DR PRINTS: PR00105; C5METHYTRASE.
 DR PROSITE: PS00094; C5_MTASE_1; FALSE_NEG.
 DR TRANSFERASE: Methyltransferase; Restriction system.
 KW ACT_SITE 81 BY SIMILARITY.
 FT ACT_SITE 81
 SO SEQUENCE 429 AA; 46547 MW; E011C7D15B33F5F3 CRC64;

Query Match 48.2%; Score 40; DB 1; Length 429;
 Best Local Similarity 61.5%; Pred. No. 30;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 4 GRELRMSDEFVD 16
 DB 129 GRDLARLVREFVD 141

RESULT 12
 ID RPSD_BORBU STANDARD; PRT: 631 AA.
 AC P52323;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE RNA polymerase sigma factor rpsd (Sigma-70).
 GN RPOD OR BB0712.
 OS *Borrelia burgdorferi* (Lyme disease spirochete).
 OC Bacteria; Spirochaetales; Spirochaetaceae; *Borrelia*.
 OX NCBI_TaxID=139;
 RN [1]
 RP SEQUENCE OF 89-631 FROM N.A.
 RC STRAIN-ATCC 35210 / B31;
 RA Pan M.;
 RA Thesis (1994), National Taiwan University, Taiwan.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 35210 / B31;
 RX MEDLINE=98065943; PubMed=9403685;
 RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
 RA Iathgra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
 RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
 RA Peterson J., Kierlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
 RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
 RA Uterback T., Watney L., McDonald L., Artiach P., Bowman C.,
 RA Galand S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
 RA Smith H.O., Venter J.C.;
 RT "Genomic sequence of a Lyme disease spirochaete, *Borrelia burgdorferi*."
 RL Nature 390:580-586(1997).
 RN [3]
 RP SEQUENCE OF 165-614 FROM N.A.
 RC STRAIN-297;
 RA Pan M., Yeh J., Tsai C.;
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES
 CC ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES AND
 CC THEN IS RELEASED. THIS IS THE PRIMARY SIGMA-FACTOR OF THIS
 CC BACTERIA.
 CC -----
 CC -1- SIMILARITY: BELONGS TO THE SIGMA-70 FACTOR FAMILY.
 CC -----
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 CC -----
 CC EMBL: U17591; AAC44104.1;
 DR EMBL: AE001171; AAC67061.1;
 DR EMBL: U68006; AAC45100.1;
 DR HSSP: P00579; ISIG.
 DR TIGR: BB0712;
 DR InterPro: IPR000943; Sigma_70.
 DR Pfam: PF00140; sigma70.1.
 DR PRINTS: PR00046; SIGMA70PCT.
 DR PROSITE: PS00715; SIGMA70.1;
 DR PROSITE: PS00716; SIGMA70.2;
 KW Transcription regulation; Sigma factor; DNA-directed RNA polymerase;
 KW DNA-binding; Complete proteome.
 FT DOMAIN 432
 FT DNA_BIND 589 608 H-T-H MOTIF (BY SIMILARITY).
 SO SEQUENCE 631 AA; 73642 MW; BD565AB7DB644796 CRC64;

Query Match 48.2%; Score 40; DB 1; Length 631;
 Best Local Similarity 50.0%; Pred. No. 45;
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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OY      3 YGRELIRMSDEFVD 16
      1 111 11111
Db      279 YOEELIRFSDVID 292

RESULT 13
6PGL_THEME STANDARD: PRT: 220 AA.
ID 6PGL_THEME STANDARD: PRT: 220 AA.
AC 09X0NB:
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 6-phosphogluconolactonase (EC 3.1.1.31) (6PGL).
OS Thermotoga maritima.
CN Bacteria; Thermotogales; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MSR8 / DSM 3109;
RX MEDLINE=99287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA Hatt D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT Evidence for lateral gene transfer between Archaea and Bacteria from
RT genome sequence of Thermotoga maritima."
RL Nature 399:323-329(1999).
CC -1- FUNCTION: HYDROLYSIS OF 6-PHOSPHOGLUCONOLACTONE TO 6-
CC PHOSPHOGLUCONATE.
CC -1- CATALYTIC ACTIVITY: 6-phospho-D-glucono-1,5-lactone + H(2)O = 6-
CC phospho-D-gluconate.
CC -1- PATHWAY: SECOND STEP IN PENTOSE PHOSPHATE PATHWAY.
CC -1- SIMILARITY: BELONGS TO THE GLUCOSAMINE/GALACTOSAMINE-6-PHOSPHATE
CC ISOMERASE FAMILY. 6-PHOSPHOGLUCONOLACTONASE SUBFAMILY.
CC -----
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CC -----
CC EMBL: AE001772; AM36230.1; -
CC DR TRIGR: TM1154; -
CC DR InterPro: IPR000457; Glucosamine_Iso.
CC DR Pfam: PF01182; Glucosamine_Iso. 1.
CC KW Hydrolase; Complete proteome.
CC SQ SEQUENCE 220 AA; 25325 MW; 9B0FD07EE01E60C3 CRC64;

Query Match 47.0%; Score 39; DB 1; Length 220;
Best Local Similarity 42.9%; Pred. No. 21;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY      1 QRYGRELIRMSDEF 14
      1 111 11111
Db      113 EKYERIRSATDQF 126

RESULT 14
RA51_SCHPO STANDARD: PRT: 365 AA.
ID RA51_SCHPO STANDARD: PRT: 365 AA.
AC P36601:
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA repair protein rhp51 (RAD51 homolog).
GN RHP51 OR RAD51 OR SPAC644.14C.
OS Schizosaccharomyces pombe (fission yeast).

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OC      2 YGRELIRMSDEF 14
      1 111 11111
OC      269 RWRRLQRLADEF 281

Eukaryota: Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94051565; PubMed=8233794;
RA Muris D.F.R., Vreeken K., Carr A.M., Broughton B.C., Lehmann A.R.,
RA Lohman P.H.M., Pastink A.;
RT "Cloning the RAD51 homologue of Schizosaccharomyces pombe."
RL Nucleic Acids Res. 21:4586-4591(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93364417; PubMed=8358431;
RA Shinohara A., Ogawa H., Matsuda Y., Ushio N., Ieko K., Ogawa T.;
RT "Cloning of human, mouse and fission yeast recombination genes
RT homologous to Rad51 and recA."
RL Nat. Genet. 4:239-243(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=94252568; PubMed=8194753;
RA Jang Y.K., Jin Y.H., Kim E.M., Hong S.H., Fabre F., Park S.D.;
RT "Cloning and sequence analysis of rhp51+, a Schizosaccharomyces pombe
RL homologue of the Saccharomyces cerevisiae Rad51 gene."
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Lyne M.H., Rajandream M.A., Barrell B.G., Brown S., Harris D.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBS databases.
CC -1- FUNCTION: REQUIRED BOTH FOR RECOMBINATION AND FOR THE REPAIR OF
CC DNA DAMAGE CAUSED BY X-RAYS.
CC -1- SIMILARITY: STRONG TO OTHER EUKARYOTIC RECA-LIKE PROTEIN; SOME, TO
CC PROKARYOTIC RECA PROTEIN.
CC -----
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CC -----
CC EMBL: Z23691; CAA0399.1; -
CC DR EMBL: D13805; BAA02963.1; -
CC DR EMBL: Z24756; CAA80879.1; -
CC DR EMBL: Z24756; CAA80878.1; ALT_INIT.
CC DR EMBL: AL355012; CAB90141.1; -
CC DR PIR: S33205; S33205.
CC DR PIR: S34713; S34713.
CC DR PIR: S42107; S42107.
CC DR PIR: S37672; S37672.
CC DR PIR: S36159; S36159.
CC DR InterPro: IPR000445; HHH.
CC DR InterPro: IPR003583; HHH.1.
CC DR InterPro: IPR001553; RecA.
CC DR Pfam: PRO0633; HHH.1.
CC DR SMART: SM00278; HHH1.1.
CC DR PROSITE: PS50162; RECA_2; 1.
CC DR PROSITE: PS50163; RECA_3; 1.
CC KW DNA damage; DNA repair; ATP-binding; DNA recombination.
CC FT NP_BIND 149 156 ATP (POTENTIAL).
CC FT CONFLICT 15 15 T -> M (IN REF. 2 AND 4).
CC SQ SEQUENCE 365 AA; 39823 MW; 9F26EB9FA4F3C2BA CRC64;

Query Match 47.0%; Score 39; DB 1; Length 365;
Best Local Similarity 53.8%; Pred. No. 37;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY      2 YGRELIRMSDEF 14
      1 111 11111
Db      269 RWRRLQRLADEF 281

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RESULT 15
VS12_REOVD STANDARD: PRT: 418 AA.
AC P03525.
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Sigma 2 protein (core protein).
GN S2.
OS Reovirus (type 3 / strain Deating).
OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
OX NCBI_TaxID=10886;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89243203; PubMed=2718385;
RA Wiener J.R., McLaughlin T., Joklik W.K.;
RT "The sequences of the S2 genome segments of reovirus serotype 3 and
RL of the dsRNA-negative mutant ts447."
RL Virology 170:340-341(1989).
[2]
RN SEQUENCE FROM N.A.
RX MEDLINE=83117734; PubMed=6961439;
RA Cashdollar L.W., Esparza J., Hudson G.R., Chmelo R.A., Lee P.W.K.,
RA Joklik W.K.;
RT "Cloning the double-stranded RNA genes of reovirus: sequence of the
RT cloned S2 gene."
RL Proc. Natl. Acad. Sci. U.S.A. 79:7644-7648(1982).
CC -1- MISCELLANEOUS: MUTANT TS447 IS TEMPERATURE SENSITIVE.
CC
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CC
CC
CC EMBL: M25780; AAA47279.1;
CC DR EMBL: J02327; -: NOT_ANNOTATED_CDS.
CC DR PIR: A31475; FOXR3D.
CC DR PIR: A04125; FOXR2D.
CC DR InterPro: IPR004317; Sigma_1_2.
CC DR Pfam: PF03084; Sigma_1_2; 1.
CC KW Core protein.
FT VARIANT 188 188 A -> V (IN MUTANT TS447).
FT VARIANT 323 323 A -> V (IN MUTANT TS447).
FT VARIANT 383 383 N -> D (IN MUTANT TS447).
FT CONFLICT 259 259 H -> Y (IN REF. 2).
FT CONFLICT 310 331 PAVSRNHGWTGRAGNQLHGFG ->
FT CONFLICT 332 418 LQCRVTSNAGLVELVTNMGSR (IN REF. 2).
FT CONFLICT 418 418 MISSING (IN REF. 2).
SQ SEQUENCE 418 AA: 47161 MW: 0E2F7824DA61DDC CRC64;

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Query Match 47.0%; Score 39; DB 1; Length 418;
Best Local Similarity 50.0%; Pred. NO. 42;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

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QY 1 ORYGRLELRMSDEPVD 16
   | : | : | | | | |
Db 326 QLHGFGVRRMATEFCD 341

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Search completed: September 20, 2002, 11:04:32
Job time: 1629 sec

RX MEDLINE-98146435; PubMed-9477341;
 Ivers A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
 RA Smith D.F.;
 RT "A physical map of the *Leishmania major* Friedlin genome.";
 RL Genome Res. 8:135-145(1998).
 DR EMBL: AL359781; CAB95305.1; -
 DR InterPro: IPR000169; THiolPROTEASE_HIS; UNKNOWN.1.
 DR PROSITE: PS00639; THIOLEPROTEASE_HIS; UNKNOWN.1.
 SQ SEQUENCE 5635 AA; 620050 MW; 64A9EB81A9B14641 CRC64;

Query Match
 Best Local Similarity 51.8%; Score 43; DB 5; Length 5635;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ORYGRRLRMS 11
 DB 1535 ORYGRRLRMS 1545

RESULT 6
 ID 09F005 PRELIMINARY; PRT; 339 AA.
 AC 09F005;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE ATRAPFLO2 PROTEIN (FRAGMENT).
 GN ATRAPFLO2.
 OS Atrichum angustatum.
 OC Eukaryota; Viridiplantae; Streptophyta; Bryophyta;
 OC Polytrichopsida; Polytrichales; Polytrichaceae; Atrichum.
 OX NCBI_Taxid=37310;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20564611; PubMed-11110908;
 RA Frohlich M.W., Estabrook G.F.;
 RT "Wilkinson Support Calculated with Exact Probabilities: An Example
 Using Floricala/LEAF Amino Acid Sequences that Compares Three
 RT Hypotheses Involving Gene Gain/Loss in Seed Plants.";
 RL Mol. Biol. Evol. 17:1914-1925(2000).
 DR EMBL: AF286055; AAC42695.1; -
 DR InterPro: IPR002910; FLO_LFY.
 DR Pfam: PF01698; FLO_LFY; 2.
 FT NON_TER 1
 SQ SEQUENCE 339 AA; 38764 MW; A978F91BD8C912CA CRC64;

Query Match
 Best Local Similarity 50.6%; Score 42; DB 10; Length 339;
 Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 GRELRMSDEFVD 16
 DB 23 GRELRMSDEFVD 35

RESULT 7
 ID 09V7Y6 PRELIMINARY; PRT; 415 AA.
 AC 09V7Y6;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CG15612 PROTEIN.
 GN CG15612.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_Taxid=7227;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-BERKELEY;
 RX MEDLINE-20196006; PubMed-10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Aguayo A., An H.-J., Andrews-Plannkoch C., Baldwin D.,
 RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bertman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brottier P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Padlos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Mei M.-H., Ibegwan C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusslein D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reiner K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wattam D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen K.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AEO03804; AAF57898.1; -
 DR FlyBase: FBgn0034193; CG15612.
 DR InterPro: IPR001849; PH.
 DR Pfam: PF00621; RhogGEF.
 DR SMART: SM00233; PH; 1.
 DR SMART: SM00325; RhogGEF; 1.
 SQ SEQUENCE 415 AA; 49479 MW; C3B0574D856DF20A CRC64;

Query Match
 Best Local Similarity 50.6%; Score 42; DB 5; Length 415;
 Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 ORYGRRLRMSDEFV 15
 DB 121 ORYGRRLRMSDEFV 135

RESULT 8
 ID 0983J4 PRELIMINARY; PRT; 457 AA.
 AC 0983J4;
 DT 01-OCT-2001 (TREMBLrel. 18, Created)
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
 DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
 DE HOMOGENTISATE 1,2-DIOXYGENASE.
 GN MLR8303.
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Phyllobacteriaceae; Mesorhizobium.
 OX NCBI_Taxid=381;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-MAF303099;
 RX MEDLINE-21082930; PubMed-11214968;
 RA Kaneke T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Watanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida T., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 Mesorhizobium loti.";
 RL DNA Res. 7:331-338(2000).
 DR EMBL: AP003013; BAB53887.1; -
 KW Dioxxygenase; Complete proteome.
 SQ SEQUENCE 457 AA; 51046 MW; 6A20B69E9A2B2BD1 CRC64;

Query Match 50.6%; Score 42; DB 16; Length 457;
 Best Local Similarity 46.7%; Pred. No. 75;
 Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 2 RYGRRLRMSDEFVD 16
 Db 425 RYGALETRDNYID 439

RESULT 9
 P71029 PRELIMINARY; PRT; 548 AA.
 AC P71029;
 DT 01-FEB-1997 (TREMblrel. 02, Created)
 DT 01-FEB-1997 (TREMblrel. 02, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE 4-METHYL-5-NITROCATACHOL OXYGENASE.
 GN DNTB.
 OS Burkholderia sp. (strain RASO).
 OC Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
 CC Burkholderia.
 OX NCBI_TaxID=69003;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-DNT;
 RX MEDLINE-96427337; PubMed-8830701;
 RA Halgler B.E., Suen W.C., Spain J.C.;
 RT "Purification and sequence analysis of 4-methyl-5-nitrocatechol
 oxygenase from Burkholderia sp. strain DNT.";
 RL J. Bacteriol. 178:6019-6024(1996).
 DR EMBL: U68411; AAC44479.1; -
 DR InterPro: IPR000733; flavo_monooxygenase.
 DR InterPro: IPR002938; Moxy_FAD_binding.
 DR InterPro: IPR003042; Rng_monooxygenase.
 DR Pfam: PF01494; FAD_binding_3; 1.
 DR Pfam: PF01360; Monooxygenase; 1.
 DR PRINTS: PR00420; RINGMOXGNSE.
 SQ SEQUENCE 548 AA; 59168 MW; 41B508A74413BC5E CRC64;

Query Match 50.6%; Score 42; DB 2; Length 548;
 Best Local Similarity 43.8%; Pred. No. 92;
 Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

OY 1 ORYGRRLRMSDEFVD 16
 Db 371 QAFSRYIRRLAPEFLD 386

RESULT 10
 ID Q960B3 PRELIMINARY; PRT; 592 AA.
 AC Q960B3;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE SD09786P.

CN CG15612.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Eukaryota; Metazoa; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stapleton M., Broksstein P., Hong L., Agbayan A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guarin C., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nuno J., Pacled J., Paragas V., Park S., Phouanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celinker S.;
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY052140; AAK93564.1; -
 SQ SEQUENCE 592 AA; 69459 MW; CC5FD772459F2A83 CRC64;

Query Match 50.6%; Score 42; DB 5; Length 592;
 Best Local Similarity 53.3%; Pred. No. 1e+02;
 Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 ORYGRRLRMSDEFV 15
 Db 298 QNRRLRLRFLD 312

RESULT 11
 ID Q9NOP8 PRELIMINARY; PRT; 653 AA.
 AC Q9NOP8;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE B67K19.2 (ZINC-FINGER PROTEIN HT2A (72 KDA TAT-INTERACTING PROTEIN))
 DE (TAT-INTERACTIVE PROTEIN, 72-KD).
 GN B67K19.2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Serna H.;
 RL Submitted (May-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-SKIN, AND MELANOMA;
 RA Strausberg R.;
 RL Submitted (Feb-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 DR EMBL: AL133284; CAB92723.1; -
 DR EMBL: BC003154; AAH03154.1; -
 DR HSSP: P29590; 1BOR.
 DR InterPro: IPR000345; Cytc_heme_bind.
 DR InterPro: IPR001258; NHL.
 DR InterPro: IPR006822; Znf-C2H2.
 DR InterPro: IPR000315; Znf-box.
 DR InterPro: IPR001841; Znf_ring.
 DR Pfam: PF01436; NHL; 6.
 DR Pfam: PF00643; ZF-B_box; 1.
 DR Pfam: PF00097; ZF-C3HC4; 1.
 DR SMART: SM00336; BBOX; 1.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS00190; CYTOCHROME_C; UNKNOWN_1.
 DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 1.
 DR PROSITE: PS00518; ZINC_FINGER_C3HC4; 1.
 KW DNA-binding; Metal-binding; Zinc; Zinc-finger.
 SQ SEQUENCE 653 AA; 71968 MW; DB5B1595CA8378FD CRC64;

Query Match 50.6%; Score 42; DB 4; Length 653;
 Best Local Similarity 61.5%; Pred. No. 1.1e+02;

Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 QRYGRELRRMSDE 13

Db 186 QRYGRELRRMSDE 198

RESULT 12

ID 099TJ8 PRELIMINARY; PRT; 876 AA.

AC 099TJ8; 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DE VALINE-TRNA LIGASE. 19, Last annotation update)

OS Staphylococcus aureus (strain N315).

OC Bacillus/Staphylococcus group; Staphylococcus.

NCBI_TaxID=158879;

SEQUENCE FROM N.A.

RA MEDLINE-21311952; PubMed-11418146;

RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

RA Cui L., Oguchi A., Aoki K.I., Nagai Y., Ito T., Kanamori M.,

RA Matsunaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y.,

RA Takahashi N.K., Sawano T., Inoue R.I., Kaito C., Sekimizu K.,

RA Hiraoka H., Kihara S., Goto S., Yabuzaki J., Kanehisa M.,

RA Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M.,

RA Ogasawara N., Hayashi H., Hiratsugu K.,

RT "Whole genome sequencing of methicillin-resistant staphylococcus

RT aureus";

RL Lancel 357:1225-1240(2001).

DR EMBL: AP003363; BAB57825.1; -

DR HSSP: P96142; 1GAX.

DR InterPro: IPR002300; trna-synt-1a.

DR InterPro: IPR001412; trna-synt-1.

DR InterPro: IPR002301; trna-synt-1le.

DR InterPro: IPR002303; trna-synt-val.

DR Pfam: PF00133; trna-synt-1; 1.

DR PRINTS: PR00986; TRNASYNTHVAL.

DR PROSITE: PS00178; AA.TRNA.LIGASE.1; 1.

KW Ligase: Complete proteome.

SO SEQUENCE 876 AA; 101723 MW; F7629339DD15155D CRC64;

Query Match 50.6%; Score 42; DB 16; Length 876;

Best Local Similarity 61.5%; Pred. No. 1.5e+02;

Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 GRELRMSDEPVD 16

Db 251 GRELRMSDEPVD 263

RESULT 14

ID 09KZC5 PRELIMINARY; PRT; 216 AA.

AC 09KZC5; 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DE HYPOTHETICAL 23.8 KDA PROTEIN.

OS Streptomyces coelicolor.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

OC Actinomycetales; Streptomycetales; Streptomycetaceae; Streptomyces.

NCBI_TaxID=1902;

SEQUENCE FROM N.A.

RA Saunders D.C., Harris D.;

RA Submitted (Apr-2000) to the EMBL/Genbank/DBJ databases.

RL [2]

RP SEQUENCE FROM N.A.

RC STRAIN-A3(2);

RA Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;

RL Submitted (Apr-2000) to the EMBL/Genbank/DBJ databases.

RP SEQUENCE FROM N.A.

RC STRAIN-A3(2);

RA Redenbach M., Kieser H.M., Denapalte D., Eichner A., Cullum J.,

RA Kinashi H., Hopwood D.A.;

RT "A set of ordered cosmid and a detailed genetic and physical map for

RT the 8 kb Streptomyces coelicolor A3(2) chromosome";

DR MOL. Microbiol. 21:77-96(1996).

DR EMBL: AL353870; CAB89025.1; -

DR InterPro: IPR003265; Endo_3c.

DR SMART: SM00478; EMD03c. 1.

KW Hypothetical protein.

SO SEQUENCE 216 AA; 23810 MW; DDD7C717D60F7AA7 CRC64;

Query Match 49.4%; Score 41; DB 2; Length 216;

Best Local Similarity 53.8%; Pred. No. 48;

Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 QRYGRELRRMSDE 13

Db 109 ERWGDPLRLRDE 121

RESULT 15

ID 09MOB1 PRELIMINARY; PRT; 447 AA.

AC 09MOB1; 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DE VALINE-TRNA LIGASE. 19, Last annotation update)

OS Staphylococcus aureus (strain Mu50).

OC Bacillus/Staphylococcus group; Staphylococcus.

NCBI_TaxID=158879;

AC 09MOB1;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE HYPOTHETICAL 50.8 KDA PROTEIN.
CN AT4G30430.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Lamar B., Stoneking T., Stumpf J., Mewes H.W., Lemcke K.,
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL161577; CAB79767.1; -
KM Hypothetical protein.
SO SEQUENCE 447 AA; 50837 MW; CB24C84F167CE3AF CRC64;

Query Match 49.48; Score 41; DB 10; Length 447;
Best Local Similarity 66.78; Pred. No. 1,1e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 5 RELRRMSDEYD 16
|||:|:| |
Db 84 RELQRIYDELYD 95

Search completed: September 20, 2002, 11:03:44
Job time: 1661 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 20, 2002, 10:35:58 : Search time 228.86 Seconds
(without alignments)
7.765 Million cell updates/sec

Title: US-09-544-664-30

Sequence: I GQVGRGLAITSDDINR 16

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 747574 seqs, 11073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	80	100.0	16	20	AAV05423 Human BAK BH3 doma
2	80	100.0	16	21	AAAB37030 Bcl2 polypeptide B
3	80	100.0	16	22	AAAB71977 Bcl2 polypeptide B
4	80	100.0	17	21	AAAB37057 Bcl2 polypeptide B
5	80	100.0	26	21	AAAB63322 Mammalian BAK Bcl-
6	80	100.0	26	22	AAAB70372 BAK BH3 consensus
7	80	100.0	27	21	AAAB37004 Bcl2 polypeptide B
8	80	100.0	28	17	AAAB62294 GD domain region F
9	80	100.0	117	19	AAAB79535 truncated BAK poly
10	80	100.0	141	16	AAAB7880 Human Cdn-1(71-211
11	80	100.0	152	16	AAAB7879 Human Cdn-1(60-211

12	80	100.0	211	16	AAAB7876 Human Cdn-1. Homo
13	80	100.0	211	16	AAAB7877 Human Cdn-2. Homo
14	80	100.0	211	17	AAAB03668 BAK protein. Homo
15	80	100.0	211	17	AAAB03669 BAK-2 protein. Ho
16	80	100.0	211	17	Bcl-2 apoptosis-re
17	80	100.0	211	19	AAAB79534 BAK polypeptide.
18	80	100.0	211	19	AAAB79535 BAK polypeptide.
19	78	97.5	16	20	AAV05423 Human BAK protein
20	78	97.5	16	21	AAAB37031 Mouse BAK BH3 doma
21	78	97.5	27	21	AAAB37005 Bcl2 polypeptide B
22	78	97.5	208	20	AAAB37052 Mouse BAK protein
23	75	93.8	16	21	AAAB05432 Bcl2 polypeptide B
24	74	92.5	31	17	AAAB05295 GD domain region F
25	69	86.2	15	17	AAAB06502 GD domain region F
26	69	86.2	15	22	AAAB5172 BH3 domain of BAK
27	47	58.8	15	22	AAAB85674 Human Bcl-2-like p
28	47	58.8	165	22	AAAB85668 Human Bcl-2-like p
29	46.5	58.1	195	22	AAAB85667 Human Bcl-2-like p
30	46.5	58.1	175	21	AAAB08500 Arabidopsis thalia
31	46.5	58.1	182	21	AAAB08499 Arabidopsis thalia
32	46.5	58.1	210	21	AAAB08498 Arabidopsis thalia
33	46.5	58.1	322	21	AAAB43239 Arabidopsis thalia
34	46.5	58.1	329	21	AAAB43238 Arabidopsis thalia
35	46.5	58.1	357	21	AAAB43237 Arabidopsis thalia
36	46	57.5	834	22	AAAB34483 E. coli cellulase p
37	46	57.5	842	22	AAAB38125 Salmonella typhi C
38	45	56.2	426	22	AAAB35705 Helicobacter pylor
39	45	56.2	426	22	AAAB35883 Human BAK BH3 doma
40	44	55.0	9	20	AAV05407 BH3 domain of huma
41	44	55.0	9	21	AAAB70831 Putative sensory t
42	44	55.0	258	22	AAAB96439 Arabidopsis thalia
43	44	55.0	291	21	AAAB24103 Arabidopsis thalia
44	44	55.0	329	21	AAAB24102 Arabidopsis thalia
45	43.5	54.4	258	21	AAAB5036 Arabidopsis thalia

ALIGNMENTS

RESULT 1	
AAV05423	AAV05423 standard; peptide; 16 AA.
XX	
AC	AAV05423:
XX	
DT	02-JUL-1999 (first entry)
XX	
DE	Human BAK BH3 domain.
XX	
KW	BH3 domain; cell death agonist; bcl homology domain; BCL-2 family;
KW	apoptosis promoter; cancer cell; virus infected cell; inflammation;
KW	autoantibody producing cell; cancer; lymphoproliferative condition;
KW	arthritis; autoimmune disease; therapy.
OS	
OS	Homo sapiens.
PN	
PN	W09916787-A1.
XX	
PD	08-APR-1999.
XX	
PF	22-SEP-1996; 98WO-US19765.
XX	
PR	07-OCT-1997; 97US-0946039.
XX	
PR	26-SEP-1997; 97US-0060133.
XX	
PA	(UNIW) UNIV WASHINGTON.
XX	
PI	Korsmeyer SJ.
XX	
DR	WPT; 1999-255058/21.
XX	
PT	Bcl homology domain 3 polypeptide
XX	

PS Example 1: Fig 4; 104pp; English.

CC This sequence represents the BH3 domain of human BAX.
 CC The invention relates to a bcl homology domain 3 (BH3 domain),
 CC derived from a proapoptotic member of the BCL-2 family. The
 CC BH3 polypeptide can be used in a method for promoting apoptosis in a
 CC target cell, especially where the cell is a cancer cell, a virus infected
 CC cell or an autonecrotic producing cell. The BH3 polypeptide can be used
 CC in therapeutic compositions for treating disease including cancer, other
 CC lymphoproliferative conditions, arthritis, inflammation, and autoimmune
 CC diseases, which may result from the down regulation of cell death
 CC regulation.

CC Sequence 16 AA:

Query Match 100.0%; Score 80; DB 20; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.2e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGVGRQLAIIIGDDINR 16
 |||
 DB 1 gvgvgrqlaiigddinr 16

RESULT 2

AAB37030 standard; peptide; 16 AA.

AAB37030:

28-FEB-2001 (first entry)

Bcl2 polypeptide BH3 domain peptide #30.

DE Bcl2 polypeptide BH3 domain peptide #30.
 XX Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;
 KW cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;
 KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;
 KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;
 KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
 KW stroke; myocardial infarction.

OS Homo sapiens.

PN WO200059526-A1.

PD 12-OCT-2000.

PF 06-APR-2000; 2000WO-US09352.

PR 07-APR-1999; 99US-0128202.

PA (UYJE-) UNIV JEFFERSON THOMAS.

PI Huang Z, Wang J, Zhang Z, Shan S, Lu Z;

DR WPI: 2000-679325/66.

PT New peptide conjugates for modulating apoptosis or for inhibiting B
 PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for
 PT treating neurodegenerative disorders, stroke, or cancer

PS Claim 18; Page 18; 74pp; English.

CC The invention relates to a peptide conjugate having the formula:
 CC (R-X)-peptide where n = 1-10; X = C=O, when the R-X group is attached
 CC to the N-terminus of the peptide, or a side chain of the peptide where
 CC the functional group of the side chain is NH2 or OH; or X = O or NH,
 CC when the R-X group is attached to the C-terminus of the peptide, or a
 CC side chain of the peptide, where the side chain functional group is COOH
 CC or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkenyl optionally
 CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,

CC phenyl optionally monosubstituted with a 1-5C straight or branched chain
 CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples
 CC of the peptide portion of the conjugate. The peptides represent analogues
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of
 CC the BH3 domain of the cell death agonist Bad. The peptide conjugate is
 CC useful for modulating apoptosis in the cells of a subject, or for
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2
 CC function. In particular, the peptide conjugate is useful for treating a
 CC subject afflicted with a cancer characterized by cancer cells that
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric,
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
 CC conjugate is also useful for treating disorders characterized by
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.

CC Sequence 16 AA:

Query Match 100.0%; Score 80; DB 21; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.2e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGVGRQLAIIIGDDINR 16
 |||
 DB 1 gvgvgrqlaiigddinr 16

RESULT 3

AAB71977 standard; peptide; 16 AA.

AAB71977:

11-MAY-2001 (first entry)

Bak BH3 peptide.

DE Bak BH3 peptide.
 XX Bak; BH3 domain; antiapoptotic; cytostatic; antimycin; apoptosis;
 KW Bcl-2; neoplasia; cancer.

OS Mammalia.

PN WO200114365-A1.

PD 01-MAR-2001.

PF 18-AUG-2000; 2000WO-US22891.

PR 20-AUG-1999; 99US-0149968.

PA (HUTC-) HUTCHINSON CANCER RES CENT FRED.

PI Hockenbery DM, Simon JA, Tzung S;

DR WPI: 2001-244291/25.

PT Novel antimycin derivatives that bind to antiapoptotic Bcl-2 family
 PT protein, useful for modulating the apoptotic state of a cell
 PS Example 6; Page 41; 60pp; English.

CC The present sequence was used in an example illustrating an invention
 CC relating to an antimycin derivative which modulates apoptosis by
 CC binding to a Bcl-2 family protein and preferentially induces apoptosis
 CC in a cell which over-expresses the Bcl-2 family protein. The antimycin
 CC derivative is used in treating an apoptosis-associated disease and for
 CC inducing apoptosis. It is also useful for treating neoplasia and drug
 CC resistance. The present sequence binds to the hydrophobic pocket of
 CC Bcl-2. A competitive binding assay was used to determine if the site of
 CC antimycin A3 interaction was the hydrophobic pocket of Bcl-2.

SO Sequence 16 AA:

Query Match 100.0%; Score 80; DB 22; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGVGRGLATIGDDINR 16
| | | | | | | | | | | | | | | |
Db 1 ggvgrglatigddinr 16

RESULT 4

ID AAB37057 standard; peptide; 17 AA.

AC AAB37057;

DT 28-FEB-2001 (first entry)

DE Bcl2 polypeptide BH3 domain peptide #57.

XX Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;
KW cardiatic; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;
KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;
KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;
KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
KW stroke; myocardial infarction.

OS Homo sapiens.

PN WC200059526-A1.

XX 12-OCT-2000.

PD 06-APR-2000; 2000WC-US09352.

PR 07-APR-1999; 99US-0128202.

XX (UYJE-) UNIT JEFFERSON THOMAS.

PI Huang Z, Wang J, Zhang Z, Shan S, Lu Z;

DR WPI; 2000-679325/66.

XX New peptide conjugates for modulating apoptosis or for inhibiting B
PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for
PT treating neurodegenerative disorders, stroke, or cancer -

PS Claim 18; Page 20; 74pp; English.

XX The invention relates to a peptide conjugate having the formula:

CC (R-X)n-peptide where n = 1-10; X = C-O, when the R-X group is attached
CC to the N-terminus of the peptide, or a side chain of the peptide where
CC the functional group of the side chain is NH2 or OH; or X = O or NH,
CC when the R-X group is attached to the C-terminus of the peptide, or a
CC side chain of the peptide, where the side chain functional group is COOH
CC or CONH2; and R = 2-18C alkyl or alkoxy; 2-14C alkyl/aryl containing one
CC or two double bonds; cyclobutyl, cyclopentyl, cyclohexyl optionally
CC monosubstituted with a 1-5C straight or branched chain alkyl group,
CC phenyl optionally monosubstituted with a 1-5C straight or branched chain
CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples
CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of
CC the BH3 domain of the cell death agonist Bad. The peptide conjugate is
CC useful for modulating apoptosis in the cells of a subject, or for
CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of
CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2
CC function. In particular, the peptide conjugate is useful for treating a
CC subject afflicted with a cancer characterized by cancer cells that
CC express Bcl-2. The cancer includes prostate, colorectal, gastric,
CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or
CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide

CC conjugate is also useful for treating disorders characterized by
CC increased apoptosis, e.g. neurodegenerative disorders, acquired
CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.

SO Sequence 17 AA:

Query Match 100.0%; Score 80; DB 21; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGVGRGLATIGDDINR 16
| | | | | | | | | | | | | | | |
Db 2 ggvgrglatigddinr 17

RESULT 5

ID AAY96322 standard; Peptide; 26 AA.

AC AAY96322;

DT 17-AUG-2000 (first entry)

DE Mammalian Bak Bcl-2 homology domain 3 domain.

XX Mammalian; apoptosis; cell death; Bcl3; apoptosis promotion; Bak;
KW apoptosis inhibition; malignant cell; autoimmune disease.

OS Mammalia.

PN WC200026228-A1.

XX 11-MAY-2000.

PD 28-OCT-1999; 99WC-US25285.

PR 02-NOV-1998; 98US-0184168.

XX (CLON-) CLONTECH LAB INC.

PI Zhu L, Yin X, Chittenden T;

DR WPI; 2000-365560/31.

XX Novel polynucleotide encoding a Bcl3 protein which is useful for
PT modulating apoptosis, especially in the treatment of cancer and
PT autoimmune diseases -

PS Disclosure: Fig 4; 47pp; English.

XX The present sequence is the mammalian Bak Bcl-2 homology domain 3
CC (BH3) domain, which was used in a sequence alignment with the same
CC domain of a putative version of the mammalian apoptosis
CC regulator Bcl3, which was designated Bcl3-ORF2. The Bcl3 protein,
CC nucleic acids and antibodies are suitable for use in promoting cell
CC death or for preventing apoptosis in malignant cells and those causing
CC autoimmune diseases.

SO Sequence 26 AA:

Query Match 100.0%; Score 80; DB 21; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGVGRGLATIGDDINR 16
| | | | | | | | | | | | | | | |
Db 3 ggvgrglatigddinr 18

RESULT 6

AAB70372

ID AAB70372 standard; Peptide: 26 AA.
 XX AAB70372;
 AC
 XX
 DT 02-MAY-2001 (first entry)
 XX
 DE BAK BH3 consensus peptide sequence SEQ ID NO:5.
 XX
 KW Bcl-XL/Bcl-2 associated cell death regulator; BAD: mutant; apoptosis;
 KW immunostimulant; neuroprotective; necrotic; antischismic; vulnary;
 KW cytosolic; antiviral; antitumor; antitumor; wound healing;
 KW immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;
 KW immunodeficiency disease; neurodegenerative disease; viral infection;
 KW ischemic cell death; reperfusion cell death; arthritis; infertility;
 KW lymphoproliferative condition; inflammation; autoimmune disease.
 XX
 OS Undefined.
 XX
 PN WO200110888-A1.
 XX
 PD 15-FEB-2001.
 XX
 PE 30-MAY-2000; 2000WO-US11864.
 XX
 PR 28-MAY-1999; 99US-0136783.
 XX
 PA (APOP-) APOPTOSIS TECHNOLOGY INC.
 XX
 PI Zhou X;
 XX
 DR WPI: 2001-138734/14.
 XX
 PT New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide;
 PT useful for screening for candidate compounds which induce or inhibit
 PT apoptosis, comprises amino acid substitutions at Ser118, Ser155 or
 PT Ser113 -
 XX
 PS Example 2: Fig 3a: 157pp: English.
 XX
 CC The present invention describes an isolated or synthetic polypeptide
 CC (1) comprising a less than full length amino acid sequence of a mutant
 CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its
 CC fragment, which contains amino acid substitutions at Ser118 of a human
 CC BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine
 CC BAD (shorter murine BAD). (1) has immunostimulant, neuroprotective,
 CC necrotic, antischismic, vulnary, cytosolic, antiviral,
 CC antitumor, antitumor, antitumor and immunosuppressive activities, and
 CC can be used as an apoptosis inducer or inhibitor. BAD polypeptides and
 CC polynucleotides can be used for screening candidate compounds and drugs
 CC for activity that promote cell survival or apoptosis. Other uses include
 CC inducing or inhibiting apoptosis in a cell. Candidate compounds
 CC identified and (mutant) BAD polypeptides are useful in treating
 CC immunodeficiency diseases, neurodegenerative diseases, ischemic cell
 CC death, reperfusion cell death, wound healing, cancer, viral infections,
 CC lymphoproliferative conditions, arthritis, infertility, inflammation and
 CC autoimmune diseases. The present sequence represents a Bcl-family member
 CC BH3 domain consensus sequence which is used in an example from the
 CC present invention.
 XX
 SQ Sequence 26 AA:
 Query Match 100.0%; Score 80; DB 22; Length 26;
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGVGRQLATIGDDINR 16
 Db 3 ggygrqlatlgddinr 18
 RESULT 7
 AAB37004

ID AAB37004 standard; peptide: 27 AA.
 XX AAB37004;
 AC
 XX
 DT 28-FEB-2001 (first entry)
 XX
 DE Bcl2 polypeptide BH3 domain peptide #4.
 XX
 KW Cytosolic; neuroprotective; anti-HIV; vitruide; cerebroprotective;
 KW apoptotic; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;
 KW apoptosis modulator; B cell lymphoma/leukemia 2; cancer; prostate;
 KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;
 KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
 KW stroke; myocardial infarction.
 XX
 OS Homo sapiens.
 XX
 PN WO200059526-A1.
 XX
 PD 12-OCT-2000.
 XX
 PE 06-APR-2000; 2000WO-US09352.
 XX
 PR 07-APR-1999; 99US-0128202.
 XX
 PA (UYJE-) UNIV JEFFERSON THOMAS.
 XX
 PI Huang Z, Wang J, Zhang Z, Shan S, Lu Z;
 XX
 DR WPI: 2000-679325/66.
 XX
 PT New peptide conjugates for modulating apoptosis or for inhibiting B
 PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for
 PT treating neurodegenerative disorders, stroke, or cancer -
 XX
 PS Claim 18; Page 17; 74pp: English.
 XX
 CC The invention relates to a peptide conjugate having the formula:
 CC (R-X)n-peptide where n = 1-10; X = C=O, when the R-X group is attached
 CC to the N-terminus of the peptide, or a side chain of the peptide where
 CC the functional group of the side chain is NH2 or OH; or X = O or NH,
 CC when the R-X group is attached to the C-terminus of the peptide, or a
 CC side chain of the peptide, where the side chain functional group is COOH
 CC or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylaryl containing one
 CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain
 CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of
 CC the BH3 domain of the cell death agonist Bad. The peptide conjugate is
 CC useful for modulating apoptosis in the cells of a subject, or for
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2
 CC function. In particular, the peptide conjugate is useful for treating a
 CC subject afflicted with a cancer characterized by cancer cells that
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric,
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
 CC conjugate is also useful for treating disorders characterized by
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
 XX
 SQ Sequence 27 AA:
 Query Match 100.0%; Score 80; DB 21; Length 27;
 Best Local Similarity 100.0%; Pred. No. 2.2e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGVGRQLATIGDDINR 16
 Db 6 ggygrqlatlgddinr 21

PD 08-JUN-1995.
 XX
 PF 30-NOV-1994; 94MO-US13930.
 XX
 PR 07-OCT-1994; 94US-0320157.
 PR 30-NOV-1993; 93US-0160067.
 XX
 PA (LXRB-) LXR BIOTECHNOLOGY INC.
 XX
 PI Barr PJ, Kiefer MC;
 XX
 DR WPI; 1995-215106/28.
 XX
 PT New nucleic acid sequences encoding Cdn apoptosis modulators - and
 PT related vectors, transformed cells, proteins and antibodies, useful
 PT or diagnosis and treatment e.g. of HIV infection, reperfusion injury
 PT etc.
 XX
 PS Disclosure; Fig.11; 66pp; English.
 XX
 CC Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in
 CC increased cell survival in response to anti-Fas-mediated apoptosis.
 CC Deletion of the N-terminal 70 amino acids of Cdn-1 improved this
 CC activity, suggesting that small, truncated Cdn-1 molecules may be
 CC potent therapeutics.
 XX
 SQ Sequence 141 AA;

Query Match 100.0%; Score 80; DB 16; Length 141;
 Best Local Similarity 100.0%; Pred. No. 1.3e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGVGRQLAIIIGDDINR 16
 DB 2 gqvgqrqalilgddlnr 17

RESULT 11
 AAR77879
 ID AAR77879 standard; Protein: 152 AA.
 XX
 AC AAR77879;
 XX
 DT 21-NOV-1995 (first entry)
 XX
 DE Human Cdn-1(60-211).
 XX
 KW Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
 KW autoimmune disease; reperfusion injury; hepatitis, osteoporosis;
 KW shock; lymphoma; eczema.
 XX
 OS Homo sapiens.
 XX
 PN WO9515084-A.
 XX
 PD 08-JUN-1995.
 XX
 PF 30-NOV-1994; 94MO-US13930.
 XX
 PR 07-OCT-1994; 94US-0320157.
 PR 30-NOV-1993; 93US-0160067.
 XX
 PA (LXRB-) LXR BIOTECHNOLOGY INC.
 XX
 PI Barr PJ, Kiefer MC;
 XX
 DR WPI; 1995-215106/28.
 XX
 PT New nucleic acid sequences encoding Cdn apoptosis modulators - and
 PT related vectors, transformed cells, proteins and antibodies, useful
 PT or diagnosis and treatment e.g. of HIV infection, reperfusion injury
 PT etc.

XX
 PS Disclosure; Fig.11; 66pp; English.
 XX
 CC Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in
 CC increased cell survival in response to anti-Fas-mediated apoptosis.
 CC Deletion of the N-terminal 59 amino acids of Cdn-1 only slightly
 CC decreased this activity, suggesting that small, truncated Cdn-1
 CC molecules may be potent therapeutics.
 XX
 SQ Sequence 152 AA;

Query Match 100.0%; Score 80; DB 16; Length 152;
 Best Local Similarity 100.0%; Pred. No. 1.5e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGVGRQLAIIIGDDINR 16
 DB 13 gqvgqrqalilgddlnr 28

RESULT 12
 AAR77876
 ID AAR77876 standard; Protein: 211 AA.
 XX
 AC AAR77876;
 XX
 DT 21-NOV-1995 (first entry)
 XX
 DE Human Cdn-1.
 XX
 KW Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
 KW autoimmune disease; reperfusion injury; hepatitis, osteoporosis;
 KW shock; lymphoma; eczema.
 XX
 OS Homo sapiens.
 XX
 PN WO9515084-A.
 XX
 PD 08-JUN-1995.
 XX
 PF 30-NOV-1994; 94MO-US13930.
 XX
 PR 07-OCT-1994; 94US-0320157.
 PR 30-NOV-1993; 93US-0160067.
 XX
 PA (LXRB-) LXR BIOTECHNOLOGY INC.
 XX
 PI Barr PJ, Kiefer MC;
 XX
 DR WPI; 1995-215106/28.
 DR N-PSDB; AA095492.
 XX
 PT New nucleic acid sequences encoding Cdn apoptosis modulators - and
 PT related vectors, transformed cells, proteins and antibodies, useful
 PT or diagnosis and treatment e.g. of HIV infection, reperfusion injury
 PT etc.
 XX
 PS Disclosure; Fig.3A-B; 66pp; English.
 XX
 CC Cdn-1 cDNA was isolated from a human heart cDNA library using a
 CC previously isolated clone as probe. Recombinant Cdn-1 was produced
 CC in Sf9 and human colon adenocarcinoma HT29 cells. Expression of
 CC Cdn-1 in WI-L2 lymphoblastoid cells resulted in increased cell
 CC survival in response to anti-Fas-mediated apoptosis.
 XX
 SQ Sequence 211 AA;

Query Match 100.0%; Score 80; DB 16; Length 211;
 Best Local Similarity 100.0%; Pred. No. 2.1e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGVGRQLAIIIGDDINR 16
 |||||||
 DB 72 ggvgrqlaIIgddInr 87

RESULT 13

AA077877
 ID AAR77877 standard; Protein: 211 AA.

XX AAR77877;
 AC AAR77877;

XX 21-NOV-1995 (first entry)
 DT 21-NOV-1995 (first entry)

XX Human Cdn-2.
 DE Human Cdn-2.

XX Cdn-2; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
 KW autoimmune disease; reperfusion injury; hepatitis; osteoporosis;
 KM shock; lymphoma; eczema.
 XX

OS Homo sapiens.
 XX

PN W09515084-A.
 XX

PD 08-JUN-1995.
 XX

PE 30-NOV-1994; 94MO-US13930.
 XX

PR 07-OCT-1994; 94US-0320157.
 XX

PR 30-NOV-1993; 93US-0160067.
 XX

PA (LXRB-) LXR BIOTECHNOLOGY INC.
 XX

PI Barr PJ, Kiefer MC;
 XX

DR WPI: 1995-215106/28.
 XX

DR N-PSDB; AA095493.
 XX

XX New nucleic acid sequences encoding Cdn apoptosis modulators - and
 PT related vectors, transformed cells, proteins and antibodies, useful
 PT or diagnosis and treatment e.g. of HIV infection, reperfusion injury
 PT etc.
 XX

PS Disclosure: Fig. 5D-E; 66pp; English.
 XX

CC Cdn-2 cDNA was isolated from a human placental genomic library
 CC using a 950 bp fragment of Cdn-1 cDNA. Expression of Cdn-2
 CC in mouse progenitor B-cell F15.12 cells decreased IL-3-induced
 CC apoptosis. The Cdn-2 protein displayed 97% amino acid identity
 CC with Cdn-1 (AAR77876).
 XX

XX Sequence 211 AA;
 SQ

Query Match 100.0%; Score 80; DB 16; Length 211;
 Best Local Similarity 100.0%; Pred. No. 2.1e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGVGRQLAIIIGDDINR 16
 |||||||
 DB 72 ggvgrqlaIIgddInr 87

RESULT 14

AA03668
 ID AAW03668 standard; Protein: 211 AA.

XX AAW03668;
 AC AAW03668;

XX 22-FEB-1997 (first entry)
 DT 22-FEB-1997 (first entry)

XX Bak protein.
 DE Bak protein.

XX Human; Bak; apoptosis; latency; virus replication;
 KW

KW Epstein-Barr virus; BHRP1; fusion protein; epitope tag;
 KW drug screening; co-precipitation; ELISA; immunoassay; antibody;
 KW protein interactive trapping; virucide; antitumour; diagnostic.
 XX

OS Homo sapiens.
 XX

PN W09633416-A1.
 XX

PD 24-OCT-1996.
 XX

PE 19-APR-1996; 96MO-US05639.
 XX

PR 20-APR-1995; 95US-0426529.
 XX

PA (LXRB-) LXR BIOTECHNOLOGY INC.
 XX

PI Barr PJ, Kiefer MC;
 XX

DR WPI: 1996-485866/48.
 XX

DR N-PSDB; AAT42138.
 XX

XX Screening for anti-viral agents - by detecting the ability of an
 PT agent to disrupt the interaction of a Bak protein and a viral
 PT protein
 XX

PS Disclosure: Fig 1: 24pp; English.
 XX

CC This Bak protein sequence represents a bcl-1 homologue which
 CC interacts with Epstein-Barr virus (EBV) early lytic cycle BHRP1
 CC protein, and is capable of modulating apoptosis. The protein may
 CC be used in complete or partial form, or as an epitope tag fusion
 CC protein, in a new virucide drug screening method, which involves
 CC combination of Bak protein and a viral protein (e.g. EBV BHRP1),
 CC exposure to a test compound, and monitoring for disruption of the
 CC interaction, e.g. by co-precipitation, protein interactive trapping
 CC or ELISA. Interaction of Bak and viral proteins allows viral
 CC replication or latency in the absence of apoptosis. Compounds which
 CC inhibit the interaction may be used as virucide, antitumour or
 CC diagnostic agents.
 XX

XX Sequence 211 AA;
 SQ

Query Match 100.0%; Score 80; DB 17; Length 211;
 Best Local Similarity 100.0%; Pred. No. 2.1e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGVGRQLAIIIGDDINR 16
 |||||||
 DB 72 ggvgrqlaIIgddInr 87

RESULT 15

AA03669
 ID AAW03669 standard; Protein: 211 AA.

XX AAW03669;
 AC AAW03669;

XX 22-FEB-1997 (first entry)
 DT 22-FEB-1997 (first entry)

XX Bak-2 protein.
 DE Bak-2 protein.

XX Human; Bak-2; apoptosis; latency; virus replication;
 KW Epstein-Barr virus; BHRP1; fusion protein; epitope tag;
 KW drug screening; co-precipitation; ELISA; immunoassay; antibody;
 KW protein interactive trapping; virucide; antitumour; diagnostic.
 XX

OS Homo sapiens.
 XX

PN W09633416-A1.
 XX

PD 24-OCT-1996.
 XX

PF 19-APR-1996; 96WO-US05639.
 XX
 PR 20-APR-1995; 95US-0426529.
 XX
 PA (LXRb-) LXR BIOTECHNOLOGY INC.
 XX
 PI Barr PJ, Kiefer MC;
 XX
 DR WPI; 1996-485886/48.
 XX N-PSDB; AAT42139.

PT Screening for anti-viral agents - by detecting the ability of an
 PT agent to disrupt the interaction of a Bak protein and a viral
 PT protein

PS Disclosure: Fig 2; 24pp; English.

CC This Bak-2 protein sequence represents a bcl-1 homologue which
 CC interacts with Epstein-Barr virus (EBV) early lytic cycle BHRF1
 CC protein, and is capable of modulating apoptosis. The protein may
 CC be used in complete or partial form, or as an epitope tag fusion
 CC protein. In a new virucide drug screening method, which involves
 CC combination of Bak-2 protein and a viral protein (e.g. EBV BHRF1),
 CC exposure to a test compound, and monitoring for disruption of the
 CC interaction, e.g. by co-precipitation, protein interaction trapping
 CC or ELISA. Interaction of Bak-2 and viral proteins allows viral
 CC replication or latency in the absence of apoptosis. Compounds which
 CC inhibit the interaction may be used as virucide, antitumour or
 CC diagnostic agents.

XX
 SQ Sequence 211 AA;

Query Match 100.0%; Score 80; DB 17; Length 211;
 Best Local Similarity 100.0%; Pred. No. 2; le-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGVGRQLAIIIGDDINR 16
 |||
 DB 72 ggyvgrqalilgddlnr 87

Search completed: September 20, 2002, 10:35:58
 Job time: 426 sec

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OM protein - protein search, using sw model

Run on: September 20, 2002, 10:37:20 ; Search time 75.64 Seconds

(without alignments)
5.167 Million cell updates/sec

Title: US-09-544-664-30

Perfect score: 80

Sequence: 1 GOVGRQLALIGDDINR 16

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters:

231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Issued Patents AA:*

- 1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/2/1aa/PTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/2/1aa/backfillseq1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	80	100.0	19	4	US-09-236-385A-35
2	80	100.0	20	4	US-09-236-385A-36
3	80	100.0	28	1	US-08-440-391-2
4	80	100.0	28	1	US-08-440-391-18
5	80	100.0	28	2	US-08-908-597A-2
6	80	100.0	28	2	US-08-908-597A-18
7	80	100.0	28	4	US-09-236-385A-2
8	80	100.0	28	4	US-09-236-385A-18
9	80	100.0	28	5	PCT-US96-06122-2
10	80	100.0	28	5	PCT-US96-06122-18
11	80	100.0	36	1	US-08-440-391-14
12	80	100.0	36	2	US-08-908-597A-14
13	80	100.0	36	2	US-09-236-385A-14
14	80	100.0	36	5	PCT-US96-06122-14
15	80	100.0	141	1	US-08-471-058-23
16	80	100.0	152	1	US-08-471-058-22
17	80	100.0	210	3	US-08-471-057-22
18	80	100.0	211	1	US-08-321-071A-16
19	80	100.0	211	1	US-08-471-058-7
20	80	100.0	211	1	US-08-471-058-9
21	80	100.0	211	1	US-08-471-058-10
22	80	100.0	211	1	US-08-471-058-11
23	80	100.0	211	2	US-08-944-530-2
24	80	100.0	211	2	US-08-944-530-4
25	80	100.0	211	3	US-08-471-057-7
26	80	100.0	211	3	US-08-471-057-9
27	80	100.0	211	3	US-08-471-057-10

28	80	100.0	211	3	US-08-471-057-11	Sequence 11, Appl
29	74	92.5	15	4	US-09-236-385A-37	Sequence 37, Appl
30	74	92.5	31	1	US-08-440-391-3	Sequence 3, Appl
31	74	92.5	31	1	US-08-440-391-16	Sequence 16, Appl
32	74	92.5	31	2	US-08-908-597A-3	Sequence 3, Appl
33	74	92.5	31	2	US-08-908-597A-16	Sequence 16, Appl
34	74	92.5	31	4	US-09-236-385A-3	Sequence 3, Appl
35	74	92.5	31	4	US-09-236-385A-16	Sequence 16, Appl
36	74	92.5	31	5	PCT-US96-06122-3	Sequence 16, Appl
37	74	92.5	31	5	PCT-US96-06122-16	Sequence 16, Appl
38	69	86.2	15	1	US-08-440-391-20	Sequence 20, Appl
39	69	86.2	15	1	US-08-440-391-10	Sequence 10, Appl
40	69	86.2	15	2	US-08-908-597A-10	Sequence 10, Appl
41	69	86.2	15	2	US-08-908-597A-20	Sequence 20, Appl
42	69	86.2	15	4	US-09-236-385A-10	Sequence 10, Appl
43	69	86.2	15	4	US-09-236-385A-20	Sequence 20, Appl
44	69	86.2	15	4	US-09-236-385A-38	Sequence 38, Appl
45	69	86.2	15	5	PCT-US96-06122-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-236-385A-35
Sequence 35, Application US/09236385A
Patent No. 6221615
GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.; and
LUTZ, Robert J.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSER: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/236,385A
FILING DATE: 25-Jan-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: MIXON, HENRY N.
REGISTRATION NUMBER: 32,073
(C) ATTORNEY DOCKET NO. 104322.147CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: Linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-09-236-385A-35

Query Match 100.0%; Score 80; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.6e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0Y 1 GOVGRQLALIGDDINR 16
|||
Db 2 GOVGRQLALIGDDINR 17

RESULT 2
US-09-236-385A-36
Sequence 36, Application US/09236385A
Patent No. 6221615
GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.; and
LUTZ, Robert J.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/236,385A
FILING DATE: 25-Jan-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
(C) ATTORNEY DOCKET NO. 104322.147C1P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 36
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 36
US-09-236-385A-36
Query Match 100.0%; Score 80; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.8e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGVGRQLATIGDDINR 16
DB 3 GGVGRQLATIGDDINR 18
RESULT 3
US-08-440-391-2
Sequence 2, Application US/08440391
Patent No. 5656725
GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.; and
LUTZ, Robert J.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,391
FILING DATE: 12-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.147
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-440-391-2
Query Match 100.0%; Score 80; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.7e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGVGRQLATIGDDINR 16
DB 6 GGVGRQLATIGDDINR 21
RESULT 4
US-08-440-391-18
Sequence 18, Application US/08440391
Patent No. 5656725
GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.; and
LUTZ, Robert J.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,391
FILING DATE: 12-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.147
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-440-391-18
Query Match 100.0%; Score 80; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.7e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGVGRQLATIGDDINR 16
DB 6 GGVGRQLATIGDDINR 21

RESULT 5
US-08-908-597A-2
Sequence 2, Application US/08908597A
Patent No. 5863795
GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.; and
APPLICANT: LUTZ, Robert J.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/908,597A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/440,391
FILING DATE: 12-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.147
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-908-597A-2

Query Match 100.0%; Score 80; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 5,7e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGVGRQLATIGDDINR 16
DB 6 GGVGRQLATIGDDINR 21

RESULT 6
US-08-908-597A-18
Sequence 18, Application US/08908597A
Patent No. 5863795
GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.; and
APPLICANT: LUTZ, Robert J.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington

STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/908,597A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/440,391
FILING DATE: 12-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.147
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-908-597A-18

Query Match 100.0%; Score 80; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 5,7e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGVGRQLATIGDDINR 16
DB 6 GGVGRQLATIGDDINR 21

RESULT 7
US-09-236-385A-2
Sequence 2, Application US/09236385A
Patent No. 6221615
GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.; and
APPLICANT: LUTZ, Robert J.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/236,385A
FILING DATE: 25-JAN-1999
CLASSIFICATION: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 28 amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-236-385A-2

Query Match 100.0%; Score 80; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.7e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGVGRQALAIIGDDINR 16
DB 6 GCGVGRQALAIIGDDINR 21

RESULT 8

US-09-236-385A-18
Sequence 18, Application US/09236385A
Patent No. 6221615

GENERAL INFORMATION:

APPLICANT: CHITTENDEN, Thomas D.; and

LUTZ, Robert J.

TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH

MODULATE APOPTOSIS

NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hale and Dorr

STREET: 1455 Pennsylvania Avenue, N.W.

CITY: Washington

STATE: D.C.

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA: US/09/236.385A

APPLICATION NUMBER: US/09/236.385A

FILING DATE: 25-Jan-1999

CLASSIFICATION: <UNKNOWN>

ATTORNEY/AGENT INFORMATION:

NAME: WIXON, HENRY N.

REGISTRATION NUMBER: 32,073

TELECOMMUNICATION INFORMATION: (C) ATTORNEY DOCKET NO. 104322.147CIP

TELEPHONE: 202-942-8400

TELEFAX: 202-942-8484

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 28 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 18:

US-09-236-385A-18

Query Match 100.0%; Score 80; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.7e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGVGRQALAIIGDDINR 16
DB 6 GCGVGRQALAIIGDDINR 21

RESULT 9

PCT-US96-06122-2

Sequence 2, Application PC/TUS9606122

GENERAL INFORMATION:

APPLICANT: IMMUNOGEN, INC.

TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS
WHICH MODULATE APOPTOSIS

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hale and Dorr

STREET: 1455 Pennsylvania Avenue, N.W.

CITY: Washington

STATE: D.C.

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/06122

FILING DATE: HEREWITH

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/440,391

FILING DATE: 12-MAY-1995

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: WIXON, HENRY N.

REGISTRATION NUMBER: 32,073

REFERENCE/DOCKET NUMBER: 104322.147PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-942-8400

TELEFAX: 202-942-8484

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 28 amino acid

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

PCT-US96-06122-2

Query Match 100.0%; Score 80; DB 5; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.7e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGVGRQALAIIGDDINR 16
DB 6 GCGVGRQALAIIGDDINR 21

RESULT 10

PCT-US96-06122-18

Sequence 18, Application PC/TUS9606122

GENERAL INFORMATION:

APPLICANT: IMMUNOGEN, INC.

TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS

WHICH MODULATE APOPTOSIS

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hale and Dorr

STREET: 1455 Pennsylvania Avenue, N.W.

CITY: Washington

STATE: D.C.

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/06122

FILING DATE: HEREWITH

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/440,391

FILING DATE: 12-MAY-1995

```

1 GENERAL INFORMATION:
2
3 APPLICANT: CHITTENDEN, Thomas D.; and
4          LUTY, Robert J.
5
6 TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
7          MODULATE APOPTOSIS
8
9 NUMBER OF SEQUENCES: 41
10
11 CORRESPONDENCE ADDRESS:
12          ADDRESSEE: Hale and Dorr
13          STREET: 1455 Pennsylvania Avenue, N.W.
14          CITY: Washington
15          STATE: D.C.
16          ZIP: 20004
17
18 COMPUTER READABLE FORM:
19

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/236,385A
FILING DATE: 25-Jan-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
(C) ATTORNEY DOCKET NO. 104322.147CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-236-385A-14

Query Match 100.0%; Score 80; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 7,6e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GOVROLATIGDDINR 16
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DB 8 GOVROLATIGDDINR 23

RESULT 14
PCT-US96-06122-14
Sequence 14, Application PC/TUS9606122
GENERAL INFORMATION:
APPLICANT: IMMUNOGEN, INC.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS
TITLE OF INVENTION: WHICH MODULE APOPTOSIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorf
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/06122
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/440,391
FILING DATE: 12-MAY-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.147PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: peptide
PCT-US96-06122-14

Query Match 100.0%; Score 80; DB 5; Length 36;
Best Local Similarity 100.0%; Pred. No. 7,6e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

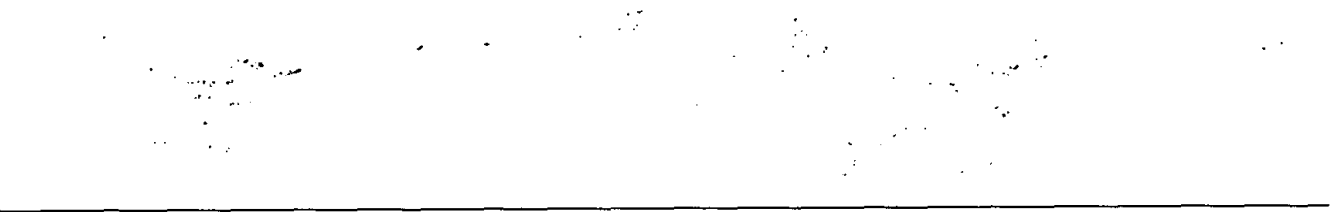
QY 1 GOVROLATIGDDINR 16
|||||
DB 8 GOVROLATIGDDINR 23

RESULT 15
US-08-471-058-23
Sequence 23, Application US/08471058
Patent No. 5770443
GENERAL INFORMATION:
APPLICANT: Kiefer, Michael C.
APPLICANT: Barr, Phillip J.
TITLE OF INVENTION: NOVEL APOPTOSIS MODULATING
TITLE OF INVENTION: PROTEINS, DNA ENCODING THE PROTEINS AND METHODS OF USE
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PALM MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,058
FILING DATE: 06-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/320,157
FILING DATE: 07-OCT-1994
APPLICATION NUMBER: 08/160,067
FILING DATE: 30-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20007.12
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-471-058-23

Query Match 100.0%; Score 80; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 3,8e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GOVROLATIGDDINR 16
|||||
DB 2 GOVROLATIGDDINR 17

Job time: 409 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 20, 2002, 10:39:09 ; Search time 95.59 Seconds
(without alignments)
16.084 Million cell updates/sec

Title: US-09-544-664-30

Perfect score: 80

Sequence: 1 GGVGROLAIGDDINR 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 28138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 28138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : PIR.71.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	80	100.0	211	2 S58873	Bak protein - huma
2	80	100.0	211	2 S58875	cdh-2 protein - hu
3	46.5	58.1	357	2 T06308	protein phosphatas
4	46	57.5	833	2 AEO364	H+/K+-exchanging A
5	46	57.5	834	1 C64779	probable copper-tr
6	46	57.5	834	2 A90696	Cu(I)-translocatio
7	46	57.5	834	2 E85546	probable ATPase yb
8	46	57.5	915	2 H82104	cation transport A
9	46	57.5	1226	2 S48824	F54F2.1 protein, -
10	45	56.2	426	2 S58684	phosphopyruvate hy
11	45	56.2	426	2 H71967	enolase - Helicoba
12	44	55.0	258	2 H75027	sy v-atpase proteo
13	44	55.0	261	2 H71213	probable chemorece
14	44	55.0	593	2 S75352	ABC-type transport
15	44	55.0	693	2 G82618	plius biogenesis p
16	44	55.0	803	1 E70041	probable copper-tr
17	43.5	54.4	355	2 H84643	probable protein p
18	43.5	54.4	532	2 JN0084	phytoene denhydrog
19	43	53.8	444	2 JQ1185	phosphopyruvate hy
20	43	53.8	446	2 T03267	probable phosphop
21	43	53.8	446	2 T02221	phosphopyruvate hy
22	43	53.8	447	2 G86940	hypothetical prote
23	43	53.8	475	2 T48031	hypothetical prote
24	43	53.8	664	2 D96633	hypothetical prote
25	43	53.8	770	2 T23999	hypothetical prote
26	43	53.8	827	2 B95969	probable H+/K+-exc
27	42	52.5	356	2 S71460	ribose-phosphate p
28	42	52.5	356	2 A53433	ribose-phosphate p
29	42	52.5	826	2 D95330	AcP copper transp

30	41	51.2	70	2 H71313	hypothetical prote
31	41	51.2	251	2 T44678	chemotaxis protein
32	41	51.2	447	2 T13091	probable minor cap
33	41	51.2	530	2 C72291	methyl-accepting c
34	41	51.2	539	2 F72288	methyl-accepting c
35	41	51.2	539	2 S22342	chaperonin HSP60 -
36	41	51.2	566	2 A72254	methyl-accepting c
37	41	51.2	570	2 H97244	membrane associate
38	41	51.2	642	2 P84172	ABC transport prot
39	41	51.2	654	2 F71298	probable methyl-ac
40	41	51.2	656	2 A72828	methyl-accepting c
41	41	51.2	656	2 E72379	methyl-accepting c
42	41	51.2	682	2 G72316	twitching motility
43	41	51.2	682	2 S40037	topoisomerase IV,
44	41	51.2	759	2 E87443	copper-transporlin
45	41	51.2	802	2 F90060	

ALIGNMENTS

RESULT 1

Bak protein - human

N:Alternate names: bcl-2 homolog; cdh-1 protein

C:Species: Homo sapiens (man)

C>Date: 15-Feb-1996 #sequence-revision 01-Mar-1996 #text-change 08-Oct-1999

C:Accession: S58873; S58872; S58874

R:Chittenden, T.; Harrington, E.A.; O'Connor, R.; Flemington, C.; Lutz, R.J.; Evan, G

Nature 374, 733-736, 1995

A:Title: Induction of apoptosis by the Bcl-2 homologue Bak.

A:Reference number: S58873; MUID:95231653

A:Accession: S58872

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-211 <F&A>

A:Cross-references: EMBL:X84213; NID:9804984; PIDN:CAA58997.1; PID:9804985

R:Kiefer, M.C.; Brauer, M.J.; Powers, V.C.; Wu, J.J.; Umansky, S.R.; Tomei, L.D.; Bar

Nature 374, 736-739, 1995

A:Title: Modulation of apoptosis by the widely distributed Bcl-2 homologue Bak.

A:Reference number: S58874; MUID:95231654

A:Accession: S58874

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-211 <KIE>

A:Cross-references: EMBL:U16811; NID:9595923; PIDN:AAA74466.1; PID:9595924

C:Genetics:

A:Gene: GDB:BAX

A:Cross-references: GDB:535887

Query Match 100.0%; Score 80; DB 2; Length 211;
Best Local Similarity 100.0%; Pred. No. 3.2e+06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGVGROLAIGDDINR 16
Db 72 GGVGROLAIGDDINR 87

RESULT 2

S58875

cdh-2 protein - human

C:Species: Homo sapiens (man)

C>Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 21-Jul-2000
 C:Accession: S58875
 R:Kleier, M.C.; Brauer, M.J.; Powers, V.C.; Wu, J.J.; Umansky, S.R.; Tomel, L.D.; Barr,
 Nature 374, 736-739, 1995
 A:Title: Modulation of apoptosis by the widely distributed Bcl-2 homologue Bak.
 A:Reference number: S58874; MUID:95231654
 A:Accession: S58875
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-211 <RLE>
 A:Cross-references: EMBL:U016812; NID:9595925; PIDN:AA74467.1; PID:9595926
 A:Note: The nucleotide sequence was submitted to the EMBL Data Library, November 1994

Query Match 100.0%; Score 80; DB 2; Length 211;
 Best Local Similarity 100.0%; Pred. No. 3.2e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 GOVGROLAIIIGDDINR 16
 |||||
 Db 72 GOVGROLAIIIGDDINR 87

RESULT 3
 706306
 Protein phosphatase 2C homolog F11C18.60 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 15-Jun-2001
 C:Accession: T06308
 R:Bevan, M.; Terry, N.; Ardies, W.; Buysaheer, C.; Dasseville, R.; De Clerck, R.; De
 ewes, H.W.; Mayer, K.F.X.; Schueller, C.
 submitted to the Protein Sequence Database, April 1999
 A:Reference number: 215589
 A:Accession: T06308
 A:Molecule type: DNA
 A:Residues: 1-357 <BEV>
 A:Cross-references: EMBL:AF049607; GSPDB:GN00062; ATSP:F11C18.60
 A:Experimental source: Cultivar Columbia; BAC clone F11C18
 C:Genetics:
 A:Gene: ATSP:F11C18.60
 A:Map position: 4
 A:Intons: 39/3; 61/1; 97/2; 148/3; 190/3; 232/1; 257/3; 275/2; 293/3
 C:Superfamily: human phosphoprotein phosphatase 1A

Query Match 58.1%; Score 46.5; DB 2; Length 357;
 Best Local Similarity 58.8%; Pred. No. 3.6;
 Matches 10; Conservative 4; Mismatches 2; Indels 1; Gaps 1;
 Oy 1 GOVGROLAIIIGDDINR 16
 |||||
 Db 104 GOVGROLAIIIGDDINR 120

RESULT 4
 AE0564
 H+/K+-exchanging ATPase (EC 3.6.1.36) - Salmonella enterica subsp. enterica serovar Typh
 C:Species: Salmonella enterica subsp. enterica serovar Typh
 A:Note: This species has also been called Salmonella typhi
 C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
 C:Accession: AE0564
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher,
 th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrer,
 S.; Mole, S.; O'Garra, P.
 Nature 413, 848-852, 2001
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
 A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
 A:Reference number: AB0502; PMID:11677608
 A:Accession: AE0564
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-833 <PAR>
 A:Cross-references: GB:AL513382; PIDN:CAD04983.1; PID:q16501768; GSPDB:GN00176

C:Genetics:
 A:Gene: STY0544
 C:Superfamily: Bacillus probable copper-transferring ATPase yvqX; ATPase nucleotide-b
 C:Keywords: hydrolase

Query Match 57.5%; Score 46; DB 2; Length 833;
 Best Local Similarity 66.7%; Pred. No. 11;
 Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 Oy 4 GROLAIIIGDDIN 15
 |||||
 Db 711 GROVAMVGDGIN 722

RESULT 5
 C64779
 probable copper-transferring ATPase (EC 3.6.1.-) - Escherichia coli
 C:Species: Escherichia coli
 C>Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 11-Jan-2000
 C:Accession: C64779
 R:Blactner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
 A.; Rose, D.J.; Mau, B.; Shaio, Y.
 Science 277, 1453-1462, 1997
 A:Title: The complete genome sequence of Escherichia coli K-12.
 A:Reference number: A64720; MUID:97426617
 A:Accession: C64779
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-834 <BLAT>
 A:Cross-references: GB:AE000154; GB:U00096; NID:q1786683; PIDN:AACT3586.1; PID:q17866
 A:Experimental source: strain K-12, substrain MG1655
 C:Genetics:
 A:Gene: ybaR
 C:Superfamily: Bacillus probable copper-transferring ATPase yvqX; ATPase nucleotide-b
 C:Keywords: ATP; copper binding; hydrolase; ion transporter; metal binding; phosphoprot
 F:928/Domain: heavy-metal-associated homology <HMA1>
 F:103-134/Domain: heavy-metal-associated homology <HMA2>
 F:189-205/Domain: transmembrane #status predicted <TM1>
 F:218-234/Domain: transmembrane #status predicted <TM2>
 F:224-568/Domain: ATPase transduction domain homology <ATP>
 F:438-454/Domain: transmembrane #status predicted <TM3>
 F:468-484/Domain: transmembrane #status predicted <TM4>
 F:631-647/Domain: transmembrane #status predicted <TM5>
 F:643-785/Domain: ATPase nucleotide-binding domain homology <ATN>
 F:806-822/Domain: transmembrane #status predicted <TM6>
 F:108,110,113/Binding site: copper (Met, Cys, Cys) #status predicted
 F:523/Active site: Asp (aspartylphosphate intermediate) #status predicted

Query Match 57.5%; Score 46; DB 1; Length 834;
 Best Local Similarity 66.7%; Pred. No. 11;
 Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 Oy 4 GROLAIIIGDDIN 15
 |||||
 Db 712 GROVAMVGDGIN 723

RESULT 6
 A0696
 Ctl1-translocation P-type ATPase [Imported] - Escherichia coli (strain O157:H7, subs
 C:Species: Escherichia coli
 C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
 C:Accession: A90696
 R:Hayaishi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C
 gashwara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shindagawa, H.
 DNA Res. 8, 11-22, 2001
 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and g
 A:Reference number: A99629; MUID:21156231; PMID:11258796
 A:Accession: A90696
 A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-834 <HAY>
A:Cross-references: PTDN:BAR33960.1; PTD:g13559994; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RMD 0509952
C:Genetics:
A:Gene: EC50537
C:Superfamily: Bacillus probable copper-transporting ATPase yvqX; ATPase nucleotide-bind

Query Match	57.5%;	Score 46;	DB 2;	Length 834;
Best Local Similarity	66.7%;	Pred. No. 11;		
Matches	8;	Conservative	3;	Mismatches 1;
				Indels 0;
				Gaps 0

```
QY      4 GRQLAIGDDIN 15
          |||:|:| |
Db      712 GRQVAMVGDCIN 723
```

```
RESULT 7
E85546
probable ATPase ybar [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C:Species: Escherichia coli
```

R:Pererna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, M.W.; Petersen, B.; White, O.; Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Diallanta, E.; Potamouis, K.; Apodaca, Nature 409, 529-533, 2001

A>Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
A:Reference number:AB5480; MUID:21074935; PMID:11206551

A:Accession: E85546
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-834 <STO>
A:Cross-references: GB:AE005174: NTD:g12513357; PIDN:AAG54833.1; GSPDB:GN00145; UWGP:Z00145
A:Experimental source: strain O157:H7, substrain EDJ933

A: Gene: ybdr
C: Superfamily: Bacillus probable copper-transporting ATPase yvqX; ATPase nucleotide-binding

Query Match	57.5%;	Score 46;	DB 2;	Length 834;
Best Local Similarity	66.7%;	Pred. No. 11;		
Matches	8.	Conservative	3.	Mismatches 1;

```
QY      4 GRQLATIGDDIN 15
          |||::|||
Db      712 GRQYAMVGDCIN 72
```

RESULT 8
H82104
cation transport ATPase, E1-E2 family VC2215 [imported] - *Vibrio cholerae* (strain N1696

C;date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: H82104
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermlaev, M.D.; Vamathevan, J.; Bess, S.; Qin, H.; Dragoli, I.; Sellers,
I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen vibrio cholerae.
A:Reference number: A82035, MUID:20406833
A:Accession: H82104
A:Status: preliminary

A: Molecule type: DNA
A: Residues: 1-915 <HEI>
A: Cross-references: GB:AE004293; GB:AE003852; NID:99656766; PIND:AAFP9359.1; GSPDB:GN00
A: Experimental source: serogroup O1; strain N16961; biotype El Tor

C;Genetics: A;Gene: VC2215 A;Map position: 1 C;Superfamily: Bacillus probable copper-transporting ATPase yvqX; ATPase nucleotide-binding

Query Match 57.5%; Score 46; DB 2; Length 915;

Best Local Similarity	64.3%	Pred. No. 12:	
Matches	9;	Conservative	3;
		Mismatches	2;
		Indels	0;
		Gaps	0.

RESULT 9
S44824
F54F2.1 protein - *Caenorhabditis elegans*

C;date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 23-mai-2004
C;Accession: S44824
R;Anderson, K.
Submitted to the EMBL Data Library September 1993

A:Reference number: S44817
A:Accession: S44824
A:Status: preliminary
A:Molecule type: DNA

C:Genetics: 58/2; 137/3; 179/1; 316/2; 393/1; 551/3; 597/2; 662/2; 899/3; 1178/3
A:introns: 58/2; 137/3; 179/1; 316/2; 393/1; 551/3; 597/2; 662/2; 899/3; 1178/3
C:Keywords: cytoskeleton, transmembrane protein

Query Match	57.5%	Score 46;	DB 2;	Length 1226;
Best Local Similarity	53.8%	Pred. No. 17;		
Matches	7;	Conservative	4;	Mismatches 2;
				Indels 0;
				Gaps 0.

```
QY      1 GQVGRQLAIGDD 13
          1 1:1:1:1:1:1
Db      359 GVFGKQLAVVGDD 37
```

RESULT 10
S58684

phosphopryuvate hydratase (EC 4.2.1.11) - Helicobacter pylori (strains 26019, 26695, 26998, 33972, 33997, 34262, 34263, 34264, 34265, 34266, 34267, 34268, 34269, 34270, 34271, 34272, 34273, 34274, 34275, 34276, 34277, 34278, 34279, 34280, 34281, 34282, 34283, 34284, 34285, 34286, 34287, 34288, 34289, 34290, 34291, 34292, 34293, 34294, 34295, 34296, 34297, 34298, 34299, 34300, 34301, 34302, 34303, 34304, 34305, 34306, 34307, 34308, 34309, 34310, 34311, 34312, 34313, 34314, 34315, 34316, 34317, 34318, 34319, 34320, 34321, 34322, 34323, 34324, 34325, 34326, 34327, 34328, 34329, 34330, 34331, 34332, 34333, 34334, 34335, 34336, 34337, 34338, 34339, 34340, 34341, 34342, 34343, 34344, 34345, 34346, 34347, 34348, 34349, 34350, 34351, 34352, 34353, 34354, 34355, 34356, 34357, 34358, 34359, 34360, 34361, 34362, 34363, 34364, 34365, 34366, 34367, 34368, 34369, 34370, 34371, 34372, 34373, 34374, 34375, 34376, 34377, 34378, 34379, 34380, 34381, 34382, 34383, 34384, 34385, 34386, 34387, 34388, 34389, 34390, 34391, 34392, 34393, 34394, 34395, 34396, 34397, 34398, 34399, 34400, 34401, 34402, 34403, 34404, 34405, 34406, 34407, 34408, 34409, 34410, 34411, 34412, 34413, 34414, 34415, 34416, 34417, 34418, 34419, 34420, 34421, 34422, 34423, 34424, 34425, 34426, 34427, 34428, 34429, 34430, 34431, 34432, 34433, 34434, 34435, 34436, 34437, 34438, 34439, 34440, 34441, 34442, 34443, 34444, 34445, 34446, 34447, 34448, 34449, 34450, 34451, 34452, 34453, 34454, 34455, 34456, 34457, 34458, 34459, 34460, 34461, 34462, 34463, 34464, 34465, 34466, 34467, 34468, 34469, 34470, 34471, 34472, 34473, 34474, 34475, 34476, 34477, 34478, 34479, 34480, 34481, 34482, 34483, 34484, 34485, 34486, 34487, 34488, 34489, 34490, 34491, 34492, 34493, 34494, 34495, 34496, 34497, 34498, 34499, 34500, 34501, 34502, 34503, 34504, 34505, 34506, 34507, 34508, 34509, 34510, 34511, 34512, 34513, 34514, 34515, 34516, 34517, 34518, 34519, 34520, 34521, 34522, 34523, 34524, 34525, 34526, 34527, 34528, 34529, 34530, 34531, 34532, 34533, 34534, 34535, 34536, 34537, 34538, 34539, 34540, 34541, 34542, 34543, 34544, 34545, 34546, 34547, 34548, 34549, 34550, 34551, 34552, 34553, 34554, 34555, 34556, 34557, 34558, 34559, 34560, 34561, 34562, 34563, 34564, 34565, 34566, 34567, 34568, 34569, 34570, 34571, 34572, 34573, 34574, 34575, 34576, 34577, 34578, 34579, 34580, 34581, 34582, 34583, 34584, 34585, 34586, 34587, 34588, 34589, 34590, 34591, 34592, 34593, 34594, 34595, 34596, 34597, 34598, 34599, 34600, 34601, 34602, 34603, 34604, 34605, 34606, 34607, 34608, 34609, 34610, 34611, 34612, 34613, 34614, 34615, 34616, 34617, 34618, 34619, 34620, 34621, 34622, 34623, 34624, 34625, 34626, 34627, 34628, 34629, 34630, 34631, 34632, 34633, 34634, 34635, 34636, 34637, 34638, 34639, 34640, 34641, 34642, 34643, 34644, 34645, 34646, 34647, 34648, 34649, 34650, 34651, 34652, 34653, 34654, 34655, 34656, 34657, 34658, 34659, 34660, 34661, 34662, 34663, 34664, 34665, 34666, 34667, 34668, 34669, 34670, 34671, 34672, 34673, 34674, 34675, 34676, 34677, 34678, 34679, 34680, 34681, 34682, 34683, 34684, 34685, 34686, 34687, 34688, 34689, 34690, 34691, 34692, 34693, 34694, 34695, 34696, 34697, 34698, 34699, 34700, 34701, 34702, 34703, 34704, 34705, 34706, 34707, 34708, 34709, 34710, 34711, 34712, 34713, 34714, 34715, 34716, 34717, 34718, 34719, 34720, 34721, 34722, 34723, 34724, 34725, 34726, 34727, 34728, 34729, 34730, 34731, 34732, 34733, 34734, 34735, 34736, 34737, 34738, 34739, 34740, 34741, 34742, 34743, 34744, 34745, 34746, 34747, 34748, 34749, 34750, 34751, 34752, 34753, 34754, 34755, 34756, 34757, 34758, 34759, 34760, 34761, 34762, 34763, 34764, 34765, 34766, 34767, 34768, 34769, 34770, 34771, 34772, 34773, 34774, 34775, 34776, 34777, 34778, 34779, 34780, 34781, 34782, 34783, 34784, 34785, 34786, 34787, 34788, 34789, 34790, 34791, 34792, 34793, 34794, 34795, 34796, 34797, 34798, 34799, 34800, 34801, 34802, 34803, 34804, 34805, 34806, 34807, 34808, 34809, 34810, 34811, 34812, 34813, 34814, 34815, 34816, 34817, 34818, 34819, 34820, 34821, 34822, 34823, 34824, 34825, 34826, 34827, 34828, 34829, 34830, 34831, 34832, 34833, 34834, 34835, 34836, 348

R. Tomb, J. F. White, O. Kellavagge, A. R. Clayton, R. A. Sutton, G. G. Frieschmann, S. Peterson, S. Loftus, B. Richardson, D. Dodson, R. Khalak, H. G. Glodet, A. McEwen, J. D. Kelley, J. M. Cotton, M. D. Weidman, J. M. Fujii, C. Bowman, C. Watthey, Nature 388, 539-547, 1997

A. Authors: Wallin, E.; Hayes, W. S.; Borodovsky, M.; Karpk, P. D.; Smith, H. O.; Fraser, J. C. *Journal of Molecular Evolution*

A;Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.
A;Reference number: A64520; MUID:97394467
A;Accession: B64539
A;status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA

A;Accession: [F426](#) <from>
A;Accession: [F426](#) <from>
A;Cross-references: GB:AE000536; GB:AE000511; NID:92313230; PIDN:AA07219.1; PID:92313230
A;Experimental source: strain 26695
A;Schmitt, M.; Odenbreit, S.; Heuermann, D.; Haas, R.
Mol. Gen. Genet. 248, 563-572, 1995
A;Title: Identification of the *hly* gene and functional characterization of the *hly* gene product in *Escherichia coli* O157:H7

A:Title: Cloning of the Helicobacter pylori tea gene and functional
A:Reference number: S58683; MUID:9607928
A:Accession: S58684
A:Molecule type: DNA
A:Residues: 1-25, '1', 27-68 <SCH>
A:Accessionformat: IMPI:751478

A:Cross-references: [Enzyme:252710](#)
C:Genetics:
A:Gene: [HP0154](#)
C:Function:
A:Description: catalyzes the reversible dehydration of 2-phospho-D-glyceric acid to P
A:Pathway: [glycolysis](#)

n:column: glycolysis
 C:Superfamily: enolase
 C;Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase; magnesium
 F:42/Binding site: magnesium 2 (Ser) #status predicted

C:Accession: G82618
 R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
 Nature 406, 151-157, 2000
 A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
 A:Reference number: A82515; NCID:20365717
 A:Note: for a complete list of authors see reference number A59328 below
 A:Accession: G82618
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-693 <SIM>
 A:Cross-references: GB:AE004014; GB:AE003849; NID:99107044; PIDN:APR84755.1; GSPDB:GN001
 A:Experimental source: strain 9a5c
 R:Stimpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carre, H
 as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
 submitted to Genbank, June 2000
 A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Fromm
 U.D.; Junqueira, M.L.; Kemper, E.L.; Kitaajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigt
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins, B
 A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
 F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmeiri, D.A
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
 A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
 M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
 A:Reference number: A59328
 A:Contents: annotation
 C:Genetics:
 A:Gene: XF1953

Query Match 55.0%; Score 44; DB 2; Length 693;
 Best Local Similarity 43.8%; Pred. No. 20;
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 OY 1 GCGGRLAIIIGDDINR 16
 1: 11 11: 11: 1: 1:
 DB 550 GAGGGAIVADEYOR 565

Search completed: September 20, 2002, 10:39:10
 Job time: 482 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 20, 2002, 11:04:32 : Search time 44.99 Seconds
(without alignments)
13.770 Million cell updates/sec

Title: US-09-544-664-30

Sequence: 1 GYGRQLAIISDINR 16

Scoring table: Gapop 10.0, Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Database: SwissProt_40*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	80	100.0	211	BAK2_HUMAN	Q13014 homo sapien
2	80	100.0	211	BAK2_HUMAN	Q16611 homo sapien
3	78	97.5	208	BAK_MOUSE	O08734 mus musculu
4	46	57.5	834	ATCQ_ECOLI	O59385 escherichia
5	46	57.5	1226	PAT2_CAEEL	P34446 caenorhabdi
6	45	56.2	426	ENO_HELIP	O92866 helicobacte
7	45	56.2	426	ENO_HELIP	P48285 helicobacte
8	44	55.0	803	ATCQ_BACSU	O32220 bacillus su
9	43.5	54.4	532	CRT1_APHSP	P21134 aphanocep
10	43	53.8	444	ENO_LYCES	P42895 lycopersico
11	43	53.8	446	ENO2_MAIZE	P26995 zea mays (m
12	43	53.8	446	ENO2_MAIZE	O42871 oryza sativ
13	43	53.8	770	YRN9_CAEEL	O09609 caenorhabdi
14	43	53.8	827	ATC2_RHIME	P58342 rhizobium m
15	43	53.8	827	ATC2_RHIME	O93543 rhizobium m
16	42	52.5	826	ATCQ_RHIME	O83841 rhizobium m
17	41	51.2	70	Y535_TREPA	O83846 treponema p
18	41	51.2	499	CPN1_MESAU	P97720 mesocricetu
19	41	51.2	539	CH60_CLOPE	P26821 clostridiu
20	41	51.2	682	PILJ_PSEAE	P42557 pseudomonas
21	41	51.2	759	PARC_CAUER	O54478 caulobacter
22	40	50.0	263	YIND_STAAU	O59605 styphlococ
23	40	50.0	428	ENO_PYRHO	P26301 zea mays (m
24	40	50.0	446	ENO1_MAIZE	P45444 emericella
25	40	50.0	4349	DYHC_EMENT	P78716 fusarium so
26	40	50.0	4349	DYHC_FUSSO	P45443 neurospora
27	40	50.0	4367	DYHC_NEUCR	O95443 drosophila
28	39	48.8	124	VAE2_DROME	P55165 gallus gall
29	39	48.8	211	CRB3_CHICK	O59369 caulobacter
30	39	48.8	351	DCUP_CAUER	O95420 pyrococcus
31	39	48.8	428	ENO_PYRAB	P42848 thermotoga
32	39	48.8	429	ENO_THEMEA	O9kpc5 vibrio chol
33	39	48.8	433	ENO_VIBCH	

ALIGNMENTS

RESULT	ID	STANDARD	PRT	211 AA	
1	BAK2_HUMAN				
AC	Q13014				
DT	01-NOV-1997 (rel. 35, Created)				
DT	01-NOV-1997 (rel. 35, Last sequence update)				
DT	16-OCT-2001 (rel. 40, Last annotation update)				
DE	Bcl-2, homologous antagonist/killer 2 (Apoptosis regulator BAK-2).				
GN	BCL2L2P1 OR BAK2				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	(1)				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=9521654; PubMed=7715731;				
RA	Kiefer M.C., Brauer M.O., Powers V.C., Wu J.J., Umansky S.R.,				
RA	Tomei L.D., Barr P.D.;				
RT	Modulation of apoptosis by the widely distributed Bcl-2 homologue				
RT	BAK-2.				
RL	Nature 374:736-739(1995).				
CC	- FUNCTION: IN THE PRESENCE OF AN APPROPRIATE STIMULUS, ACCELERATES				
CC	PROGRAMMED CELL DEATH BY BINDING TO, AND ANTAGONIZING THE A				
CC	REPRESSOR BCL-2 OR ITS ADENOVIRUS HOMOLOG B19.19K PROTEIN.				
CC	- SUBUNIT: FORMS HETERODIMERS WITH BCL-2, B19.19K PROTEIN, AND BCL-				
CC	X(L).				
CC	- SUBCELLULAR LOCATION: Membrane-associated (potential).				
CC	- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES, WITH				
CC	HIGHEST LEVELS IN THE HEART AND SKELETAL MUSCLE.				
CC	- DOMAIN: INACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND				
CC	BAK FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION				
CC	WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.				
CC	- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 1 (BH1).				
CC	- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 2 (BH2).				
CC	- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 3 (BH3).				
CC	- CAUTION: THIS COULD BE THE PRODUCT OF A PSEUDOGENE.				
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	EMBL: U16812; AAA74467.1; -				
DR	HSSP: Q16611; 1BX1.				
DR	InterPro: IPR002475; BCL2_family.				
DR	InterPro: IPR000712; BCL2.				
DR	Pfam: PF00452; BCL-2_1.				
DR	SMART: SM00337; BCL_1.				
DR	PROSITE: PS01080; BHL_1.				
DR	PROSITE: PS01258; BH2_1.				
DR	PROSITE: PS01259; BH3_1.				

```

DR PROSITE: P550062; BCL2 FAMILY; 1.
KM APOPTOSIS; Transmembrane.
FT DOMAIN 74 88 BH3.
FT DOMAIN 117 136 BH1.
FT DOMAIN 159 184 BH2.
FT TRANSMEM 188 205 POTENTIAL.
SQ SEQUENCE 211 AA; 23411 MW; 703875EC4DCC1D3 CRC64;

Query Match 100.0%; Score 80; DB 1; Length 211;
Best Local Similarity 100.0%; Pred. No. 3 9e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GONGROLAIIIGDDINR 16
DB 72 GONGROLAIIIGDDINR 87

RESULT 2
BAK_HUMAN STANDARD; PRT; 211 AA.
ID Q1611; O92533;
AC 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Bcl-2 homologous antagonist/killer (Apoptosis regulator BAK).
GN BAK1 OR BAK
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;

BAK_HUMAN STANDARD; PRT; 211 AA.
ID Q1611; O92533;
AC 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Bcl-2 homologous antagonist/killer (Apoptosis regulator BAK).
GN BAK1 OR BAK
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;

SEQUENCE FROM N.A.
RC TISSUE-B-cell;
RA MEDLINE-95231652; PubMed-7715729;
RA Parow S.N., White J.H.M., Martiou I., Raven T., Pun K.-T.,
RA Grinham C.J., Martiou J.C., Brown R.;
RT "Cloning of a bcl-2 homologue by interaction with adenovirus E1B
RT 19k.";
RL Nature 374:731-733(1995).

SEQUENCE FROM N.A.
RC TISSUE-B-cell;
RA MEDLINE-95231653; PubMed-7715730;
RA Chittenden T., Harrington E.A., O'Connor R., Flemington C., Lutz R.J.,
RA Evan G.I., Guild B.C.;
RT "Induction of apoptosis by the Bcl-2 homologue BAK.";
RL Nature 374:733-736(1995).

SEQUENCE FROM N.A.
RC TISSUE-B-cell;
RA MEDLINE-95231654; PubMed-7715731;
RA Kleier M.C., Brauer M.J., Powers V.C., Wu J.J., Umansky S.R.,
RA Tomel L.D., Barr P.J.;
RT "Modulation of apoptosis by the widely distributed Bcl-2 homologue
RT BAK.";
RL Nature 374:736-739(1995).

SEQUENCE FROM N.A.
RC TISSUE-B-cell;
RA MEDLINE-95231655; PubMed-7715732;
RA Williams S.;
RT Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

SEQUENCE OF 96-206 FROM N.A.
RC TISSUE-B-cell;
RA MEDLINE-95231656; PubMed-7715733;
RA Williams S.;
RT Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.

MUTAGENESIS AND FUNCTION OF BH3 DOMAIN.
RA MEDLINE-96091131; PubMed-8521816;
RA Chittenden T., Flemington C., Houghton A.B., Ebb R.G., Gallo G.J.,
RA Elango B., Chinnappa G., Lutz R.J.;
RT "A conserved domain in BAK, distinct from BH1 and BH2, mediates cell
RT death and protein binding functions.";
RL EMO J. 14:5589-5596(1995).

STRUCTURE BY NMR OF 72-87.

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RX MEDLINE-97172562; PubMed-9020082;
RA Sattler M., Liang H., Nettlesheim D., Meadows R.P., Harlan J.E.,
RA Eperstadt M., Yoon H.S., Shuker S.B., Chang B.S., Mann A.J.;
RA Thompson C.B., Fesk S.W.;
RT "Structure of Bcl-xL-Bak peptide complex: recognition between
RT regulators of apoptosis.";
RL Science 275:983-986(1997).

FUNCTION: IN THE PRESENCE OF AN APPROPRIATE STIMULUS, ACCELERATES
PROGRAMMED CELL DEATH BY BINDING TO, AND ANTAGONIZING THE A
REPRESSOR BCL-2 OR ITS ADENOVIRUS HOMOLOG E1B 19K PROTEIN.
SUBUNIT: FORMS HETERODIMERS WITH BCL-2, E1B 19K PROTEIN, AND BCL-
X(L).
SUBCELLULAR LOCATION: Membrane-bound (Potential).
TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES, WITH
HIGHEST LEVELS IN THE HEART AND SKELETAL MUSCLE.
DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND
BAK FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 1 (BH1).
SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 2 (BH2).
SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 3 (BH3).
SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

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EMBL: X84213; CAAS6897.1;
EMBL: U23765; AAA93066.1;
EMBL: U16811; AAA74466.1;
EMBL: 293017; CA65626.1;
EMBL: D88397; BAA13606.1;
EMBL: D88396; BAA13606.1; JOINED.
PDB: 1BXL; 29-OCT-97.
MTM: 600516;
InterPro: IPR002475; BCL2 family.
InterPro: IPR000712; BCL2.
Pfam: PF00452; BCL-2; 1.
SMART: SM00337; BCL-2; 1.
PROSITE: PS01080; BH1; 1.
PROSITE: PS01258; BH2; 1.
PROSITE: PS01259; BH3; 1.
PROSITE: PS50062; BCL2 FAMILY; 1.
APOPTOSIS; Transmembrane; 3D-structure.
DOMAIN 74 88 BH3.
DOMAIN 117 136 BH1.
DOMAIN 159 184 BH2.
TRANSMEM 188 205 POTENTIAL.
SQ SEQUENCE 211 AA; 23409 MW; A2200FE72A46D04E CRC64;

Query Match 100.0%; Score 80; DB 1; Length 211;
Best Local Similarity 100.0%; Pred. No. 3 9e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GONGROLAIIIGDDINR 16
DB 72 GONGROLAIIIGDDINR 87

RESULT 3
BAK_MOUSE STANDARD; PRT; 208 AA.
ID Q08734;
AC 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-2002 (Rel. 41, Last annotation update)
DE Bcl-2 homologous antagonist/killer (Apoptosis regulator BAK)

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GN BAK1 OR BAK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId:10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SWISS; TISSUE=Liver;
 RX MEDLINE=97446138; PubMed=9299236;
 RA Ulrich E., Kaufmann-Zeh A., Hueber A.O., Williamson J.,
 RT Chittenden T., Ma A., Evan G.I.;
 "gene structure", cDNA sequence, and expression of murine Bak, a
 proapoptotic Bcl-2 family member.";
 RL Genomics 44:195-200(1997).
 CC -1- FUNCTION: IN THE PRESENCE OF AN APPROPRIATE STIMULUS, ACCELERATES
 PROGRAMED CELL DEATH BY BINDING TO, AND ANTAGONIZING THE A
 REPRESSOR BCL-2 OR ITS ADENOVIRUS HOMOLOG E1B 19K PROTEIN (BY
 SIMILARITY).
 CC -1- SUBUNIT: FORMS HETERODIMERS WITH BCL-2, E1B 19K PROTEIN, AND BCL-
 X(L) (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Membrane-associated (Potential).
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED.
 CC -1- DOMAIN: INTRAC B3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND
 BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
 WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
 CC APOPTOTIC MEMBERS OF THE BCL-2 FAMILY (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 1 (BH1).
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 2 (BH2).
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 3 (BH3).
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
 CC -----
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 CC -----
 CC EMBL: Y13231; CAA73684.1; -.
 DR HSSP: Q16611; IBXL.
 DR MGD: MGI:1097161; Bak1.
 DR InterPro: IPR002475; BCL2_family.
 DR InterPro: IPR000712; Bcl_2.
 DR Pfam: PF00452; Bcl_2; 1.
 DR SMART: SM00337; BCL; 1.
 DR PROSITE: PS01080; BH1; 1.
 DR PROSITE: PS01258; BH2; 1.
 DR PROSITE: PS01259; BH3; 1.
 DR PROSITE: PS50062; BCL2_FAMILY; 1.
 DR Apoptosis; Transmembrane.
 KW DOMAIN 71 85 BH3.
 FT DOMAIN 114 133 BH1.
 FT DOMAIN 166 181 BH2.
 FT TRANSMEM 185 202 POTENTIAL.
 SQ SEQUENCE 208 AA; 23300 MW; DAFCL1BL6OC523C9 CRC64;

Query Match 97.5%; Score 78; DB 1; Length 208;
 Best Local Similarity 93.8%; Pred. No. 8.2e-06;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GOVGROLATIGDDINR 16
 Db 69 GOVGROLATIGDDINR 84

RESULT 4
 ID ATCU_ECOLI STANDARD; PRT; 834 AA.
 AC Q59385; P78245;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Probable copper-transporting ATPase (EC 3.6.3.4).
 GN YBAR OR B0484.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC Escherichia.
 OX NCBI_TaxId=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RA Das S., Chuang E., Vulpe C., Goldman J., Girschler J.,
 RL Submitted (JUN-1996) to the EMBL/Genbank/DBD databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Roberts D., Allen E., Araujo R., Aparicio A., Chung E., Davis K.,
 RA Duncan M., Federspiel N., Hyman R., Kallman S., Komp C., Kurd O.,
 RA Lew H., Lin D., Nemeth A., Oefner P., Schramm S., Davis R.W.;
 RL Submitted (JAN-1997) to the EMBL/Genbank/DBD databases.
 CC -1- FUNCTION: INVOLVED IN COPPER TRANSPORT.
 CC -1- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + ORTHOPHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- SIMILARITY: BELONGS TO THE CARLON TRANSPORT ATPASES FAMILY
 CC (E1-E2 ATPASES). SUBFAMILY IB.
 CC -1- SIMILARITY: CONTAINS 2 HMA DOMAINS.
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 CC -----
 CC EMBL: U58330; AAB02268.1; -.
 DR EMBL: AE000154; AAC73586.1; -.
 DR EMBL: UB2664; AAB40238.1; -.
 DR HSSP: P04129; IAFI.
 DR EcoGene; EGI3246; ybar.
 DR InterPro: IPR001757; E1-E2_ATPase.
 DR InterPro: IPR001934; HMA.
 DR Pfam: PF001454; Hydrolyase.
 DR Pfam: PF00403; HMA; 2.
 DR Pfam: PF00702; Hydrolyase; 1.
 DR PRINTS: PR00119; CATAPASE.
 DR PROSITE: PS00154; ATPASE_E1_E2; 1.
 DR PROSITE: PS01047; HMA_1; 1.
 DR PROSITE: PS50846; HMA_2; 2.
 KW Hydrolyase; Transmembrane; Phosphorylation; ATP-binding; Copper;
 KM Metal-binding; Repeat; Complete proteome.
 FT TRANSMEM 187 207 POTENTIAL.
 FT TRANSMEM 218 238 POTENTIAL.
 FT TRANSMEM 254 274 POTENTIAL.
 FT TRANSMEM 284 304 POTENTIAL.
 FT TRANSMEM 384 458 POTENTIAL.
 FT TRANSMEM 464 484 POTENTIAL.
 FT TRANSMEM 485 505 POTENTIAL.
 FT TRANSMEM 627 647 POTENTIAL.
 FT TRANSMEM 733 753 POTENTIAL.
 FT TRANSMEM 779 799 POTENTIAL.
 FT TRANSMEM 801 821 POTENTIAL.
 FT DOMAIN 4 65 HMA 1.
 FT DOMAIN 100 163 HMA 2.

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FT METAL 110 110 COPPER (POTENTIAL).
FT METAL 113 113 COPPER (POTENTIAL).
FT MOD_RES 523 523 PHOSPHORYLATION (PROBABLE).
FT CONFLICT 162 181 EAIEDAKRREEROEFAVAT ->
FT CONFLICT 508 508 KRLKMTLNASASKRPPLA (IN REF. 1).
FT CONFLICT 576 576 A -> R (IN REF. 1).
FT CONFLICT 576 576 O -> R (IN REF. 1).
SQ SEQUENCE 834 AA; 87873 MW; CF84A18FE20BE6F6 CRC64;

Query Match 57.5%; Score 46; DB 1; Length 834;
Best Local Similarity 66.7%; Pred. No. 6.4;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 4 GROLAIIGDDIN 15
Db 712 GQVAVMGDGIN 723

RESULT 5
PART2_CAEEL STANDARD; PRT; 1226 AA.
AC P34446;
DT 01-FEB-1994 (Rel. 28; Created)
DT 01-FEB-1994 (Rel. 28; Last sequence update)
DT 01-MAR-2002 (Rel. 41; Last annotation update)
DE Integrin alpha pat-2 precursor.
CN PAT-2 OR P54F2.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae.
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=BRISTOL N2.
RC MEDLINE=94150718; PubMed=7966398;
RA Wilson R., Atascough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rikken L., Roopra A., Saunders D., Shownkeen R.,
RA Sims M., Smalton N., Smith A., Smith M., Sonhammer E., Staden R.,
RA Sulston J., Thierly-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Woldman P.;
*2.2 MB of contiguous nucleotide sequence from chromosome III of C.
RT elegans.
RL Nature 368:32-38(1994).
CC -1- FUNCTION: POSSIBLE ROLE IN CELL-CELL INTERACTIONS (BY SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA PAT-2
CC ASSOCIATES WITH BETA PAT-3.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.
CC -1- SIMILARITY: CONTAINS 7 FG-GAP REPEATS.
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CC -----
CC EMBL: L23645; AAK26134.1; -
CC PIR: S44824; S44824.
CC HSP: P11215; IABX.
CC WormPep: F54F2.1; CE00194.
CC InterPro: IPR000413; Integrin_alpha.
CC Pfam: PF01839; FG-GAP; 5.
CC Pfam: PF00357; Integrin_A; 1.
CC PRINTS: PRO1185; INTEGRINA.

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DR SMART: SM00191; Int_alpha; 5.
DR PROSITE: PS00242; INTEGRIN_ALPHA; 1.
KM Integrin, Cell adhesion; Receptor; Glycoprotein; Transmembrane;
KW Signal; Repeat.
FT CHAIN 26 1226 POTENTIAL.
FT DOMAIN 26 1134 INTEGRIN ALPHA PAT-2.
FT TRANSMEM 1155 1177 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 1178 1226 POTENTIAL.
FT REPEAT 40 103 CYTOPLASMIC (POTENTIAL).
FT REPEAT 120 172 FG-GAP 1.
FT REPEAT 189 243 FG-GAP 2.
FT REPEAT 244 297 FG-GAP 3.
FT REPEAT 300 372 FG-GAP 4.
FT REPEAT 373 433 FG-GAP 5.
FT REPEAT 437 485 FG-GAP 6.
FT REPEAT 485 508 FG-GAP 7.
FT CARBOHYD 108 108 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 679 679 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 775 775 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 819 819 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1226 AA; 135939 MW; B9169AD75B88901D CRC64;

Query Match 57.5%; Score 46; DB 1; Length 1226;
Best Local Similarity 53.8%; Pred. No. 9.6;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Oy 1 GQVAVMGDGIN 13
Db 359 GVEGQIAVWGDD 371

RESULT 6
ENO_HELPJ STANDARD; PRT; 426 AA.
ID ENO_HELPJ
AC Q9ZMS6;
DT 16-OCT-2001 (Rel. 40; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 16-OCT-2001 (Rel. 40; Last annotation update)
DE Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-
DE glycerate hydro-lyase).
DE ENO OR JHP0142.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=85963;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Dolg P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Glison R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Voyis G.F.,
RA Trust T.J.;
*Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori.
RL Nature 397:176-180(1999).
CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate -> phosphoenolpyruvate +
CC H(2)O.
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
CC THE DIMER (BY SIMILARITY).
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
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CC -----
DR EMBL: AE001453; AAD05723.1; -.
DR HSSP: P00924; 4ENL.
DR InterPro: IPR000941; Enolase.
DR Pfam: PF00113; Enolase; 1.
DR PRINTS: PR00148; ENOLASE.
DR ProDom: PD000902; Enolase; 1.
DR ProSITE: PS00164; ENOLASE; 1.
DR Lyase: Glycolysis; Magnesium; Complete proteome.
KM ACT_SITE 155 155 BY SIMILARITY.
FT METAL 242 242 MAGNESIUM (BY SIMILARITY).
FT METAL 286 286 MAGNESIUM (BY SIMILARITY).
FT METAL 313 313 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 426 AA; 46554 MW; EDFA73EAB8B77BEE CRC64;

Query Match 56.2%; Score 45; DB 1; Length 426;
Best Local Similarity 46.2%; Pred. No. 4.6;
Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 2 QVGRQLATIGDDI 14
DB 303 ELGRQIOLVGDDL 315

RESULT 7
ENO_HELPY STANDARD; PRT; 426 AA.
ID ENO_HELPY
AC P48285;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-
DE glycerate hydro-lyase).
GN ENO OR HP0154.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=26695 / ATCC 700392;
RX MEDLINE=97394467; PubMed=9252185;
RA Tomb J.-F., White O., Kervatage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
RA Nelson K., Quackenbush J., Zhou L., Kirness E.F., Peterson S.,
RA Loftus B., Richardson D., Dodson R., Khalak H.G., Hickey E.K.,
RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
RA Cotton M.D., Weldman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
RA Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori."
RL Nature 388:539-547(1997).
RN [2]
RP SEQUENCE OF 1-178 FROM N.A.
RC STRAIN=ATCC 53726 / 84-183;
RX MEDLINE=95286262; PubMed=7768597;
RA Thompson S.A., Blaser M.J.;
RT Isolation of the Helicobacter pylori reca gene and involvement of
RT the reca region in resistance to low pH.;
RL Infect. Immun. 63:2185-2193(1995).
CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate -> phosphoenolpyruvate +
CC H(2O).
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
CC THE DIMER (BY SIMILARITY).
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

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CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC -----
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CC -----
DR EMBL: AE000536; AAD07219.1; -.
DR HSSP: P00924; 4ENL.
DR TIGR: HP0154; -.
DR InterPro: IPR000941; Enolase.
DR Pfam: PF00113; Enolase; 1.
DR PRINTS: PR00148; ENOLASE.
DR ProDom: PD000902; Enolase; 1.
DR ProSITE: PS00164; ENOLASE; 1.
DR Lyase: Glycolysis; Magnesium; Complete proteome.
KM ACT_SITE 155 155 BY SIMILARITY.
FT METAL 242 242 MAGNESIUM (BY SIMILARITY).
FT METAL 286 286 MAGNESIUM (BY SIMILARITY).
FT METAL 313 313 MAGNESIUM (BY SIMILARITY).
FT METAL 313 313 MAGNESIUM (BY SIMILARITY).
FT CONFLICT 26 26 V -> I (IN REF. 2).
FT CONFLICT 85 85 I -> T (IN REF. 2).
SQ SEQUENCE 426 AA; 46534 MW; 7B7A0B87A5DFB398 CRC64;

Query Match 56.2%; Score 45; DB 1; Length 426;
Best Local Similarity 46.2%; Pred. No. 4.6;
Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 2 QVGRQLATIGDDI 14
DB 303 ELGRQIOLVGDDL 315

RESULT 8
ATCU_BACSU STANDARD; PRT; 803 AA.
ID ATCU_BACSU
AC G32220;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Potential copper-transporting ATPase (EC 3.6.3.4).
GN YVGH.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
RT Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RL -1- FUNCTION: INVOLVED IN COPPER TRANSPORT (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + H(2O) -> ADP + ORTHOPHOSPHATE.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
CC (E1-E2 ATPASES). SUBFAMILY 1B.
CC -1- SIMILARITY: CONTAINS 2 HMA DOMAINS.
CC -----
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CC -----
DR EMBL: Z99121; CAB15355.1; -.
DR HSSP: P04129; IAFJ.

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DR Sublist: BG14106; YV9X.
DR InterPro: IPR001366; Cad_ATPase.
DR InterPro: IPR000579; Cu_P_ATPase.
DR InterPro: IPR001756; Cu_ATPase.
DR InterPro: IPR001577; Cu_ATPase.
DR InterPro: IPR001757; El-E2_ATPase.
DR InterPro: IPR001802; Hg_scarvenger.
DR InterPro: IPR001934; HMA.
DR InterPro: IPR001454; Hydrolyase.
DR Pfam: PF00122; El-E2_ATPase. 1.
DR Pfam: PF00403; HMA; 2.
DR Pfam: PF00702; Hydrolyase. 1.
DR PRINTS: PR00119; CATATPASE.
DR PRINTS: PR00940; CATATPASE.
DR PRINTS: PR00941; CATATPASE.
DR PRINTS: PR00942; CATATPASE.
DR PRINTS: PR00946; HSCAVENGER.
DR PROSITE: PS00154; ATPASE_E1_E2. 1.
DR PROSITE: PS01047; HMA_1; 2.
DR PROSITE: PS00846; HMA_2; 2.
DR Hydrolyase; Transmembrane; Phosphorylation; Magnesium; ATP-binding;
KW Metal-binding; Copper; Repeat; Complete proteome.
FT TRANSMEM 163 183 POTENTIAL.
FT TRANSMEM 197 217 POTENTIAL.
FT TRANSMEM 229 249 POTENTIAL.
FT TRANSMEM 260 280 POTENTIAL.
FT TRANSMEM 416 436 POTENTIAL.
FT TRANSMEM 448 468 POTENTIAL.
FT TRANSMEM 610 630 POTENTIAL.
FT TRANSMEM 704 724 POTENTIAL.
FT TRANSMEM 767 787 POTENTIAL.
FT DOMAIN 7 73 HMA 1.
FT METAL 17 17 COPPER (POTENTIAL).
FT METAL 20 20 COPPER (POTENTIAL).
FT METAL 85 85 COPPER (POTENTIAL).
FT METAL 88 88 COPPER (POTENTIAL).
FT MOD_RES 500 500 PHOSPHORYLATION (BY SIMILARITY).
FT METAL 699 699 MAGNESIUM (BY SIMILARITY).
FT METAL 703 703 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 803 AA; 86024 MW; D9C8DA5D40326C6B CRC64;

Query Match 55.08; Score 44; DB 1; Length 803;
Best Local Similarity 66.78; Pred. NO. 13;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 4 GROLAIGDDIN 15
DB 691 GROLAIGDDIN 702

RESULT 9
CRTL_APHSP STANDARD; PRT; 532 AA.
AC P21134;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-2002 (Rel. 41, Last annotation update)
DE Phytene dehydrogenase (EC 1.14.99.-) (Phytene desaturase).
GN CRTL.
OS Aphnocapsa sp.
OC Bacteria; Cyanobacteria; Chroococcales; Aphnocapsa.
OX NCBI_TaxID=1120;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PC6 6714;
RX MEDLINE=90382685; PubMed=2119326;
RA Schmidt A., Sandmann G.;
RT Cloning and nucleotide sequence of the crtI gene encoding phytene
RT dehydrogenase from the cyanobacterium Aphnocapsa PCC6714.";
RL Gene 91:113-117(1990).

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CC -1- FUNCTION: THIS ENZYME CONVERTS PHYTOENE INTO ZETA-CAROTENE VIA THE
CC INTERMEDIARY OF PHYTOFLUENE BY THE SYMMETRICAL INTRODUCTION OF TWO
CC DOUBLE BONDS AT THE C-11 AND C-11' POSITIONS OF PHYTOENE.
CC -1- COFACTOR: NAD, NADP, OR FAD (PROBABLE).
CC -1- PATHWAY: CAROTENOID BIOSYNTHESIS.
CC -1- SIMILARITY: BELONGS TO THE PHYTOENE DEHYDROGENASE FAMILY.
CC -----
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CC -----
DR EMBL: M55647; AAA62573.1; -.
DR PIR: JN0084; JN0084.
KW Carotenoid biosynthesis; Oxidoreductase; FAD; Flavoprotein; NAD.
FT NP_BIND 22 49 FAD (ADP PART) (POTENTIAL).
SQ SEQUENCE 532 AA; 56754 MW; 06290C5A914B19F CRC64;

Query Match 54.48; Score 43.5; DB 1; Length 532;
Best Local Similarity 47.48; Pred. No. 10;
Matches 9; Conservative 5; Mismatches 2; Indels 3; Gaps 1;

OY 1 GQVGRLOAI---IGDDINR 16
DB 141 GQVGRLOAI---IGDDINR 159

RESULT 10
ENO_LYCES STANDARD; PRT; 444 AA.
AC P26300;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-
DE glycerate hydro-lyase).
GN Pchl.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. SUPERSONIC;
RX MEDLINE=93044507; PubMed=1841726;
RA van der Straeten D., Rodrigues-Pousada R.A., Goodman H.M.,
RA van Montagu M.;
RT Plant enolase: gene structure, expression, and evolution.";
RL Plant Cell 3:719-735(1991).
CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate -> phosphoenolpyruvate +
CC H(2)O.
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
CC THE DIMER (BY SIMILARITY).
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC -----
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CC -----
DR EMBL: X58108; CAA41115.1; -.
DR PIR: J01185; J01185.

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DR HSSP: P56252; 1PDZ.
 DR Mendel: 611; LYES: Pgh1.2.
 DR InterPro: IPR000941; ENOLASE.
 DR Pfam: PF00113; ENOLASE.1.
 DR PRINTS: PR00148; ENOLASE.
 DR ProDom: PD000902; ENOLASE.1.
 DR PROSITE: PS00164; ENOLASE.1.
 DR Lyase: Glycolysis; Magnesium.
 KW ACT_SITE 163 163 BY SIMILARITY.
 FT METAL 250 250 MAGNESIUM (BY SIMILARITY).
 FT METAL 300 300 MAGNESIUM (BY SIMILARITY).
 FT METAL 327 327 MAGNESIUM (BY SIMILARITY).
 SO SEQUENCE 444 AA; 47798 MW; 73C384181ED620A0 CRC64;

Query Match
 Best Local Similarity 46.2%; Score 43; DB 1; Length 446;
 Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 QVGRQAIIGDDI 14
 DB 317 EIGEVOIVGDDL 329
 : : 1 : 1 : 1 : 1 :
 : : 1 : 1 : 1 : 1 :
 : : 1 : 1 : 1 : 1 :

RESULT 11
 ENO2_MAIZE STANDARD; PRT; 446 AA.
 ID ENO2_MAIZE STANDARD; PRT; 446 AA.
 AC P42895;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Enolase 2 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 2).
 GN ENO2.
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
 OC Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. B73; TISSUE=Root;
 RX MEDLINE=99063764; PubMed=9847102;
 RA Lal S.K., Lee C., Sachs M.M.;
 RT "Differential regulation of enolase during anaerobiosis in maize.";
 RL Plant Physiol. 118:1285-1293(1998).
 CC -1 CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate + H(2O).
 CC -1 COPFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
 CC -1 PATHWAY: GLYCOLYSIS.
 CC -1 SUBUNIT: HOMODIMER.
 CC -1 SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1 SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
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 CC -----
 CC EMBL: U19793; AAC04187.1; -.
 DR HSSP: P56252; 1PDZ.
 DR MaizeDB: 30060; -.
 DR Mendel: 16623; Zeama:Pgh1.16623.
 DR InterPro: IPR000941; ENOLASE.
 DR Pfam: PF00113; ENOLASE.1.
 DR PRINTS: PR00148; ENOLASE.
 DR ProDom: PD000902; ENOLASE.1.
 DR PROSITE: PS00164; ENOLASE.1.
 DR Lyase: Glycolysis; Magnesium; Multigene family.
 KW

FT ACT_SITE 164 164 BY SIMILARITY.
 FT METAL 251 251 MAGNESIUM (BY SIMILARITY).
 FT METAL 302 302 MAGNESIUM (BY SIMILARITY).
 FT METAL 329 329 MAGNESIUM (BY SIMILARITY).
 SO SEQUENCE 446 AA; 48162 MW; DC27708CF92F6850 CRC64;

Query Match
 Best Local Similarity 46.2%; Score 43; DB 1; Length 446;
 Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 QVGRQAIIGDDI 14
 DB 319 EIGEVOIVGDDL 331
 : : 1 : 1 : 1 : 1 :
 : : 1 : 1 : 1 : 1 :
 : : 1 : 1 : 1 : 1 :

RESULT 12
 ENO_ORYZA STANDARD; PRT; 446 AA.
 ID ENO_ORYZA STANDARD; PRT; 446 AA.
 AC Q42971;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) (OSE1).
 GN Oryza sativa (Rice).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Euphorbiaceae; Oryzaeae; Oryza.
 OX NCBI_TaxID=4530;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. TAINING 67; TISSUE=Seed;
 RA Hsing Y.-I.C., Tsao C.-W., Hsieh J.-S., Chen Z.-Y., Shu T.-F.,
 RA Chow T.-Y.;
 RT "A rice early embryogenesis-specific enolase cDNA";
 RL (In) Plant Gene Register PGR95-084.
 CC -1 CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate + H(2O).
 CC -1 COPFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER.
 CC -1 PATHWAY: GLYCOLYSIS.
 CC -1 SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1 SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1 DEVELOPMENTAL STAGE: EXPRESSED DURING EARLY EMBRYOGENESIS.
 CC -1 SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
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 CC -----
 CC EMBL: U09450; AAC49173.1; -.
 DR HSSP: P56252; 1PDZ.
 DR InterPro: IPR000941; ENOLASE.
 DR Pfam: PF00113; ENOLASE.1.
 DR PRINTS: PR00148; ENOLASE.
 DR ProDom: PD000902; ENOLASE.1.
 DR PROSITE: PS00164; ENOLASE.1.
 KW Lyase: Glycolysis; Magnesium.
 KW ACT_SITE 164 164 BY SIMILARITY.
 FT METAL 251 251 MAGNESIUM (BY SIMILARITY).
 FT METAL 302 302 MAGNESIUM (BY SIMILARITY).
 FT METAL 329 329 MAGNESIUM (BY SIMILARITY).
 SO SEQUENCE 446 AA; 47986 MW; FECDB1319246D477 CRC64;

Query Match
 Best Local Similarity 46.2%; Score 43; DB 1; Length 446;
 Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 2 QVGRQLAIGDDI 14
 Db 319 EIGEOVQIVGDDL 331

RESULT 13
 ID YRN9_CAEEL STANDARD: PRT: 770 AA.

AC 009609;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Hypothetical 84.2 kDa protein R07B1.9 in chromosome X.

GN R07B1.9.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 CC Rhabditidae; Peloderinae; Caenorhabditis.
 NCBI_TaxID=6239;

RM SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Kershaw J.;
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.

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DR EMBL: Z48621; CAAB8546.1;
 DR Wormpep: R07B1.9; CE01635.
 KM Hypothetical protein.
 SQ SEQUENCE 770 AA: 84235 MW: 428A80C594ACBBDB8 CRC64;

Query Match 53.8%; Score 43; DB 1; Length 770;
 Best Local Similarity 56.2%; Pred. No. 18;
 Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 GOVGRQLAIGDDINR 16
 Db 738 GQCGSPANVGVDDPNR 753

RESULT 14
 ID ATC2_RHIME STANDARD: PRT: 827 AA.

AC P58342;
 DT 01-MAR-2002 (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DE Copper-transporting ATPase 2 (EC 3.6.3.4).
 GN ACTP2 OR ATC2 OR R81018 OR S8A21578.

OS Rhizobium meliloti (Sinorhizobium meliloti).
 OC Plasmid psymb (megaplasmid 2).
 CC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 CC Rhizobiaceae; Sinorhizobium.

NCBI_TaxID=382;
 RM SEQUENCE FROM N.A.
 RC STRAIN=1021;

RA MEDLINE=21396508; PubMed=11481431;
 RA Finn T.M., Meldner S., Wong K., Buhrmester J., Chain P.,
 RA Vorholter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,
 RA Golding B., Piehler A.;
 RT "The complete sequence of the 1,683-kb psymb megaplasmid from the N2-
 RT fixing endosymbiont Sinorhizobium meliloti."
 RT Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
 CC -1- FUNCTION: INVOLVED IN COPPER TRANSPORT (BY SIMILARITY).

CC -1- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + ORTHOPHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
 CC (E1-E2 ATPASES). SUBFAMILY 1B.

CC -1- SIMILARITY: CONTAINS 2 HMA DOMAINS.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).

DR EMBL: A1603645; CAC49418.1;
 DR PROSITE: PS00154; ATPASE_E1_E2; 1.
 DR PROSITE: PS01047; HMA_1; 2.
 KM Hydrolyase; Transmembrane; Phosphorylation; Magnesium; ATP-binding;
 KM Metal-binding; Copper; Repeat; Plasmid; Complete proteome.

FT TRANSMEM 174 194 POTENTIAL.
 FT TRANSMEM 210 230 POTENTIAL.
 FT TRANSMEM 246 266 POTENTIAL.
 FT TRANSMEM 271 291 POTENTIAL.
 FT TRANSMEM 430 450 POTENTIAL.
 FT TRANSMEM 458 478 POTENTIAL.
 FT TRANSMEM 771 793 POTENTIAL.
 FT TRANSMEM 797 819 POTENTIAL.

FT DOMAIN 16 81 HMA 1.
 FT DOMAIN 83 149 HMA 2.
 FT METAL 26 26 COPPER (POTENTIAL).
 FT METAL 29 29 COPPER (POTENTIAL).
 FT METAL 93 93 COPPER (POTENTIAL).
 FT METAL 96 96 COPPER (POTENTIAL).
 FT MOD_RES 515 515 PHOSPHORYLATION (BY SIMILARITY).
 FT METAL 714 714 MAGNESIUM (BY SIMILARITY).
 FT METAL 718 718 MAGNESIUM (BY SIMILARITY).
 SQ SEQUENCE 827 AA: 85861 MW: A3DBDFDD1315FBC CRC64;

Query Match 53.8%; Score 43; DB 1; Length 827;
 Best Local Similarity 64.3%; Pred. No. 20;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 2 QVGRQLAIGDDIN 15
 Db 704 QGGRSVAFIGDGIN 717

RESULT 15
 ID ATC2_RHIME STANDARD: PRT: 827 AA.

AC O9X5X3;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Copper-transporting ATPase (EC 3.6.3.4).

GN ACTP.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 CC Rhizobiaceae; Sinorhizobium.

NCBI_TaxID=382;
 RM SEQUENCE FROM N.A.
 RC STRAIN=MSM419;

RA Reeve W.G., Tiwari R.P., Kale N.B., Dilworth M.J., Glenn A.R.;
 RA "The role of copper and P-type ATPase in the acid-tolerance of
 RA Rhizobium leguminosarum by vicila and Sinorhizobium meliloti."
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: INVOLVED IN COPPER TRANSPORT (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + ORTHOPHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY

```

CC      (E1-E2 ATPASES). SUBFAMILY 1B.
CC      -1- SIMILARITY: CONTAINS 2 HMA DOMAINS.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: AF129004; AAD27639.1; -.
DR      HSP: O04656; IAWO.
DR      InterPro: IPR001366; Cat_ATPase.
DR      InterPro: IPR000579; Cat_P_ATPase.
DR      InterPro: IPR001757; E1-E2_ATPase.
DR      InterPro: IPR001802; HG_scarvenger.
DR      InterPro: IPR001934; HMA.
DR      InterPro: IPR001454; Hydrolase.
DR      Pfam: PF00122; E1-E2_ATPase; 1.
DR      Pfam: PF00403; HMA; 2.
DR      Pfam: PF00702; Hydrolase; 1.
DR      PRINTS: PR00119; CATATPASE.
DR      PRINTS: PR00940; CATPATPASE.
DR      PRINTS: PR00941; CDATPASE.
DR      PRINTS: PR00946; HGSCAVENGER.
DR      PROSITE: PS00154; ATPASE_E1_E2; 1.
DR      PROSITE: PS01047; HMA_1; 2.
DR      PROSITE: PS00846; HMA_2; 2.
DR      Hydrolase; Transmembrane; Phosphorylation; Magnesium; ATP-binding;
KW      Metal-binding; Copper; Repeat.
FT      TRANSMEM 174 194 POTENTIAL.
FT      TRANSMEM 210 230 POTENTIAL.
FT      TRANSMEM 248 268 POTENTIAL.
FT      TRANSMEM 271 291 POTENTIAL.
FT      TRANSMEM 430 450 POTENTIAL.
FT      TRANSMEM 458 478 POTENTIAL.
FT      TRANSMEM 541 561 POTENTIAL.
FT      TRANSMEM 569 589 POTENTIAL.
FT      TRANSMEM 727 747 POTENTIAL.
FT      TRANSMEM 773 793 POTENTIAL.
FT      TRANSMEM 795 815 POTENTIAL.
FT      DOMAIN 16 81 HMA 1.
FT      METAL 83 149 HMA 2.
FT      METAL 26 26 COPPER (POTENTIAL).
FT      METAL 29 29 COPPER (POTENTIAL).
FT      METAL 93 93 COPPER (POTENTIAL).
FT      METAL 96 96 COPPER (POTENTIAL).
FT      MOD_RES 515 515 PHOSPHORYLATION (BY SIMILARITY).
FT      METAL 714 714 MAGNESIUM (BY SIMILARITY).
FT      METAL 718 718 MAGNESIUM (BY SIMILARITY).
SQ      SEQUENCE 827 AA; 86239 MF; 707E2148DDA5004 CRC64;

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Query Match          53.8%; Score 43; DB 1; Length 827;
Best Local Similarity 64.3%; Pred. No. 20;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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QY      2 OVEROLAITGDDIN 15
       1 1 1 1 1 1 1 1 1
DB      704 QGGRSVAFIGDGIN 717

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Search completed: September 20, 2002, 11:04:33
Job time: 1630 sec

GenCore version 4.5
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OM protein - protein search, using SW model

Run on: September 20, 2002, 11:03:44 : Search time 172.19 Seconds
(without alignments)
16.075 Million cell updates/sec

Title: US-09-544-664-30

Perfect score: 80

Sequence: 1 GOVGR0LATIGDDINR 16

Scoring table: GAPOP 10.0, GAPEXT 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP_ARCHAEA:19:1
2: SP_BACTERIA:19:1
3: SP_FUNGI:19:1
4: SP_HUMAN:19:1
5: SP_INVERTEBRATE:19:1
6: SP_MAMMAL:19:1
7: SP_MHC:19:1
8: SP_ORNITHINE:19:1
9: SP_PHASE:19:1
10: SP_PLANT:19:1
11: SP_RODENT:19:1
12: SP_VIRUS:19:1
13: SP_VIRUS:19:1
14: SP_UNCLASSIFIED:19:1
15: SP_VIRUS:19:1
16: SP_BACTERIA:19:1
17: SP_ARCHAEA:19:1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	80	100.0	80	6 077738	077738 sus.scrofa
2	79	98.8	163	6 09M256	09M256 ovls.aries
3	78	97.5	151	11 091KX5	091KX5 mus.musculi
4	78	97.5	209	11 09JX59	09JX59 rattus.norv
5	46.5	58.1	357	10 09S253	09S253 aradidopsi
6	46.5	57.5	915	16 09K227	09K227 vibrio.chol
7	44	55.0	258	17 09UXV1	09UXV1 pyrococcus
8	44	55.0	261	17 057733	057733 pyrococcus
9	44	55.0	556	10 09LH16	09LH16 aradidopsi
10	44	55.0	593	16 P73239	P73239 synochocyst
11	44	55.0	608	10 09PC35	09PC35 aradidopsi
12	44	55.0	693	16 09PC32	09PC32 xyella.fas
13	43.5	54.4	355	10 081716	081716 aradidopsi
14	43	53.8	421	16 098KM2	098KM2 rhizobium
15	43	53.8	447	16 09CD42	09CD42 mycobacteri
16	43	53.8	475	10 09LZ01	09LZ01 aradidopsi

17	43	53.8	664	10 022716	022716 aradidopsi
18	42	52.5	326	4 014558	014558 homo.sapien
19	42	52.5	326	4 096108	096108 homo.sapien
20	42	52.5	326	11 085168	085168 rattus.norv
21	42	52.5	326	11 080204	080204 mus.musculi
22	42	52.5	369	11 080256	080256 mus.musculi
23	42	52.5	369	11 080256	080256 mus.musculi
24	42	52.5	369	11 080256	080256 mus.musculi
25	42	52.5	369	11 080256	080256 mus.musculi
26	42	52.5	369	11 080256	080256 mus.musculi
27	42	52.5	369	11 080256	080256 mus.musculi
28	42	52.5	369	11 080256	080256 mus.musculi
29	42	52.5	369	11 080256	080256 mus.musculi
30	42	52.5	369	11 080256	080256 mus.musculi
31	42	52.5	369	11 080256	080256 mus.musculi
32	42	52.5	369	11 080256	080256 mus.musculi
33	42	52.5	369	11 080256	080256 mus.musculi
34	42	52.5	369	11 080256	080256 mus.musculi
35	42	52.5	369	11 080256	080256 mus.musculi
36	42	52.5	369	11 080256	080256 mus.musculi
37	42	52.5	369	11 080256	080256 mus.musculi
38	42	52.5	369	11 080256	080256 mus.musculi
39	42	52.5	369	11 080256	080256 mus.musculi
40	42	52.5	369	11 080256	080256 mus.musculi
41	42	52.5	369	11 080256	080256 mus.musculi
42	42	52.5	369	11 080256	080256 mus.musculi
43	42	52.5	369	11 080256	080256 mus.musculi
44	42	52.5	369	11 080256	080256 mus.musculi
45	42	52.5	369	11 080256	080256 mus.musculi

ALIGNMENTS

RESULT 1	PRELIMINARY:	PRT:	80 AA.
ID 077738	AC 077738	PT 01-NOV-1998 (TREMUR1.08, Created)	
PT 01-NOV-1998 (TREMUR1.08, Last sequence update)	DT 01-DEC-2001 (TREMUR1.19, Last annotation update)	DE BAK PROTEIN (FRAGMENT)	
DE BAK PROTEIN (FRAGMENT)	CN BAK	OS sus.scrofa (pig)	
OS sus.scrofa (pig)	OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:	OC Mammalia: Eutheria: Cetartiodactyla: Suina: Suidae: Sus.	
OC Mammalia: Eutheria: Cetartiodactyla: Suina: Suidae: Sus.	CX NCBI_TaxID=9823:	RN [1]	
RN [1]	RP SOURCE FROM N.A.	RP Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darner D.:	
RP Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darner D.:	RT "Expression of apoptosis-associated genes in hibernating and stunned	RT myocardium of pig."	
RT myocardium of pig."	RL Submitted (JAN-1998) to the EMBL/Genbank/DBJ databases.	DR EMBL: AJ001204; CAA04598.1; -	
DR EMBL: AJ001204; CAA04598.1; -	DR HSSP: Q16611; 1BXL	DR InterPro: IPR002475; BCL2_family.	
DR InterPro: IPR002475; BCL2_family.	DR InterPro: IPR000712; BCL-2.	DR Pfam: PF00452; BCL-2.1.	
DR Pfam: PF00452; BCL-2.1.	DR SMART: SM00337; BCL-1.	DR PROSITE: PS00662; BCL1_FAMILY: 1.	
DR PROSITE: PS00662; BCL1_FAMILY: 1.	DR PROSITE: PS01259; BH3: 1.	FT NON_TER	
FT NON_TER	FT NON_TER	FT NON_TER	
FT NON_TER	SEQUENCE	80 AA: 80 MW: 8818 MW: FDIAP3BD7D59C86 CRC64:	
SEQUENCE	80 AA: 80 MW: 8818 MW: FDIAP3BD7D59C86 CRC64:	Query Match	
Query Match	Best local similarity	100.0%; Score 80; DB 6; Length 80;	
Best local similarity	Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1 GOVGR0LATIGDDINR 16	
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1 GOVGR0LATIGDDINR 16	23 GOVGR0LATIGDDINR 38	


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RA Terryn N., Ardiles W., Buysshaert C., Dasseville R., De Clerck R.,
RA De Keyser A., Neyt P., Rouze P., Van Den Daele H., Villaroel R.,
RA Gielen J., Van Montagu M., Mewes H.W., Lemcke K., Mayer K.F.X.,
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
RA Bossert L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jiang P.X., Jones T., Kamuya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinzaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RA "Arabidopsis cDNA clones.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL049607; CAB40756.1; -
DR EMBL: AL161579; CAB79904.1; -
DR EMBL: AY057611; AAL14406.1; -
DR HSSP: P35813; 1A60.
DR InterPro: IPR000222; PP2C.
DR InterPro: IPR001932; PP2C_domain.
DR Pfam: PF00481; PP2C; 2.
DR SMART: SM00332; PP2C; 1.
DR SMART: SM00331; PP2C_SIG; 1.
DR PROSITE: PS01032; PP2C; 1.
DR SEQUENCE 357 AA; 39203 MW; 98EE1A09818CA0D3 CRC64;

Query Match 58.1%; Score 46.5; DB 10; Length 357;
Best Local Similarity 58.8%; Pred. No. 13;
Matches 10; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

QY 1 GQVGRQLAITGDINDR 16
DB 104 GQGRGRELAVGDKINK 120

RESULT 6
OQKP27 PRELIMINARY; PRT; 915 AA.
AC GQKP27;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE CATION TRANSPORT ATPASE, E1-E2 FAMILY.
GN VC2215.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subphylum; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-EL TOR N16961 / SEROTYPE O1;
RX MEDLINE-20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RA "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae.";
RL Nature 406:477-483(2000).
DR EMBL: AE004293; AAF93559.1; -
DR HSSP: P04129; IAF.
DR TIGR: VC2215; -
DR InterPro: IPR000579; Cat_P_ATPaseA.
DR InterPro: IPR001757; E1-E2_ATPase.

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DR InterPro: IPR001802; HG_scavenger.
DR InterPro: IPR001934; HMA.
DR InterPro: IPR001454; Hydrolyase.
DR InterPro: IPR000150; Hypothet_cof.
DR Pfam: PF00122; E1-E2_ATPase; 1.
DR Pfam: PF00403; HMA; 3.
DR Pfam: PF00702; Hydrolyase; 1.
DR PRINTS: PR00119; CATAPARSE.
DR PRINTS: PR00940; CATAPARSEA.
DR PROSITE: PS00154; ATPASE_E1_E2; UNKNOWN_1.
DR PROSITE: PS01229; COF_2; UNKNOWN_1.
DR PROSITE: PS01047; HMA; 1.
KW Complete proteome.
SQ SEQUENCE 915 AA; 97311 MW; 2F31EE2640AD0D20 CRC64;

Query Match 57.5%; Score 46; DB 16; Length 915;
Best Local Similarity 64.3%; Pred. No. 44;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 QVGRQLAITGDINDR 15
DB 786 QQGRKVMAMIGDGIN 799

RESULT 7
OQUXV1 PRELIMINARY; PRT; 258 AA.
AC QQUXV1;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE SV-ATPASE PROTEOLIPID.
GN PAB1189.
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
OX NCBI_TaxID=29292;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-ORSAY;
RA Heilig R.;
RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
RT structure and evolution.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ248288; CAB50662.1; -
DR InterPro: IPR004089; Chemotaxis_transducer.
DR InterPro: IPR004090; Me_chemotaxis.
DR Pfam: PF00015; MCPsignal; 1.
DR PRINTS: PR00260; CHEMTRNSDUCR.
DR SMART: SM00283; MA; 1.
KW Complete proteome.
SQ SEQUENCE 258 AA; 29033 MW; EDEB44AC4B515112 CRC64;

Query Match 55.0%; Score 44; DB 17; Length 258;
Best Local Similarity 43.8%; Pred. No. 23;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 GQVGRQLAITGDINDR 16
DB 122 GFAGRGFAVAVDEIR 137

RESULT 8
O57733 PRELIMINARY; PRT; 261 AA.
AC O57733;
DT 01-AUG-1998 (TREMblrel. 07, Created)
DT 01-AUG-1998 (TREMblrel. 07, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE 261AA LONG HYPOTHETICAL CHEMORECEPTOR PROTEIN.
GN PH1970.

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OS Pyrococcus horikoshii.
 OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
 NC NCBL_TaxID=53953;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-073;
 RX MEDLINE=98344137; PubMed=9679194;
 RA Kawarabayashi Y., Sawada M., Horikawa H., Halkawa Y., Hino Y.,
 Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
 Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
 Funahashi T., Tanaka T., Kudo Y., Yamazaki J., Kishida N., Oguchi A.,
 Aoki K.-I., Yoshizawa H., Nakamura Y., Nobb F.T., Horikoshi K.,
 Masuchi Y., Shizuya H., Kikuchi H.;
 RA "Complete sequence and gene organization of a hyper-
 thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
 RT Thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
 RL DNA Res. 5:55-76(1998)
 DR EMBL: AP000007; BAA31097.1;
 DR InterPro: IPR004089; Chemotaxis_transducer.
 DR Pfam: PF00015; MCPsignal; 1.
 DR SMART: SM00283; MA; 1.
 KW Complete proteome.
 SQ SEQUENCE 261 AA; 29234 MW; 2FDDC7CC08223D46 CRC64;

Query Match 55.0%; Score 44; DB 17; Length 261;
 Best Local Similarity 43.8%; Pred. No. 24;
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Oy 1 GCGGRLAIGDDINR 16
 Db 125 GEAGRGFAVVADEIRR 140

RESULT 9
 ID 09LH6 PRELIMINARY; PRT; 556 AA.
 AC 09LH6;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE G1AIAFP0301.1 (HYPOTHETICAL 63.0 KDA PROTEIN).
 GN T21B14.12.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eucosids II; Brassicales; Brassicaceae; Arabidopsis.
 NC NCBL_TaxID=3702;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-COLUMBIA;
 RX Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
 RL Submitted (MAV-2000) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-COLUMBIA;
 RX PubMed=10907853;
 RA Nakamura Y.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
 RT Sequence features of the regions of 4,251,695 bp covered by ninety P1,
 RT TAC and BAC clones.";
 RL DNA Res. 7:217-221(2000).
 [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RX MEDLINE=21016720; PubMed=11130713;
 RA Salanoubat M., Lemcke K., Rieger M., Ansoerg W., Unseld M.,
 Faltmann B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
 Delesny M., Boutry M., Grivell L.A., Mache R., Paulgomech P.,
 De Simone V., Choise N., Artiguenave F., Robert C., Brottier P.,
 Wincker P., Cattellico L., Weissenbach J., Safran W., Queller F.,
 Schefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
 Wurthmann E., Drzonek H., Erfle H., Jordan N., Bangerter S.,
 Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,

RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,
 Conrad A., Hornischer K., Kaen G., Loenert T.H., Norisick G.,
 RA Reichelt J., Scharfe M., Schuen O., Bargues M., Terol J., Clement J.,
 RA Navarro P., Collado C., Perez-Perez A., Oltmawelder B., Duchemin D.,
 RA Cooke R., Laurie M., Berger-Llauró C., Purnelle B., Masuy D.,
 RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
 RA Montfort A., Argitrou A., Flores M., Liguori R., Vitale D.,
 RA Mannhaupt G., Haase D., Schoof H., Rüd S., Zaccaria P., Mewes H.-W.,
 RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
 RA Rooney T., Rizzo M., Wals A., Ulteback T., Fujii C.Y., Shea T.P.,
 RA Creasy T.H., Haas B., Maiti R., Mu D., Peterson J., Van Aken S.,
 RA Pail G., Miltsher J., Sellers P., Gill J.E., Feldblyum T.V.,
 RA Preus D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
 RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
 RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida T.,
 RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakayama S., Nakazaki N., Shino S., Takeuchi C., Wada T.,
 RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
 RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
 RT thaliana.";
 RL Nature 408:820-822(2000).
 DR EMBL: AP002040; BAB03118.1;
 DR EMBL: AC069473; AAC51057.1;
 KW Hypothetical protein.
 SQ SEQUENCE 556 AA; 63004 MW; F697359ABB7213F CRC64;

Query Match 55.0%; Score 44; DB 10; Length 556;
 Best Local Similarity 53.8%; Pred. No. 55;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 4 GRLAIGDDINR 16
 Db 262 GRLVFGDSLNR 274

RESULT 10
 ID P73239 PRELIMINARY; PRT; 593 AA.
 AC P73239;
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE ABC TRANSPORTER.
 GN SLR2019.
 OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 NC NCBL_TaxID=1148;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97061201; PubMed=8905231;
 RA Kaneko T., Sato S., Kocani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hirose M., Sugita M., Sasamoto S., Kimura T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
 RA Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
 RA Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions.";
 RL DNA Res. 3:109-136(1996).
 CC -I- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
 CC (ABC TRANSPORTERS).
 CC EMBL: D90904; BAA17266.1;
 DR InterPro: IPR003593; AAA.
 DR InterPro: IPR001140; ABC_transporter_tmam.
 DR InterPro: IPR003439; ABC_transporter.
 DR InterPro: IPR001687; ATP_GTP_A.
 DR Pfam: PF00064; ABC_membrane; 1.
 DR Pfam: PF00005; ABC_tran; 1.
 DR SMART: SM00382; AAA; 1.
 DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
 KW ATP-binding; Complete proteome; Transport.
 SQ SEQUENCE 593 AA; 65761 MW; DA48CE3DDDAC6C9 CRC64;

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Query Match          55.0%; Score 44; DB 16; Length 593;
Best Local Similarity 61.5%; Pred. No. 59;
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OY 4 GROLATIGDDINR 16
  11:111:1111:
DB 128 GRMLATLNDINDNO 140

RESULT 11
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AC O9FC35;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE EMBL|CA82953.1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_Taxid=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-COLUMBIA;
RA Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,
RA Tabata S.;
RT *Structural analysis of Arabidopsis thaliana chromosome 5. XI.*;
RL Submitted (MAY-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; A002033.2; BAB09804.1; -.
DR InterPro: IPR000531; TrnB_box.
DR PROSITE: PS00430; TrnB_DEPENDENT_REC_1; UNKNOWN.1.
SQ SEQUENCE 608 AA; 67925 MW; 7355DF42E697586C CRC64;

Query Match          55.0%; Score 44; DB 10; Length 608;
Best Local Similarity 53.8%; Pred. No. 60;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 4 GROLATIGDDINR 16
  11:111:111:11
DB 321 GRRLVFGDSLNR 333

RESULT 12
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DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
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DE XFL1953.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xylella.
OX NCBI_Taxid=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-9A5C;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvaranga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Britones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carter H.,
RA Colaço N.B., Colombo A., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
RA Facinani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.R.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohne M., Furlan L.R.,
RA Gantier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hohnselt J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,

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RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.V., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A.Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silveira J.F., Silvestri M.L.Z., Sigueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsubako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa."
RL Nature 406:151-159(2000).
DR EMBL; AE004014; AAF84755.1; -.
DR HSSP: P02942; 1007.
DR InterPro: IPR004089; Chemotaxis_transducer.
DR InterPro: IPR004090; Me_chemotaxis.
DR Pfam: PF00015; MCP_signal; 1.
DR PRINTS: PR00260; CHEMTRNSDCR.
DR SMART: SM00283; MA; 1.
DR Complete proteome.
SQ SEQUENCE 693 AA; 74235 MW; EAD48C73BF573D80 CRC64;

Query Match          55.0%; Score 44; DB 16; Length 693;
Best Local Similarity 43.8%; Pred. No. 70;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

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  11:111111:11:1
DB 550 GEAGRGFAIVADVDOR 565

RESULT 13
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AC O81716;
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DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE HYPOTHETICAL 39.4 KDA PROTEIN.
DE AT2G25070.
GN Arabidopsis thaliana (Mouse-ear cress).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_Taxid=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., Vanaken S.E., Umeyam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Coppenhaver G.P., preuss D., Niernan W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana."
RL Nature 402:761-768(1999).
RN [12]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
[13]
RP SEQUENCE FROM N.A.

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Fri Sep 20 11:03:13 2002

Job time: 1663 sec

us-09-544-664-30.rspt

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 20, 2002, 10:35:58 ; Search time 228.86 Seconds
(without alignments)
7.765 Million cell updates/sec

Title: US-09-544-664-32
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Searched: 747574 seqs, 11073796 residues

Total number of hits satisfying chosen parameters: 747574

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81	100.0	16	21 AAB37032	Bcl2 polypeptide B
2	81	100.0	24	20 AAY05411	Human Bcl-2 domain
3	81	100.0	26	17 AAM06298	CD domain region f
4	81	100.0	26	21 AAY96323	Mammalian Bax, Bcl-2
5	81	100.0	26	22 AAB70373	Bax BH3 consensus
6	81	100.0	27	21 AAB37006	Bcl2 polypeptide B
7	81	100.0	34	20 AAY05430	Human Bax BH3 domain
8	81	100.0	78	21 AAY70818	Human neuroprotect
9	81	100.0	131	20 AAY34149	Human truncated Bax
10	81	100.0	192	16 AAR71406	Human Bax protein
11	81	100.0	192	20 AAY34150	Human wild-type Bax

12	81	100.0	192	20 AAY05435	Human BAX protein
13	81	100.0	192	20 AAM87804	A human Bcl-2 asso
14	81	100.0	192	20 AAM87809	A human Bcl-2 asso
15	81	100.0	192	21 AAY70827	Human BAX alpha pr
16	81	100.0	192	21 AAY69202	Amino acid sequenc
17	81	100.0	192	22 AAB74121	Human bcl-2 associ
18	81	100.0	192	22 AAB74126	Human bcl-2 associ
19	81	100.0	192	22 AAB46286	Human Bcl protein
20	81	100.0	192	22 AAB35129	Human Bax. Homo s
21	81	100.0	192	22 AAB50539	Human Bax protein
22	81	100.0	197	21 AAY76512	Truncated Bax amin
23	81	100.0	221	18 AAM10688	Bax omega protein
24	81	100.0	331	20 AAY39263	Coding region of c
25	78	96.3	16	20 AAY05426	Mouse Bax BH3 doma
26	78	96.3	16	21 AAB37033	Bcl2 polypeptide B
27	78	96.3	24	21 AAY70824	Mouse neuroprotect
28	78	96.3	27	21 AAB37007	Bcl2 polypeptide B
29	78	96.3	78	21 AAY70819	Mouse neuroprotect
30	78	96.3	192	16 AAR71407	Mouse Bax protein
31	78	96.3	192	20 AAY05434	Mouse Bax protein
32	78	96.3	192	20 AAM87805	Murine Bcl-2 assoc
33	78	96.3	192	20 AAM87808	Murine Bcl-2 assoc
34	78	96.3	192	21 AAY70828	Mouse Bax alpha pr
35	78	96.3	192	22 AAB74122	Murine bcl-2 assoc
36	78	96.3	192	22 AAB74125	Murine bcl-2 assoc
37	78	96.3	192	22 AAB35128	Murine Bax. Mus s
38	77	95.1	15	20 AAY05412	Human Bax BH3 doma
39	77	92.6	16	20 AAY05425	Human Bax BH3 doma
40	73	90.1	16	21 AAB37034	Bcl2 polypeptide B
41	71	87.7	15	17 AAM06296	Bcl2 polypeptide B
42	71	87.7	15	22 AAB85171	BH3 domain of Bax
43	71	87.7	15	22 AAB61183	Human Bax BH3 doma
44	71	87.7	70	21 AAY70816	Human neuroprotect
45	68	84.0	70	21 AAY70817	Mouse neuroprotect

ALIGNMENTS

RESULT	ID	Sequence	Score	Length	Description
1	AAB37032	standard; peptide; 16 AA.	81	16	Bcl2 polypeptide BH3 domain peptide #32.
XX	AC	AAB37032:	81	16	28-FEB-2001 (first entry)
XX	DT	28-FEB-2001 (first entry)	81	16	Bcl2 polypeptide BH3 domain peptide #32.
XX	DE	Bcl2 polypeptide BH3 domain peptide #32.	81	16	Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;
XX	KW	cardiac; Bcl-2 superfamily; BH3 domain; cell death agonist; Bax;	81	16	apoptosis modulator; B cell lymphoma/leukemia 2; cancer; prostate;
XX	KW	colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;	81	16	melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
XX	KW	stroke; myocardial infarction.	81	16	
XX	OS	Homo sapiens.	81	16	
XX	PN	W0200059526-A1.	81	16	
XX	PD	12-OCT-2000.	81	16	
XX	PF	06-APR-2000; 2000MO-US09352.	81	16	
XX	PR	07-APR-1999; 99US-0128202.	81	16	
XX	PA	(UYJE-) UNIV JEFFERSON THOMAS.	81	16	
XX	PI	Huang Z, Wang J, Zhang Z, Shan S, Lu Z;	81	16	
XX	DR	WPI; 2000-679325/66.	81	16	
XX	PT	New peptide conjugates for modulating apoptosis or for inhibiting B	81	16	

PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for
PT treating neurodegenerative disorders, stroke, or cancer -
XX
PS Claim 18; Page 18; 74pp; English.

CC The invention relates to a peptide conjugate having the formula:
CC (R-X)_n-peptide where n = 1-10; X = C=O, when the R-X group is attached
CC to the N-terminus of the peptide, or a side chain of the peptide where
CC the functional group of the side chain is NH₂ or OH; or X = O or NH,
CC when the R-X group is attached to the C-terminus of the peptide, or a
CC side chain of the peptide, where the side chain functional group is COOH
CC or CONH₂; and R = 2-18C alkyl or alkoxy, 2-14C alkenyl containing one
CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally
CC monosubstituted with a 1-5C straight or branched chain alkyl group,
CC phenyl optionally monosubstituted with a 1-5C straight or branched chain
CC alkyl group, or benzyl. The peptides AAM37601-B37058 represent examples
CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of
CC the Bcl-2 domain of the cell death agonist bcl-2. The peptide conjugate is
CC useful for modulating apoptosis in the cells of a subject, or for
CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of
CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2
CC function. In particular, the peptide conjugate is useful for treating a
CC subject afflicted with a cancer characterized by cancer cells that
CC express Bcl-2. The cancer includes prostate, colorectal, gastric,
CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or
CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
CC conjugate is also useful for treating disorders characterized by
CC increased apoptosis, e.g. neurodegenerative disorders, acquired
CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
XX

Query Match	100.0%	Score 81	DB 21	Length 16
Best Local Similarity	100.0%	Pred. NO. 9.3e-07		
Matches 16	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	KKUSECTKRIQDELD	16	
db	1	kkiseclkrigdeids	16	

RESULT 2
AAV05411
ID AAV05411 standard; peptide; 24 AA.
XX
XX AC
XX AAV05411;
DT 02-JUL-1999 (first entry)
XX
XX
DE Human BAX BH3 domain.
XX
XX BH3 domain; cell death agonist; bcl homology domain; BCL-2 family;
KW apoptosis promoter; cancer cell; virus infected cell; inflammation;
KW autoantibody producing cell; cancer; lymphoproliferative condition;
KW arthritis; autoimmune disease; therapy.

OS	Homo sapiens.
XX	
PN	MO9916787-A1.
XX	
PD	08-APR-1999.
XX	
PF	22-SEP-1998; 98MO-US19765
XX	
PR	07-OCT-1997; 97US-0946039
PR	26-SEP-1997; 97US-0060133
XX	
PA	(UNIT) UNIV WASHINGTON.
XX	
P1	Korameyer SJ;
XX	

DR	WPI; 1999-255058/21.
XX	
PT	Bcl homology domain 3 polypeptide
XX	
PS	Claim 4; Fig 17a; 104pp; English.

CC This sequence represents a bcl homology domain 3 (BH3 domain) of the
CC invention, derived from a proapoptotic member of the BCL-2 family. The
CC BH3 polypeptide can be used in a method for promoting apoptosis in a
CC target cell, especially where the cell is a cancer cell, a virus infected
CC cell, or an autacombody producing cell. The BH3 polypeptide can be used
CC in therapeutic compositions for treating disease including cancer, other
CC lymphoproliferative conditions, arthritis, inflammation, and autoimmune
CC diseases, which may result from the down regulation of cell death
CC regulation.

Seq	Sequence	24 AA:
Query	Match	100.0%; Score 81; DB 20; Length 24;
	Best Local Similarity	100.0%; Pred. No. 1,4e-06;
Matches	16; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 KKLSECLKRTGDELDLS	16
db	5 KKLSECLKRTGDELDLS	20

RESULT	3	
AAW06298		
ID	AAW06298	standard; Peptide: 26 AA.
XX		
AC	AAW06298;	
XX		
DT	29-JUL-1997	(first entry)
XX		
DE	GD domain region for Bax amino acid residues 52-77.	
XX		
KW	Apoptosis; follicular lymphoma; tumour; p53; antibody.	
XX		
OS	Synthetic.	
XX		
PN	WO9635951-A1.	
XX		
PD	14-NOV-1996.	
XX		
PE	06-MAY-1996; 96WO-US06122.	
XX		
PR	12-MAY-1995; 95US-0440391.	
XX		
PA	(IMMU-) IMMUNOGEN INC.	
XX		
PI	Chiltenden TD, Lutz RJ;	
XX		
DR	WPI; 1996-518805/51.	
XX		
DR	N-PSDB; AAT42431.	
XX		
PT	Peptide(s) comprising GD domains - have similar activities to wild	
PT	type Bax, and cause cellular apoptosis for treatment of viral	
PT	Infection	
XX		
PS	Claim 2; Page 52; 69pp; English.	

The term GD domain refers to a protein domain first identified in Bak and shown to be essential for the interaction of Bak with Bcl-x(l) and for Bak's cell killing function; and to peptides and/or molecules capable of mimicking its structure and/or function. The present sequence represents a GD domain corresponding to amino acid residues 52-77 of Bak. An antibody raised against a GD domain may be used to screen a cDNA expression library for clones comprising cDNA inserts encoding immunoreactive proteins. Truncated GD domain peptides have been shown to maintain the protein binding and cell killing function exhibited by wild type Bak. These molecules may induce apoptosis in

CC tumour cell. These peptides act independently of p53 status. Bak or
 CC CD domain mimetics that inhibit Bcl-2 may be selectively toxic to
 CC certain tumours, e.g. follicular lymphoma, which depend on high levels
 CC of Bcl-2 for their continued growth and survival. CD domain mimetics
 CC may also be used for combating viral infections by causing apoptosis
 CC of infected cells.

XX Sequence 26 AA:

Query Match 100.0%; Score 81; DB 17; Length 26;

Best Local Similarity 100.0%; Pred. No. 1.5e-06; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KKLSECLKRIQDELD 16
 |||
 DB 6 KKLSECLKRIQDELD 21

RESULT 4

AA96323 ID AAY96323 standard; Peptide: 26 AA.

XX AAY96323;

DT 17-AUG-2000 (first entry)

DE Mammalian Bax Bcl-2 homology domain 3 domain.

XX Mammal; apoptosis; cell death; BRC3; apoptosis promotion; Bax;

KW apoptosis inhibition; malignant cell; autoimmune disease.

XX Mammalia.

PN WO200026228-A1.

XX 11-MAY-2000.

PD 28-OCT-1999; 99WO-US25285.

XX 02-NOV-1998; 98US-0184168.

PR (CLON-) CLONTECH LAB INC.

XX Zhu L, Yin X, Chittenden T;

PI WPI: 2000-365560/31.

DR Novel polynucleotide encoding a BRC3 protein which is useful for

XX modulating apoptosis, especially in the treatment of cancer and

PT autoimmune diseases -

PS Disclosure; Fig 4; 47pp; English.

XX The present sequence is the mammalian Bax Bcl-2 homology domain 3

CC (BH3) domain, which was used in a sequence alignment with the same

CC domain of a putative version of the mammalian apoptosis

CC regulator BRC3, which was designated BRC3-ORF2. The BRC3 protein,

CC nucleic acids and antibodies are suitable for use in promoting cell

CC death or for preventing apoptosis in malignant cells and those causing

CC autoimmune diseases.

XX Sequence 26 AA:

Query Match 100.0%; Score 81; DB 21; Length 26;

Best Local Similarity 100.0%; Pred. No. 1.5e-06; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KKLSECLKRIQDELD 16
 |||
 DB 3 KKLSECLKRIQDELD 18

RESULT 5

AAB70373 ID AAB70373 standard; Peptide: 26 AA.

XX AAB70373;

DT 02-MAY-2001 (first entry)

DE BAX BH3 consensus peptide sequence SEQ ID NO:6.

XX Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;

KW immunostimulant; neuroprotective; neurotrophic; antiischemic; vulnery;

KW cytostatic; antiviral; antiarthritic; antiinflammatory; wound healing;

KW immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;

KW immunodeficiency disease; neurodegenerative disease; viral infection;

KW ischaemic cell death; reperfusion cell death; arthritis; infertility;

KW lymphoproliferative condition; inflammation; autoimmune disease.

XX Unidentified.

OS WO200110888-A1.

PN 15-FEB-2001.

XX 30-MAY-2000; 2000WO-US11864.

PF 28-MAY-1999; 99US-0136783.

PR (APOF-) APOPTOSIS TECHNOLOGY INC.

XX Zhou X;

PI WPI: 2001-138734/14.

DR New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,

XX useful for screening for candidate compounds which induce or inhibit

XX apoptosis, comprises amino acid substitutions at Ser118, Ser155 or

PT Ser113 -

XX Example 2; Fig 3a; 157pp; English.

PS The present invention describes an isolated or synthetic polypeptide

CC (1) comprising a less than full length amino acid sequence of a mutant

CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its

CC fragment, which contains amino acid substitutions at Ser118 of a human

CC BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine

CC BAD (shorter murine BAD). (1) has immunostimulant, neuroprotective,

CC neurotrophic, antiischemic, vulnery, cytostatic, antiviral,

CC antiarthritic, antiinflammatory and immunosuppressive activities, and

CC can be used as an apoptosis inducer or inhibitor. BAD polypeptides and

CC polynucleotides can be used for screening candidate compounds and drugs

CC for activity that promote cell survival or apoptosis. Other uses include

CC inducing or inhibiting apoptosis in a cell. Candidate compounds

CC identified and (mutant) BAD polypeptides are useful in treating

CC immunodeficiency diseases, neurodegenerative diseases, ischemic cell

CC death, reperfusion cell death, wound healing, cancer, viral infections,

CC lymphoproliferative conditions, arthritis, infertility, inflammation and

CC autoimmune diseases. The present sequence represents a Bcl-family member

CC BH3 domain consensus sequence which is used in an example from the

CC present invention.

XX Sequence 26 AA:

Query Match 100.0%; Score 81; DB 22; Length 26;

Best Local Similarity 100.0%; Pred. No. 1.5e-06; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KKLSECLKRIQDELD 16
 |||
 DB 3 KKLSECLKRIQDELD 18

RESULT 6
 AAB37006
 ID AAB37006 standard; peptide: 27 AA.
 XX
 AC AAB37006;
 XX
 DT 28-FEB-2001 (first entry)
 XX
 DE Bcl2 polypeptide BH3 domain peptide #6.
 XX
 KM Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;
 KM cardiact; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;
 KM apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;
 KM colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;
 KM melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
 KM stroke; myocardial infarction.
 XX
 OS Homo sapiens.
 XX
 PN WO200059526-A1.
 XX
 PD 12-OCT-2000.
 XX
 PF 06-APR-2000; 2000WO-US093552.
 XX
 PR 07-APR-1999; 99US-0128202.
 XX
 PA (UYJE-) UNIV JEFFERSON THOMAS.
 XX
 PI Huang Z, Wang J, Zhang Z, Shan S, Lu Z;
 XX
 DR WPI: 2000-679325/66.
 XX
 PT New peptide conjugates for modulating apoptosis or for inhibiting B
 cell lymphoma/leukemia 2 (bcl-2) function, especially useful for
 PT treating neurodegenerative disorders, stroke, or cancer
 XX
 PS Claim 18; Page 17; 74pp; English.
 XX
 CC The invention relates to a peptide conjugate having the formula:
 CC (R-X)-n-peptide where n = 1-10; X = C=O, when the R-X group is attached
 CC to the N-terminus of the peptide, or a side chain of the peptide where
 CC the functional group of the side chain is NH2 or OH; or X = O or NH,
 CC when the R-X group is attached to the C-terminus of the peptide, or a
 CC side chain of the peptide, where the side chain functional group is COOH
 CC or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkenyl optionally
 CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain
 CC alkyl group, or benzyl. The peptides AAB37001-837058 represent examples
 CC of the peptide portion of the conjugate. The peptides represent analogues
 CC of a bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of
 CC the BH3 domain of the cell death agonist Bad. The peptide conjugate is
 CC useful for modulating apoptosis in the cells of a subject, or for
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockade of
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2
 CC function. In particular, the peptide conjugate is useful for treating a
 CC subject afflicted with a cancer characterized by cancer cells that
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric,
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
 CC conjugate is also useful for treating disorders characterized by
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
 XX
 SO Sequence 27 AA:

Query Match 100.0%; Score 81; DB 21; Length 27;
 Best Local Similarity 100.0%; Pred. No. 1.6e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KKLSECLKRIQDELDS 16
 |||
 Db 6 KKLSECLKRIQDELDS 21

RESULT 7
 AAY05430
 ID AAY05430 standard; peptide: 34 AA.
 XX
 AC AAY05430;
 XX
 DT 02-JUL-1999 (first entry)
 XX
 DE Human BAX BH3 domain.
 XX
 KM BH3 domain; cell death agonist; bcl homology domain; Bcl-2 family;
 KM apoptosis promoter; cancer cell; virus infected cell; inflammation;
 KM autoantibody producing cell; cancer; lymphoproliferative condition;
 KM arthritis; autoimmune disease; therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO9916787-A1.
 XX
 PD 08-APR-1999.
 XX
 PE 22-SEP-1998; 98WO-US19765.
 XX
 PR 07-OCT-1997; 97US-0946039.
 XX
 PR 26-SEP-1997; 97US-0060133.
 XX
 PA (UNIM) UNIV WASHINGTON.
 XX
 PI Korsmeyer SJ;
 XX
 DR WPI: 1999-255058/21.
 XX
 PT Bcl homology domain 3 polypeptide
 PT
 PT Example 10; Fig 17a; 104pp; English.
 XX
 PS This sequence represents a bcl homology domain 3 (BH3 domain) of the
 CC invention, derived from a proapoptotic member of the BCL-2 family. The
 CC BH3 polypeptide can be used in a method for promoting apoptosis in a
 CC target cell, especially where the cell is a cancer cell, a virus infected
 CC cell or an autoantibody producing cell. The BH3 polypeptide can be used
 CC in therapeutic compositions for treating disease including cancer, other
 CC lymphoproliferative conditions, arthritis, inflammation, and autoimmune
 CC diseases, which may result from the down regulation of cell death
 CC regulation.
 XX
 SO Sequence 34 AA:

Query Match 100.0%; Score 81; DB 20; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 KKLSECLKRIQDELDS 16
 |||
 Db 5 KKLSECLKRIQDELDS 20

RESULT 8
 AAY70818
 ID AAY70818 standard; Protein: 78 AA.
 XX
 AC AAY70818;
 XX
 DT 31-JUL-2000 (first entry)
 XX
 DE Human neuroprotective truncated BAX protein, tBAX78.
 XX

KW Human; truncated BAX protein; tBAX78; BAX alpha; BCL-2 family;
 KW neuron; anti-apoptotic; cerebroprotective; neuroprotective; neuroactive;
 KW apoptosis; treatment; neurodegenerative disease; peripheral nerve injury;
 KW spinal cord injury; head trauma; stroke.
 XX
 OS Homo sapiens.
 XX
 XX Key
 FH Region
 FT 1..58
 FT /note= "N-terminal region of BAX alpha"
 FT 59..73
 FT /label= BH3_domain
 FT
 PN MO200023083-A1.
 XX
 PD 27-APR-2000.
 XX
 PF 22-OCT-1999; 99MO-US24747.
 XX
 PR 22-OCT-1998; 98US-0177315.
 XX
 PA (UNIM) UNIV WASHINGTON.
 XX
 PI Johnson EM, Easton R;
 XX
 DR WPI; 2000-339513/29.
 XX
 PT Truncated BAX polypeptides useful for preventing apoptosis of neurons
 PT for the treatment of nervous system disorders -
 XX
 PS Claim 4; Page 33; 43pp; English.
 XX
 CC The present sequence is a specifically claimed truncated BAX protein
 CC tBAX78 which inhibits neuronal apoptosis induced by trophic factor
 CC deprivation. The protein consists of first 78 amino acids of human
 CC BAX alpha, that includes the N-terminal region and BH3
 CC domain. It lacks the BH1, BH2 and C-terminal transmembrane domains of
 CC the full-length BAX alpha. The tBAX protein lacking only the
 CC transmembrane domain has been shown to have anti-apoptotic activity.
 CC The present sequence is used to treat diseases associated with neuronal
 CC apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury,
 CC spinal cord injury, head trauma and stroke.
 CC
 SQ Sequence 78 AA:
 Query Match 100.0%; Score 81; DB 21; Length 78;
 Best Local Similarity 100.0%; Pred. No. 4,8e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 KKLSECLKRIQDELDS 16
 DB 57 KKLSECLKRIQDELDS 72
 RESULT 9
 ID AAY34149 standard; Protein: 131 AA.
 AC AAY34149;
 XX
 XX 30-NOV-1999 (first entry)
 DE Human truncated Bax protein.
 XX
 XX Apoptosis; adenovirus; dimeric; Bcl-2; p53; cancer; gene therapy.
 OS Homo sapiens.
 XX
 XX Key
 FH Domain
 FT 59..101
 FT /note= "Portion of BH3 domain essential for dimerisation"
 FT

PN MO9946371-A2.
 XX
 PD 16-SEP-1999.
 XX
 PF 11-MAR-1999; 99MO-US05359.
 XX
 PR 11-MAR-1998; 98US-0077541.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI McDonnell TJ, Swisher SG, Fang B, Bruckheimer EM, Sarkiss MG;
 PI Ji L, Koch JA;
 DR WPI; 1999-551404/46.
 DR N-PSDB; AA219763.
 XX
 PT New adenovirus vectors, used for killing or inhibiting the growth of
 PT cells and for treating cancers -
 XX
 PS Claim 26; Page 148-149; 151pp; English.
 XX
 CC This sequence represents a human truncated Bax protein. The cDNA
 CC contains a single base deletion relative to the wild-type (AA219764),
 CC causing a frameshift which leads to translation of a premature stop
 CC codon, resulting in a truncated protein. However, the domain responsible
 CC for its function is still present in the truncated protein. Bax (Bcl-2
 CC associated x protein) is a proapoptotic member of the Bcl-2 gene family.
 CC Bax functions as a primary response gene in the p53-regulated apoptotic
 CC pathway. The Bax gene promoter has 4 p53 binding sites and the
 CC expression of Bax is upregulated at the transcriptional level by p53, and
 CC Bax mRNA and protein expression have been shown to increase following
 CC induction of p53. Bax protein can function as a homodimer, or it can
 CC heterodimerise with other Bcl-2 gene family members such as the
 CC antiapoptotic protein Bcl-2. Heterodimerisation of Bcl-2 family members
 CC provides a means of controlling cell death via the "rheostat" model. This
 CC model suggests that the relative amounts of Bcl-2 and Bax determine the
 CC susceptibility of a cell to undergo apoptosis. If Bcl-2 is in excess,
 CC Bcl-2/Bax heterodimers predominate and cell death is inhibited. If Bax is
 CC in excess, however, Bax homodimers predominate and the cell becomes
 CC susceptible to apoptosis following exposure to an apoptotic stimulus.
 CC Additionally, Bax can function in its monomeric form to accelerate cell
 CC death. Use of novel adenoviral vectors containing this Bax gene may
 CC augment and complement wild-type p53 gene therapy, which induces a G1
 CC cell cycle arrest and/or apoptosis in malignant cells carrying p53
 CC mutations. In addition, Bax overexpression could provide the apoptotic
 CC effect of p53 without the need for p53 itself.
 CC
 SQ Sequence 131 AA:
 Query Match 100.0%; Score 81; DB 20; Length 131;
 Best Local Similarity 100.0%; Pred. No. 8,3e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 KKLSECLKRIQDELDS 16
 DB 57 KKLSECLKRIQDELDS 72
 RESULT 10
 ID AAR71406 standard; Protein: 192 AA.
 AC AAR71406;
 XX
 XX 15-NOV-1995 (first entry)
 DE Human Bax protein.
 XX
 XX Human; bcl-2; alpha; beta; proto-oncogene; hematopoietic cell line;
 KW apoptosis; membrane-associated cytoplasmic protein; B cell; T cell;
 KW proliferation; cell cycle progression; Bax; apoptotic cell death;
 KW apoptosis; cytokine; death repressor; BH1; BH2; cancer therapy;

KW hyperplasia: immunodeficiency disease; AIDS; neurodegeneration;
 KW ischemic cell death.

XX Homo sapiens.

OS MO9505750-A.

XX 02-MAR-1995.

XX 24-AUG-1994; 94MO-US09701.

XX 26-AUG-1993; 930S-0112208.

XX 25-MAY-1994; 94US-0248819.

XX (UNIT) UNIT WASHINGTON.

XX KORMEYER SJ;

XX WPI; 1995-106605/14.

XX N-PSDB; AA097606.

XX Methods for producing and identifying mutant bcl-2 proteins -
 PT that lack death repressor activity and/or lacks binding to Bax.

XX Disclosure: Fig 3; 133pp; English.

CC This sequence represents human Bax protein. Bax is a protein which is
 CC associated with the human bcl-2 alpha and beta proteins, the sequences
 CC of which are given in AA071404-05 respectively. bcl-2 is encoded by a
 CC proto-oncogene and is capable of inhibiting apoptosis in many
 CC hematopoietic cell systems. bcl-2 is a 26 kD membrane-associated
 CC cytoplasmic protein and is thought to function by enhancing the survival
 CC of hematopoietic cells of B and T origins rather than directly promoting
 CC proliferation of these cell types. bcl-2 has not been shown to directly
 CC promote cell cycle progression nor does it necessarily alter the dose
 CC response to limiting concentrations of IL-3. bcl-2 has been shown to
 CC form heterodimers with this 21 kD protein, Bax. Overexpressed Bax
 CC accelerates apoptotic cell death induced by cytokine deprivation in an
 CC IL-3 dependent cell line, and it also acts to counter the death repressor
 CC activity of bcl-2. Therefore, the ratio between bcl-2 and Bax determines
 CC cell survival or death following an apoptotic stimulus. The invention
 CC gives a mutant form of bcl-2 in which there is at least one amino acid
 CC substitution or deletion in the BH1 or BH2 domains. This makes the
 CC mutant protein substantially incapable of binding Bax and/or incapable
 CC of death repressor activity. Down regulation of bcl-2 is useful in
 CC cancer therapy, controlling hyperplasias and eliminating self-reactive
 CC clones in autoimmunity by favouring death effector molecules. Up
 CC regulating bcl-2 is beneficial in treatment and diagnosis of immuno-
 CC deficiency diseases, including AIDS and neurodegenerative and ischemic
 CC cell death.

XX Sequence 192 AA;

Query Match 100.0%; Score 81; DB 16; Length 192;

Best Local Similarity 100.0%; Pred. NO. 1.2e-05; Mismatches 0; Indels 0; Gaps 0;

XX 1 KKLSECLKRIQDELDS 16

XX 57 KKLSECLKRIQDELDS 72

RESULT 11

ID AAY34150 standard; Protein; 192 AA.

XX AAY34150;

XX 30-NOV-1999 (first entry)

XX Human wild-type Bax protein.

XX

KW Apoptosis; adenovirus; dimeric; Bcl-2; p53; cancer; gene therapy.

XX Homo sapiens.

XX Key Location/Qualifiers

XX FT Domain 59..101 /note="Portion of BH3 domain essential for dimerisation"

XX MO9946371-A2.

XX 16-SEP-1999.

XX 11-MAR-1999; 99WO-US05359.

XX 11-MAR-1998; 98US-0077541.

XX (TEXA) UNIT TEXAS SYSTEM.

XX McDonnell TJ, Swisher SG, Fang B, Bruckheimer EM, Sarkiss MG;

XX Ji L, Roth JA;

XX WPI; 1999-551404/46.

XX N-PSDB; AA219764.

XX New adenovirus vectors, used for killing or inhibiting the growth of
 PT cells and for treating cancers -

XX Disclosure: Page 149-150; 151pp; English.

CC This sequence represents human wild-type Bax protein. A naturally
 CC occurring mutant protein (AAY34149) was also isolated. Bax (Bcl-2
 CC associated X protein) is a proapoptotic member of the Bcl-2 gene family.
 CC Bax functions as a primary response gene in the p53-regulated apoptotic
 CC pathway. The Bax gene promoter has 4 p53 binding sites and the
 CC expression of Bax is upregulated at the transcriptional level by p53, and
 CC Bax mRNA and protein expression have been shown to increase following
 CC induction of p53. Bax protein can function as a homodimer, or it can
 CC heterodimerise with other Bcl-2 gene family members such as the
 CC antiapoptotic protein Bcl-2. Heterodimerisation of Bcl-2 family members
 CC provides a means of controlling cell death via the "rheostat" model. This
 CC model suggests that the relative amounts of Bcl-2 and Bax determine the
 CC susceptibility of a cell to undergo apoptosis. If Bcl-2 is in excess,
 CC Bcl-2/Bax heterodimers predominate and cell death is inhibited. If Bax is
 CC in excess, however, Bax homodimers predominate and the cell becomes
 CC susceptible to apoptosis following exposure to an apoptotic stimulus.
 CC Additionally, Bax can function in its monomeric form to accelerate cell
 CC death. Use of novel adenoviral vectors containing the Bax gene may
 CC augment and complement wild-type p53 gene therapy, which induces a G1
 CC cell cycle arrest and/or apoptosis in malignant cells carrying p53
 CC mutations. In addition, Bax overexpression could provide the apoptotic
 CC effect of p53 without the need for p53 itself.

XX Sequence 192 AA;

Query Match 100.0%; Score 81; DB 20; Length 192;

Best Local Similarity 100.0%; Pred. NO. 1.2e-05; Mismatches 0; Indels 0; Gaps 0;

XX 1 KKLSECLKRIQDELDS 16

XX 57 KKLSECLKRIQDELDS 72

RESULT 12

ID AAY05435 standard; peptide; 192 AA.

XX AAY05435;

XX 02-JUL-1999 (first entry)

XX Human BAX protein sequence.

XX

XX BH3 domain: cell death agonist; bcl homology domain; Bcl-2 family;
 KW apoptosis promoter; cancer cell; virus infected cell; inflammation;
 KW autoantibody producing cell; cancer; lymphoproliferative condition;
 KW arthritis; autoimmune disease; therapy.
 XX
 OS Homo sapiens.
 PN MO9916787-A1.
 XX
 PD 08-APR-1999.
 XX
 PF 22-SEP-1998; 98WO-US19765.
 XX
 PR 07-OCT-1997; 97US-0946039.
 XX
 PR 26-SEP-1997; 97US-0060133.
 XX
 PA (UNIW) UNIV WASHINGTON.
 XX
 PI Korsmeyer SJ.
 XX
 DK WPI; 1999-255058/21.
 XX
 PT Bcl homology domain 3 polypeptide
 XX
 PS Disclosure; Fig 21c; 104pp; English.
 XX
 CC This sequence represents the human BAX protein.
 CC The invention relates to a bcl homology domain 3 (BH3 domain),
 CC derived from a proapoptotic member of the BCL-2 family. The
 CC BH3 polypeptide can be used in a method for promoting apoptosis in a
 CC target cell, especially where the cell is a cancer cell, a virus infected
 CC cell or an autanibody producing cell. The BH3 polypeptide can be used
 CC in therapeutic compositions for treating disease including cancer, other
 CC lymphoproliferative conditions, arthritis, inflammation, and autoimmune
 CC diseases, which may result from the down regulation of cell death
 CC regulation.
 CC
 XX
 SQ Sequence 192 AA:

Query Match 100.0%; Score 81; DB 20; Length 192;
 Best Local Similarity 100.0%; Pred. No. 1.2e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLSECLKRIQDELD 16
 |||||||
 DB 57 KKLSECLKRIQDELD 72

RESULT 13
 AAM87804
 ID AAM87804 standard; Protein: 192 AA.
 XX
 AC AAM87804;
 XX
 DT 10-MAR-1999 (first entry)
 XX
 DE A human Bcl-2 associated protein designated Bax.
 XX
 KW Human; Bcl-2 associated protein; Bax; bcl-2; antibody; modulator;
 KW bcl-2-related function; apoptosis.
 XX
 OS Homo sapiens.
 XX
 OS Key Location/Qualifiers
 FH 97..118
 FT /note="BH1 domain"
 FT 146..168
 FT /note="BH2 domain"
 XX
 PN US5856171-A.
 XX

PD 05-JAN-1999.
 XX
 PF 10-NOV-1994; 94US-0337646.
 XX
 PR 10-NOV-1994; 94US-0337646.
 PR 26-AUG-1993; 93US-0112208.
 PR 25-MAY-1994; 94US-0248819.
 XX
 PA (UNIW) UNIV WASHINGTON.
 XX
 PI Korsmeyer SJ;
 XX
 DK WPI; 1999-105119/09.
 DR N-PSDB; AAV84005.
 XX
 PT DNA composition encoding bcl-2 two-hybrid and reporter system - for
 PT identifying modulators of bcl-2 function
 XX
 PS Example 1; Columns 71-74; 105pp; English.
 XX
 CC The present sequence represents a human Bcl-2 associated protein
 CC designated Bax. The Bax protein is used in a composition which
 CC comprises a bcl-2 family member polypeptide, a naturally occurring
 CC Bax polypeptide and an antibody that binds to the Bax polypeptide.
 CC The composition is used to identify modulators of bcl-2-related
 CC function, e.g. substances that inhibit binding of Bax to bcl-2,
 CC which would be potentially useful as drugs for modulating
 CC apoptosis.
 CC
 XX
 SQ Sequence 192 AA:

Query Match 100.0%; Score 81; DB 20; Length 192;
 Best Local Similarity 100.0%; Pred. No. 1.2e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLSECLKRIQDELD 16
 |||||||
 DB 57 KKLSECLKRIQDELD 72

RESULT 14
 AAM87809
 ID AAM87809 standard; Protein: 192 AA.
 XX
 AC AAM87809;
 XX
 DT 10-MAR-1999 (first entry)
 XX
 DE A human Bcl-2 associated protein designated Bax.
 XX
 KW Human; Bcl-2 associated protein; Bax; bcl-2; antibody; modulator;
 KW bcl-2-related function; apoptosis.
 XX
 OS Homo sapiens.
 XX
 OS Key Location/Qualifiers
 FH 97..118
 FT /note="BH1 domain"
 FT 146..168
 FT /note="BH2 domain"
 XX
 PN US5856171-A.
 XX
 PD 05-JAN-1999.
 XX
 PF 10-NOV-1994; 94US-0337646.
 XX
 PR 10-NOV-1994; 94US-0337646.
 PR 26-AUG-1993; 93US-0112208.
 PR 25-MAY-1994; 94US-0248819.
 XX
 PA (UNIW) UNIV WASHINGTON.
 XX
 PI Korsmeyer SJ;
 XX
 DK WPI; 1999-105119/09.
 DR DNA composition encoding bcl-2 two-hybrid and reporter system - for

PF Identifying modulators of bcl-2 function
 XX
 PS Example 7; Fig 7; 105pp; English.
 XX
 CC The present sequence represents a human Bcl-2 associated protein
 CC designated Bax. The Bax protein is used in a composition which
 CC comprises a bcl-2 family member polypeptide, a naturally occurring
 CC Bax polypeptide and an antibody that binds to the Bax polypeptide.
 CC The composition is used to identify modulators of bcl-2-related
 CC function, e.g. substances that inhibit binding of Bax to bcl-2,
 CC which would be potentially useful as drugs for modulating
 CC apoptosis.
 XX
 SO Sequence 192 AA:
 XX
 Query Match 100.0%; Score 81; DB 20; Length 192;
 Best Local Similarity 100.0%; Pred. No. 1.2e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 KKLSECLKRIGDELDS 16
 DB 57 KKLSECLKRIGDELDS 72
 RESULT 15
 AAY70827
 ID AAY70827 standard; Protein: 192 AA.
 XX
 AC AAY70827;
 XX
 D7 31-JUL-2000 (first entry)
 XX
 DE Human BAX alpha protein.
 XX
 KW Human; truncated BAX protein; tBAX; BAX alpha; BCL-2 family; head trauma;
 KW neuron; anti-apoptotic; cerebroprotective; neuroprotective; neuroactive;
 KW apoptosis; treatment; neurodegenerative disease; peripheral nerve injury;
 KW spinal cord injury; stroke; pro-apoptotic; PCD; programmed cell death.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 1..58
 FT Domain /label= "N-terminal_region
 FT 59..73
 FT Domain /label= "BH3_domain
 FT /note= "BCL-2 Homology domain 3"
 FT 98..118
 FT Domain /label= "BH1_domain
 FT 150..165
 FT Domain /label= "BH2_domain
 FT 169..188
 FT Domain /label= "Transmembrane_domain
 PN WO200023083-A1.
 XX
 PD 27-APR-2000.
 XX
 PE 22-OCT-1999; 99WO-US24747.
 XX
 PR 22-OCT-1998; 98US-0177315.
 XX
 PA (UNIV) UNIV WASHINGTON.
 XX
 PI Johnson EM, Easton R;
 XX
 DR WPI: 2000-339513/29.
 XX
 PT Truncated BAX polypeptides useful for preventing apoptosis of neurons
 PT for the treatment of nervous system disorders
 XX
 PS Disclosure; Page 35-36; 43pp; English.

XX
 CC The present sequence is a human BAX alpha protein, a pro-apoptotic
 CC protein which is a member of BCL-2 family of proteins that are involved
 CC in regulation of neuronal programmed cell death. The patent discloses
 CC specific truncated proteins derived from BAX alpha which inhibit neuronal
 CC apoptosis induced by trophic factor deprivation. The anti-apoptotic
 CC truncated BAX (tBAX) proteins include tBAX70, tBAX78 and their mutants.
 CC These proteins contain the N-terminal region and at least a portion of
 CC the BH3 domain of BAX alpha and lack the BH1, BH2 and C-terminal
 CC transmembrane domains. The tBAX protein lacking only the
 CC transmembrane domain has been shown to have anti-apoptotic activity.
 CC The tBAX proteins are used to treat diseases associated with neuronal
 CC apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury,
 CC spinal cord injury, head trauma and stroke.
 XX
 SO Sequence 192 AA:
 XX
 Query Match 100.0%; Score 81; DB 21; Length 192;
 Best Local Similarity 100.0%; Pred. No. 1.2e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 KKLSECLKRIGDELDS 16
 DB 57 KKLSECLKRIGDELDS 72
 Search completed: September 20, 2002, 10:35:59
 Job time: 427 sec

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OM protein - protein search, using sw model

Run on: September 20, 2002, 10:37:21 Search time 75.64 seconds
(without alignments)
5.167 Million cell updates/sec

Title: US-09-544-664-32

Sequence: 1 KRLSECLKRIQDELDS 16

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Issued Patents AA: *
1: /cgn2_6/prodata/2/1aa/5A.COMB.pep.*
2: /cgn2_6/prodata/2/1aa/5B.COMB.pep.*
3: /cgn2_6/prodata/2/1aa/6A.COMB.pep.*
4: /cgn2_6/prodata/2/1aa/6B.COMB.pep.*
5: /cgn2_6/prodata/2/1aa/PCTUS.COMB.pep.*
6: /cgn2_6/prodata/2/1aa/Dackfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	20	4	US-09-236-385A-40
2	81	100.0	26	1	US-08-440-391-6
3	81	100.0	26	1	US-08-440-391-6
4	81	100.0	26	2	US-08-908-597A-6
5	81	100.0	26	2	US-08-908-597A-6
6	81	100.0	26	4	US-09-236-385A-6
7	81	100.0	26	4	US-09-236-385A-6
8	81	100.0	26	5	PCT-US96-06122-6
9	81	100.0	26	5	PCT-US96-06122-6
10	81	100.0	34	1	US-08-440-391-13
11	81	100.0	34	2	US-08-440-391-13
12	81	100.0	34	4	US-09-236-385A-13
13	81	100.0	34	5	PCT-US96-06122-13
14	81	100.0	42	1	US-08-798-897-22
15	81	100.0	42	2	US-08-978-523-22
16	81	100.0	192	1	US-08-112-208C-2
17	81	100.0	192	1	US-08-112-208C-9
18	81	100.0	192	1	US-08-248-819A-9
19	81	100.0	192	1	US-08-248-819A-9
20	81	100.0	192	1	US-08-607-269-25
21	81	100.0	192	1	US-08-471-058-13
22	81	100.0	192	2	US-08-337-646A-2
23	81	100.0	192	2	US-08-337-646A-2
24	81	100.0	192	2	US-08-856-531-2
25	81	100.0	192	2	US-08-856-531-2
26	81	100.0	192	2	US-08-856-034-2
27	81	100.0	192	2	US-08-856-034-2

28	81	100.0	192	3	US-08-471-057-13	Sequence 13, Appl
29	81	100.0	192	4	US-09-127-048-7	Sequence 7, Appl
30	81	100.0	192	4	US-08-927-326-2	Sequence 2, Appl
31	81	100.0	192	4	US-08-927-326-9	Sequence 9, Appl
32	81	100.0	192	5	PCT-US95-04600-25	Sequence 25, Appl
33	81	100.0	221	1	US-08-616-732A-9	Sequence 9, Appl
34	81	100.0	221	4	US-09-037-742B-9	Sequence 9, Appl
35	78	96.3	192	1	US-08-112-208C-3	Sequence 3, Appl
36	78	96.3	192	1	US-08-112-208C-8	Sequence 8, Appl
37	78	96.3	192	1	US-08-248-819A-3	Sequence 8, Appl
38	78	96.3	192	1	US-08-248-819A-8	Sequence 8, Appl
39	78	96.3	192	2	US-08-337-646A-3	Sequence 3, Appl
40	78	96.3	192	2	US-08-337-646A-8	Sequence 8, Appl
41	78	96.3	192	2	US-08-856-531-3	Sequence 3, Appl
42	78	96.3	192	2	US-08-856-531-8	Sequence 8, Appl
43	78	96.3	192	2	US-08-856-034-3	Sequence 3, Appl
44	78	96.3	192	2	US-08-856-034-8	Sequence 8, Appl
45	78	96.3	192	4	US-09-127-048-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-236-385A-40
Sequence 40, Application US/09236385A
Patent No. 6221615

GENERAL INFORMATION:

APPLICANT: CHITTENDEN, Thomas D.; and

INVENTOR: Robert J.

TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH

MODULATE APOPTOSIS

NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:

ADDRESS: Hale and Port

STREET: 1455 Pennsylvania Avenue, N.W.

CITY: Washington

STATE: D.C.

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/236,385A

FILING DATE: 25-Jan-1999

CLASSIFICATION: <unknown>

ATTORNEY/AGENT INFORMATION:

NAME: WIXON, HENRY N.

REGISTRATION NUMBER: 32,073

TELECOMMUNICATION INFORMATION: (C) ATTORNEY DOCKET NO. 104322.147CIP

TELEPHONE: 202-942-8400

TELEFAX: 202-942-8484

INFORMATION FOR SEQ ID NO: 40

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 40

US-09-236-385A-40

Query Match 100.0%; Score 81; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 4, 1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRLSECLKRIQDELDS 16
DB 3 KRLSECLKRIQDELDS 18

RESULT 2
US-08-440-391-6
Sequence 6, Application US/08440391
Patent No. 5656725
GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.; and
APPLICANT: LUTZ, Robert J.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440.391
FILING DATE: 12-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.147
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ. ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-440-391-6

Query Match 100.0%; Score 81; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLSECLKRIGDELDS 16
Db 6 KKLSECLKRIGDELDS 21

RESULT 3
US-08-440-391-24
Sequence 24, Application US/08440391
Patent No. 5656725
GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.; and
APPLICANT: LUTZ, Robert J.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/440.391
FILING DATE: 12-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.147
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ. ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-440-391-24

Query Match 100.0%; Score 81; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLSECLKRIGDELDS 16
Db 6 KKLSECLKRIGDELDS 21

RESULT 4
US-08-908-597A-6
Sequence 6, Application US/08908597A
Patent No. 5863795
GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.; and
APPLICANT: LUTZ, Robert J.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/908.597A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/440.391
FILING DATE: 12-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.147
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ. ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-908-597A-6

Query Match 100.0%; Score 81; DB 2; Length 26;

Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLSECLKRIIDELDS 16
|||||
Db 6 KKLSECLKRIIDELDS 21

RESULT 5

US-08-908-597A-24
Sequence 24, Application US/08908597A
Patent No. 5863795

GENERAL INFORMATION:

APPLICANT: CHITTENDEN, Thomas D.; and
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/908,597A
FILING DATE:
CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/440,391
FILING DATE: 12-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.

REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.147
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-908-597A-24

Query Match 100.0%; Score 81; DB 2; Length 26;

Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLSECLKRIIDELDS 16
|||||
Db 6 KKLSECLKRIIDELDS 21

RESULT 6

US-09-236-385A-6
Sequence 6, Application US/09236385A
Patent No. 6221615

GENERAL INFORMATION:

APPLICANT: CHITTENDEN, Thomas D.; and
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS

NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr

US-09-236-385A-6

STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/236,385A
FILING DATE: 25-Jan-1999
CLASSIFICATION: <unknown>

ATTORNEY/AGENT INFORMATION:

NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073

TELECOMMUNICATION INFORMATION: (C) ATTORNEY DOCKET NO. 104322.147CIP

TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-236-385A-6

Query Match 100.0%; Score 81; DB 4; Length 26;

Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLSECLKRIIDELDS 16
|||||
Db 6 KKLSECLKRIIDELDS 21

RESULT 7

US-09-236-385A-24
Sequence 24, Application US/09236385A
Patent No. 6221615

GENERAL INFORMATION:

APPLICANT: CHITTENDEN, Thomas D.; and
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/236,385A
FILING DATE: 25-Jan-1999
CLASSIFICATION: <unknown>

ATTORNEY/AGENT INFORMATION:

NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073

TELECOMMUNICATION INFORMATION: (C) ATTORNEY DOCKET NO. 104322.147CIP

TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484

INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:

LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-236-385A-24

Query Match 100.0%; Score 81; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. NO. 5,4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KKLSECLKRIQDELDS 16
|||||
DB 6 KKLSECLKRIQDELDS 21

RESULT 8
PCT-US96-06122-6
Sequence 6, Application PC/TUS9606122
GENERAL INFORMATION:

APPLICANT: IMMUNOGEN, INC.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS
TITLE OF INVENTION: WHICH MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/06122
FILING DATE: HEREWITH

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/440,391
FILING DATE: 12-MAY-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.147PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US96-06122-6

Query Match 100.0%; Score 81; DB 5; Length 26;
Best Local Similarity 100.0%; Pred. NO. 5,4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KKLSECLKRIQDELDS 16
|||||
DB 6 KKLSECLKRIQDELDS 21

RESULT 9
PCT-US96-06122-24
Sequence 24, Application PC/TUS9606122
GENERAL INFORMATION:

APPLICANT: IMMUNOGEN, INC.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS
TITLE OF INVENTION: WHICH MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/06122
FILING DATE: HEREWITH

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/440,391
FILING DATE: 12-MAY-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.147PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484

INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US96-06122-24

Query Match 100.0%; Score 81; DB 5; Length 26;
Best Local Similarity 100.0%; Pred. NO. 5,4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KKLSECLKRIQDELDS 16
|||||
DB 6 KKLSECLKRIQDELDS 21

RESULT 10
US-08-440-391-13
Sequence 13, Application US/08440391
Patent No. 5656725
GENERAL INFORMATION:

APPLICANT: CHITTENDEN, Thomas D.; and
APPLICANT: LUTZ, Robert J.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,391
FILING DATE: 12-MAY-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.147
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-440-391-13

Query Match 100.0%; Score 81; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 7.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KKLSECLKRIIDELDS 16
|||||
DB 8 KKLSECLKRIIDELDS 23

RESULT 11
US-08-908-597A-13
Sequence 13, Application US/08908597A
Patent No. 5863795
GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.; and
APPLICANT: LUTZ, Robert J.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/908,597A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/440,391
FILING DATE: 12-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.147
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-908-597A-13

Query Match 100.0%; Score 81; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 7.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KKLSECLKRIIDELDS 16
|||||
DB 8 KKLSECLKRIIDELDS 23

RESULT 12
US-09-236-385A-13
Sequence 13, Application US/09236385A
Patent No. 6221615
GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.; and
APPLICANT: LUTZ, Robert J.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/236,385A
FILING DATE: 25-Jan-1999
CLASSIFICATION: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-236-385A-13

Query Match 100.0%; Score 81; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 7.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KKLSECLKRIIDELDS 16
|||||
DB 8 KKLSECLKRIIDELDS 23

RESULT 13
PCT-US96-06122-13
Sequence 13, Application PC/TUS9606122
GENERAL INFORMATION:
APPLICANT: IMMUNOGEN, INC.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS
WHICH MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/06122
FILING DATE: HEREMITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/440,391
FILING DATE: 12-MAY-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.147PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-0596-06122-13

Query Match 100.0%; Score 81; DB 5; Length 34;
Best local Similarity 100.0%; Pred. No. 7.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLSECLKRIIGDELDS 16
DB 8 KKLSECLKRIIGDELDS 23

RESULT 14
US-08-798-897-22
Sequence 22, Application US/08798897
Patent No. 5789201
GENERAL INFORMATION:
APPLICANT: Gustella, John
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-798-897-22

Query Match 100.0%; Score 81; DB 1; Length 42;
Best local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLSECLKRIIGDELDS 16
DB 27 KKLSECLKRIIGDELDS 42

RESULT 15
US-08-978-523-22
Sequence 22, Application US/08978523
Patent No. 5883229
GENERAL INFORMATION:
APPLICANT: Gustella, John
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-978-523-22

Query Match 100.0%; Score 81; DB 2; Length 42;
Best local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLSECLKRIIGDELDS 16
DB 27 KKLSECLKRIIGDELDS 42

Search completed: September 20, 2002, 10:37:21
Job time: 409 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 20, 2002, 10:39:10
(Search time 95.59 seconds
(without alignments)
16.084 Million cell updates/sec

Title: US-09-544-664-32

Perfect score: 81

Sequence: 1 KRLSECLKRIQDELD 16

Scoring table: BLOSUM62

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR_71:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	81	100.0	179	2	JC7255
2	81	100.0	192	2	A47538
3	81	100.0	218	2	B47538
4	78	96.3	192	2	D47538
5	75	92.6	133	2	I53295
6	49	60.5	669	2	A90506
7	47	58.0	862	1	FAD0AA
8	44	54.3	500	2	S64220
9	43	53.1	92	2	F71868
10	43	53.1	197	2	PC2235
11	43	53.1	213	2	E69057
12	43	53.1	217	2	E71098
13	43	53.1	339	2	S08981
14	43	53.1	1002	2	AP1909
15	42.5	52.5	460	2	C96964
16	42	51.9	677	2	T36106
17	42	51.9	1325	2	T42722
18	41	50.6	151	2	S61384
19	41	50.6	345	2	AF1936
20	41	50.6	772	2	T25469
21	41	50.6	1280	2	T34357
22	40	49.4	118	2	D64347
23	40	49.4	126	2	G64311
24	40	49.4	159	2	AB0413
25	40	49.4	177	2	S25492
26	40	49.4	349	2	B35114
27	40	49.4	382	2	H72255
28	40	49.4	384	2	A64230
29	40	49.4	435	2	A86492

ALIGNMENTS

30	40	49.4	435	2	H72129	hypothetical prote
31	40	49.4	460	2	B87455	DNA repair protein
32	40	49.4	485	2	F64165	hypothetical prote
33	40	49.4	713	2	JC2534	RING protein - rat
34	40	49.4	968	2	C82452	hypothetical prote
35	40	49.4	1193	2	A86193	hypothetical prote
36	40	49.4	1413	2	D84481	probable retroelem
37	40	49.4	1465	2	T23056	hypothetical prote
38	39	48.1	112	2	AD1756	hypothetical gene
39	39	48.1	229	2	B97053	radc protein ortho
40	39	48.1	256	2	T45895	hypothetical prote
41	39	48.1	257	2	G88021	protein M10D9.2 [1
42	39	48.1	294	2	H84115	ribokinase trsk [1
43	39	48.1	317	2	A59292	probable type II m
44	39	48.1	327	2	C69419	phosphate ABC tran
45	39	48.1	375	2	D97268	toxic anion resist

RESULT 1
JC7255
Bax-delta protein - human
C:Species: Homo sapiens (man)
C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 17-Nov-2000
C:Accession: JC7255
R:Schmitt, E.; Paquet, C.; Beauchemin, M.; Deyver-Bertrand, J.; Bertrand, R.
Biochem. Biophys. Res. Commun. 270, 868-879, 2000
A:Title: Characterization of Bax-delta, a cell death-inducing isoform of Bax.
A:Reference number: JC7255
A:Accession: JC7255
A:Molecule type: mRNA
A:Residues: 1-179 <SCH>
A:Cross-references: GB:AF247393
A:Experimental source: cancer promyelocytic cells
C:Comment: This protein, a member of the Bcl-2 family, has a proapoptotic effect. It
clivellion.
C:Superfamily: bcl transforming protein
C:Keywords: transmembrane protein

Query Match 100.0%; Score 81; DB 2; Length 179;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 KRLSECLKRIQDELD 16
DB 57 KRLSECLKRIQDELD 72

RESULT 2
A47538
bcl-2-associated protein x, alpha splice form - human
N:Alternate names: BAX; programmed cell death membrane protein x alpha
C:Species: Homo sapiens (man)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
R:Oltvai, Z.N.; Millman, C.L.; Korsmeyer, S.J.
Cell 74, 609-619, 1993
A:Title: Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerate
A:Reference number: A47538; MUID:93364978
A:Accession: A47538
A:Molecule type: mRNA
A:Residues: 1-192 <OLT>
A:Cross-references: GB:I22473; NID:g388165; PIDD:AAA03619.1; PIDD:g388166
A>Note: the amino end of the mature protein is blocked
C:Genetics:
A:Gene: GDB:BAX
A:Cross-references: GDB:228082; OMIM:600040
A:Map position: 19q13.3-19q13.4
C:Superfamily: bcl transforming protein
C:Keywords: alternative splicing; blocked amino end; heterodimer; homodimer; transmem

F:172-191/Domain: transmembrane #status predicted <TM1>

Query Match	100.0%;	Score 81;	DB 2;	Length 192;
Best Local Similarity	100.0%;	Pred. No. 1.6e-05;		
Matches 16; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

```
QY      1 KKLSECLKRIGDELD 16
          |||||
Db      57 KKLSECLKRIGDELD 72
```

RESULT
B47538

bcl-2-associated protein x, beta splice form - human
 A:Alternate names: BAX; programmed cell death membrane protein x beta
 C:Species: Homo sapiens (man)
 C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
 C:Accession: B47538
 R:Oltvai, Z.N.; Millman, C.L.; Korsmeyer, S.J.
 Cell 74, 609-619, 1993
 A:Title: bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerates F
 A:Reference number: A47358; MUID:93364978
 A:Accession: B47538
 A:Molecule type: mRNA
 A:Residues: 1-218 <OLT>
 A:Cross-references: GB:L22474; NID:g388167; PID:AAA03620.1; PID:g388168
 A>Note: the amino end of the mature protein is blocked
 C:Genetics:
 A:Gene: GDB:BAX
 A:Cross-references: GDB:228082; OMIM:600040
 A:Map position: 19q13.3-19q13.4
 C:Superfamily: bcl transforming protein
 C:Keywords: alternative splicing; blocked amino end; cytosol; heterodimer; homodimer

```
Query Match      100.0%; Score 81; DB 2; length 218;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

OY      1 KKLSECLKRIGDELD 16
          |||||
Db      57 KKLSECLKRIGDELD 72

```

RESULT
D47538

bcl-2-associated protein x⁺ mouse
 N:Alternate names: Bax; programmed cell death membrane protein x
 C:Species: Mus musculus (house mouse)
 C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
 C:Accession: D47358
 R:Oliva, Z.N.; Millman, C.L.; Korsmeyer, S.J.
 R:Title: Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerates
 A:Reference number: A47538; MUID:93364978
 A:Accession: D47538
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-192
 A:Cross-references: GB:L22472
 C:Genetics:
 A:Gene: bax
 C:Superfamily: bcl transforming protein

Query Match	96.3%	Score 78;	DB 2;	Length 192;
Best Local Similarity	93.8%	Pred. No. 4.9e-05;		
Matches 15; Conservative	1;	Mismatches 0;	Indels 0;	Gaps 0;

```
QY      1 KKLSECLKRIGDELD 16
          |||||:|||||||
Db      57 KKLSECLRRIGDELD 72
```

RESULT 5
153295

Query Match	92.68;	Score 75;	DB 2;	Length 133;
Best Local Similarity	87.58;	Pred. No. 0.0001;		
Matches 14; Conservative	2;	Mismatches 0;	Indels 0;	Gaps 0;

```
QY      1 KKLSECLRIGDELD 16
          |||||:|||||:
Db      21 KKLSECLRIGDELDN 36
```

RESULT 6

A9050b
ser/chr protein kinase, probable [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C:Accession: A90506
R:She, O.; Singh, R.K.; Confalonieri, F.; Zivanovic, V.; Allard, G.; Awaletz, M.J.; Ch
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder
arrett, R.A.; Ragan, M.A.I.; Sensen, C.W.; Van der Oost, J.
Submitted to Genbank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: A90506
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-669 <XNU>
A:Cross-references: GB:AE006641; NID:913816645; PIDN:AAK3304.1; GSPDB:GN00155
A:Genetics:
A:Gene: SS03207

Query Match	60.58;	Score 49;	DB 2;	Length 669;
Best Local Similarity	50.08;	Pred. No. 6.9;		
Matches	7;	Conservative	0;	Indels 0;
		Mismatches		Gaps 0;

```
QY      3 LSECLKRI GDELD S 16  
          ::|::| | | | | :  
Db     175 VAOCMERIGDELEA 188
```

RESULT 7
FADOAA

alpha-actinin slime mold (*Dictyostelium discoideum*)
C:Species: *Dictyostelium discoideum*
C/Date: 30-Jun-1991 #sequence-revision 30-Jun-1991 #text-change 22-Jun-1999
C/Accession: S00103; A23006
R:Noegel, A.; Wilke, W.; Schleicher, M.
FEBS Lett. 221, 391-396, 1987
A>Title: Calcium-sensitive non-muscle alpha-actinin contains EF-hand structures and h
Reference number: S00103; M00D:87304850

A:Accession: S00103
A:Molecule type: mRNA
A:Residues: 1-862 <NO>
A:Cross-references: EMBL:Y00689; NID:g7177; PIDN:CA6865.1; PID:g7178
R:Witte, W.; Schleicher, M.; Lotzsch, F.; Noegel, A.
J. Cell Biol. 103, 969-975, 1986
A:Title: Studies on the transcription, translation, and structure of alpha-actinin in D.
A:Reference number: A29006; MUID:86304574
A:Accession: A29006
A:Molecule type: DNA
A:Residues: 92-359, 'P', 361-500, 'T', 502-505 <WT>
A:Cross-references: EMBL:X04324; NID:g7202; PIDN:CA2785.1; PID:g929034
C:Superfamily: alpha-actinin; alpha-actinin actin-binding domain homology; calmodulin re
C:Keywords: actin binding; calcium binding; duplication; EF hand; homodimer
F:21-236/Domain: alpha-actinin actin-binding domain homology <ACT>
F:266-377/Domain: spectrin/dystrophin repeat homology <SP1>
F:386-493/Domain: spectrin/dystrophin repeat homology <SP2>
F:502-607/Domain: spectrin/dystrophin repeat homology <SP3>
F:616-717/Domain: spectrin/dystrophin repeat homology <SP4>
F:730-762/Domain: calmodulin repeat homology <EF1>
F:766-798/Domain: calmodulin repeat homology <EF2>

Query Match 58.0%; Score 47; DB 1; Length 862;
Best Local Similarity 69.2%; Pred. No. 18;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 KLSKCKLRIGDEL 14
| | | | | | | | | |
Db 754 EFSCKLRIGDEL 766

RESULT 8
S64220
hypothetical protein YGL202w - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein G1253
C:Species: Saccharomyces cerevisiae
C:Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 29-Oct-1999
C:Accession: S64220
R:Bjournson, A.J.; McKeaynolds, A.D.K.; Wright, L.F.
submitted to the Protein Sequence Database, May 1996
A:Reference number: S64218
A:Accession: S64220
A:Molecule type: DNA
A:Residues: 1-500 <BO>
A:Cross-references: EMBL:Z72724; NID:g1322833; PIDN:CA96914.1; PID:e243502; PID:g132283
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SCD:ARO8
A:Cross-references: SGD:S0003170; MIPS:YGL202w
A:Map position: 7L

Query Match 54.3%; Score 44; DB 2; Length 500;
Best Local Similarity 64.3%; Pred. No. 33;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 KKLSECKLRIGDEL 14
| | | | | | | | | |
Db 479 EKLTEGKLRIGDEL 492

RESULT 9
F71868
hypothetical protein jhp0948 - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
C:Accession: F71868
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
Ives, C.; Gibson, R.; Moberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path

A:Reference number: A71800; MUID:99120557
A:Accession: F71868
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-92 <AR>
A:Cross-references: GB:AE001524; GB:AE001439; NID:g4155523; PIDN:AA006526.1; PID:g415
A:Experimental source: strain J99
C:Genetics:
A:Gene: jhp0948

Query Match 53.1%; Score 43; DB 2; Length 92;
Best Local Similarity 53.3%; Pred. No. 9.2;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 KKLSECKLRIGDEL 15
| | | | | | | | | |
Db 58 KKLSECKLRIGDEL 72

RESULT 10
PC2235
grpe protein - Synechococcus sp. (strain PCC 7942) (fragment)
C:Species: Synechococcus sp.
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 03-Nov-2000
C:Accession: PC2235; PC2156
R:Nimura, K.; Yoshikawa, H.; Takahashi, H.
Biochem. Biophys. Res. Commun. 201, 466-471, 1994
A:Title: Identification of dnaK multigene family in Synechococcus sp. PCC7942.
A:Reference number: PC2156; MUID:94257019
A:Accession: PC2235
A:Molecule type: DNA
A:Residues: 1-197 <NM>
A:Cross-references: DDBJ:D28550; NID:g507816; PIDN:BA05902.1; PID:dl006452; PID:g507
C:Genetics:
A:Gene: grpe
A:Superfamily: heat shock protein grpe
C:Keywords: heat shock; stress-induced protein

Query Match 53.1%; Score 43; DB 2; Length 197;
Best Local Similarity 72.7%; Pred. No. 19;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 KKLSECKLRIG 11
| | | | | | | | | |
Db 120 KQLVDCLRIG 130

RESULT 11
E69057
molybdopterin-guanine dinucleotide biosynthesis MoA related protein - Methanobacteri
C:Species: Methanobacterium thermoautotrophicum
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C:Accession: E69057
R:Smith, D.R.; Doucette-Stamm, L.A.; Delonghery, C.; Lee, H.; Dupois, J.; Aldredge, T.
Qiu, D.; Spadafora, R.; Viciare, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jivani,
K.; S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fu
A:Reference number: A69000; MUID:98037514
A:Accession: E69057
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-213 <MT>
A:Cross-references: GB:AE000803; GB:AE000666; NID:g2621179; PIDN:AA84649.1; PID:g262
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH143

Query Match 53.1%; Score 43; DB 2; Length 213;
Best Local Similarity 42.9%; Pred. No. 21;

Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 LSECCLKRIGDELD 16
DB 130 MKECFRRLQDSCDA 143

RESULT 12

E71098

Probable arom protein - Pyrococcus horikoshii

C:Species: Pyrococcus horikoshii

C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000

C:Accession: E71098

R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Hatakeyama, Y.; Hiro, Y.; Yamamoto, S.; Sekin

M.; Ohnuki, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi

DNA Res. 5, 55-76, 1998

A:Title: Complete sequence and gene organization of the genome of a hyperthermophilic

A:Reference number: A71000; MUID:98344137

A:Accession: E71098

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-217 <RAM>

A:Cross-References: GB:AP000004; NID:93236131; PIDN:BAM30147.1; PID:93257464

A:Experimental source: strain OT3

A:Note: This accession replaces an interim accession for a sequence replaced by GenBank

C:Genetics:

A:Gene: PHJ049

C:Superfamily: arom protein

Query Match 53.1%; Score 43; DB 2; Length 217;

Best Local Similarity 43.8%; Pred. No. 21;

Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 KRLSECLKRIGDELD 16

DB 74 KRLQECIDKLEKVD 89

RESULT 13

S08981

Malate dehydrogenase (EC 1.1.1.37) - Methanothermobacter ferredoxin

C:Species: Methanothermobacter ferredoxin

C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 18-Sep-1998

C:Accession: S08981; S08689

R:Honka, E.; Fabry, S.; Miermann, T.; Palm, P.; Hensel, R.

Eur. J. Biochem. 188, 623-632, 1990

A:Title: Properties and primary structure of the L-malate dehydrogenase from the extreme

A:Reference number: S08981; MUID:90235834

A:Accession: S08981

A:Molecule type: DNA

A:Residues: 1-339 <HON>

A:Cross-References: EMBL:X51840

R:Honka, E.; Fabry, S.; Miermann, T.; Palm, P.; Hensel, R.

submitted to the EMBL Data Library, February 1990

A:Reference number: S08689

A:Accession: S08689

A:Molecule type: DNA

A:Residues: 1-339 <HON>

A:Cross-References: EMBL:X51714

C:Genetics:

A:Start codon: TTG

C:Superfamily: malate dehydrogenase ylbC

C:Keywords: oxidoreductase; tricarboxylic acid cycle

Query Match 53.1%; Score 43; DB 2; Length 339;

Best Local Similarity 66.7%; Pred. No. 32;

Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 KRLSECLKRIGDELD 15

DB 320 KRLVEKLEIADLN 334

RESULT 14

AF1909

Two component hybrid sensor and regulator all0824 [imported] - Anabaena sp. (strain P

C:Species: Anabaena sp.

A:Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002

C:Accession: AF1909

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu

Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium

A:Reference number: AB1807; MUID:21595285; PMID:11759640

A:Accession: AF1909

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1002 <KUR>

A:Cross-References: GB:BA000019; PIDN:BAE72781.1; PID:917130169; GSPDB:GN00179

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: all0824

Query Match 53.1%; Score 43; DB 2; Length 1002;

Best Local Similarity 46.7%; Pred. No. 93;

Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 KRLSECLKRIGDELD 15

DB 571 KRLQTKRIGDNLN 565

RESULT 15

C96964

SAM-dependent methyltransferase related to tRNA(uracyl-5'-)-methyltransferase (trmA) fa

C:Species: Clostridium acetobutylicum

C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001

C:Accession: C96964

R:Rolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L

J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium

A:Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: C96964

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-460 <KUR>

A:Cross-References: GB:AE001437; PIDN:AAK78502.1; PID:915023386; GSPDB:GN00168

A:Experimental source: Clostridium acetobutylicum ATCC824

C:Genetics:

A:Gene: CAC0523

Query Match 52.5%; Score 42.5; DB 2; Length 460;

Best Local Similarity 71.4%; Pred. No. 52;

Matches 10; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 2 KRLSECLKRIGDELD 15

DB 103 KRLVEKLEIADLN 115

Search completed: September 20, 2002, 10:39:12
Job time: 484 sec

Fri Sep 20 11:03:14 2002

us-09-544-664-32.rpr

Page 5

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 20, 2002, 11:04:33 : Search time 44.99 Seconds
(without alignments)

13.770 Million cell updates/sec

Title: US-09-544-664-32

Sequence: 1 KXISECLKRIQDELDS 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	81	100.0	192	1	BAXA_BOVIN
2	81	100.0	192	1	BAXA_HUMAN
3	81	100.0	218	1	BAXA_HUMAN
4	78	96.3	192	1	BAXA_MOUSE
5	78	96.3	192	1	BAXA_MOUSE
6	47	58.0	862	1	BAXA_RAT
7	44	54.3	500	1	AKOB_YEAST
8	43	53.1	197	1	GRPE_SYNP7
9	43	53.1	197	1	MOBA_METTH
10	43	53.1	246	1	KAD_ARATH
11	43	51.9	339	1	MDH_MERPE
12	42	51.9	1325	1	G160_MOUSE
13	41	50.6	499	1	C71R_ARATH
14	40	49.4	118	1	Y380_METJA
15	40	49.4	126	1	Y095_METJA
16	40	49.4	143	1	YORH_TTV1
17	40	49.4	152	1	VG28_BPT4
18	40	49.4	349	1	TRPD_PSEAE
19	40	49.4	384	1	ODP2_MYCSE
20	40	49.4	485	1	YAB4_HAEIN
21	40	49.4	497	1	C716_ARATH
22	40	49.4	588	1	BIN1_MOUSE
23	40	49.4	588	1	BIN1_MOUSE
24	40	49.4	713	1	DDX4_RAT
25	39	48.1	234	1	RBSK_BACHD
26	39	48.1	404	1	Y256_METJA
27	39	48.1	702	1	DDX4_MOUSE
28	39	48.1	724	1	DDX4_HUMAN
29	39	48.1	1033	1	YDK9_SCHPO
30	38	46.9	162	1	ATPE_BACHD
31	38	46.9	197	1	YET4_METJA
32	38	46.9	242	1	TRPD_BACCA
33	38	46.9	281	1	KHSE_THEMA

34	38	46.9	381	1	BECA_STRPA	085502 streptococc
35	38	46.9	402	1	ODP2_MYCEN	P75392 mycoplasma
36	38	46.9	471	1	GATL_YEAST	P17648 saccharomyc
37	38	46.9	483	1	NIFD_KLEPN	P00466 klebsiella
38	38	46.9	499	1	C81E_GLYEC	P93147 glycyrrhiza
39	38	46.9	520	1	TR14_FUSSP	Q12612 fusarium sp
40	38	46.9	533	1	ENDR_BOVIN	P07106 bos taurus
41	38	46.9	552	1	HMA1_CUCSA	P93111 cucumis sat
42	38	46.9	669	1	PROD_DROME	Q04499 drosophila
43	38	46.9	704	1	PCCA_RAT	P14882 rattus norv
44	38	46.9	890	1	IMB2_HUMAN	Q92973 homo sapien
45	38	46.9	941	1	LOM2_ARATH	P93655 arabidopsis

ALIGNMENTS

RESULT 1
BAXA_BOVIN STANDARD; PRT: 192 AA.
ID BAXA_BOVIN
AC 002703;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Apoptosis regulator BAX, membrane isoform alpha.
GN BAX.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_Taxid:9913;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HOLSTEIN; TISSUE-Thymus;
RX MEDLINE-98162580; PubMed-9501056;
RA Reyes R.A., Cockrell G.L.;
RT "Increased ratio of bcl-2/bax expression is associated with bovine
leukemia virus-induced leukemogenesis in cattle."
RT Virology 242:184-192(1998).
RL
CC -1- FUNCTION: ACCELERATES PROGRAMED CELL DEATH BY BINDING TO, AND
ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ANOLOGYRUS
HOMOLOG E1B 19K PROTEIN. INDUCES THE RELEASE OF CYTOCHROME C,
ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS. BAX DEFICIENCY
LEADS TO LYMPHOID HYPERPLASIA AND MALE STERILITY, BECAUSE OF THE
CESSATION OF SPERM PRODUCTION (BY SIMILARITY).
CC -1- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,
E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Membrane-bound (By similarity).
CC -1- ALTERNATIVE PRODUCTS: A 21 kDa MEMBRANE PROTEIN ALPHA AND THE TWO
CYTOPLASMIC PROTEINS BETA AND GAMMA ARE GENERATED BY ALTERNATIVE
SPLICING.
CC -1- DOMAIN: INTACT B3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND
BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC APOPTOTIC MEMBERS OF THE BCL-2 FAMILY (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 1 (BH1).
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 2 (BH2).
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 3 (BH3).
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC
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CC
CC EMBL: U92569; AAC48806.1; -
DR HSSP: Q07817; IMAZ.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; BCL_2.
DR Pfam: PF00452; BCL-2; 1.

DR SMART: SM00337; BCL: 1.
 DR PROSITE: PS01080; BH1: 1.
 DR PROSITE: PS01258; BH2: 1.
 DR PROSITE: PS01259; BH3: 1.
 DR PROSITE: PS00062; BCL2 FAMILY: 1.
 KW Apoptosis: Transmembrane; Alternative splicing.
 FT DOMAIN 59 73 BH3.
 FT DOMAIN 98 118 BH1.
 FT DOMAIN 150 165 BH2.
 FT TRANSMEM 172 192 POTENTIAL.
 SQ SEQUENCE 192 AA: 21259 MW: 68455BABFD5F87E CRC64:

Query Match 100.0%; Score 81; DB 1; Length 192;
 Best Local Similarity 100.0%; Pred. No. 7e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KKLSECLKRIQDELDS 16
 DB 57 KKLSECLKRIQDELDS 72

RESULT 2
 BAXA_HUMAN STANDARD; PRT; 192 AA.
 ID BAXA_HUMAN
 AC 007812;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Apoptosis regulator BAX, membrane isoform alpha.
 GN BAX.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-B-cell;
 RX MEDLINE-93364978; PubMed-8358790;
 RA Oliva Z.N., Millman C.L., Korsmeyer S.J.;
 RT "Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that
 accelerates programmed cell death.";
 RL Cell 74:609-619(1993).
 RN [2]
 RP MUTAGENESIS, AND FUNCTION OF BH3 DOMAIN.
 RX MEDLINE-96091131; PubMed-8521816;
 RA Chittenden T., Flemington C., Houghton A.B., Ebb R.G., Gallo G.J.,
 RA Elangovan B., Chinnadurai G., Lutz R.J.;
 RT "A conserved domain in Bax, distinct from BH1 and BH2, mediates cell
 death and protein binding functions.";
 RL EMBO J. 14:5589-5596(1995).
 RN [3]
 RP VARIANT T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA ARG-67.
 RX MEDLINE-98200607; PubMed-9531611;
 RA Melierink J.P.P., Mensink E.J.B.M., Wang K., Sedlak T.W.,
 RA Sloetjes A.W., de Witte T., Waksman G., Korsmeyer S.J.;
 RT "Hematopoietic malignancies demonstrate loss-of-function mutations of
 BAX.";
 RL Blood 91:2991-2997(1998).
 CC -1- FUNCTION: ACCELERATES PROGRAMED CELL DEATH BY BINDING TO, AND
 ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS
 HOMOLOG E1B 19K PROTEIN. INDUCES THE RELEASE OF CYTOCHROME C,
 ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS.
 CC -1- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,
 E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1.
 CC -1- SUBCELLULAR LOCATION: Membrane-bound
 CC -1- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE
 CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY
 ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
 CC -1- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAX, BAD AND
 BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
 WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.

CC APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
 CC -1- DISEASE: DEFECTS IN BAX ARE FOUND IN SOME PATIENTS WITH T-CELL
 ACUTE LYMPHOBLASTIC LEUKEMIA.
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 1 (BH1).
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 2 (BH2).
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 3 (BH3).
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
 CC -----
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 CC -----

DR EMBL: L22473; AAA03619.1; -
 DR PIR: A47538; A47538.
 DR HSSP: Q07817; 1MAZ.
 DR MIM: 600040;
 DR InterPro: IPR002475; BCL2 family.
 DR InterPro: IPR000712; Bcl_2.
 DR Pfam: PF00452; Bcl-2; 1.
 DR SMART: SM00337; BCL: 1.
 DR PROSITE: PS00062; BCL2 FAMILY: 1.
 DR PROSITE: PS01080; BH1: 1.
 DR PROSITE: PS01258; BH2: 1.
 DR PROSITE: PS01259; BH3: 1.
 KW Apoptosis: Transmembrane; Alternative splicing; Disease mutation.
 FT DOMAIN 59 73 BH3.
 FT DOMAIN 98 118 BH1.
 FT DOMAIN 150 165 BH2.
 FT TRANSMEM 172 192 POTENTIAL.
 FT VARIANT 67 67 G -> R (IN T-CELL ACUTE LYMPHOBLASTIC
 LEUKEMIA).
 FT
 SQ SEQUENCE 192 AA: 21184 MW: 60000A7DEE494 CRC64:
 FT

Query Match 100.0%; Score 81; DB 1; Length 192;
 Best Local Similarity 100.0%; Pred. No. 7e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KKLSECLKRIQDELDS 16
 DB 57 KKLSECLKRIQDELDS 72

RESULT 3
 BAXB_HUMAN STANDARD; PRT; 218 AA.
 ID BAXB_HUMAN
 AC 007814;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Apoptosis regulator BAX, cytoplasmic isoform beta.
 GN BAX.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-B-cell;
 RX MEDLINE-93364978; PubMed-8358790;
 RA Oliva Z.N., Millman C.L., Korsmeyer S.J.;
 RT "Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that
 accelerates programmed cell death.";
 RL Cell 74:609-619(1993).
 CC -1- FUNCTION: ACCELERATES PROGRAMED CELL DEATH BY BINDING TO, AND
 ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS
 HOMOLOG E1B 19K PROTEIN.
 CC -1- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,

```

CC      E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1.
CC      -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC      -1- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE
CC      CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY
CC      ALTERNATIVE SPLICING.
CC      -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
CC      -1- DOMAIN: INTERACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND
CC      BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
CC      WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC      -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOMOLOGY DOMAIN 1 (BH1).
CC      -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOMOLOGY DOMAIN 2 (BH2).
CC      -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOMOLOGY DOMAIN 3 (BH3).
CC      -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC      -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: L22474; AAA03620.1; -.
CC      PIR: B47538; B47538.
CC      HSSP: Q07817; IMAZ.
CC      MIM: 600040; -.
CC      InterPro: IPR002475; BCL2_family.
CC      InterPro: IPR000712; BCL_2.
CC      Pfam: PF00452; Bcl-2; 1.
CC      SMART: SM00337; BCL_1.
CC      PROSITE: PS01080; BH1; 1.
CC      PROSITE: PS01258; BH2; 1.
CC      PROSITE: PS01259; BH3; 1.
CC      PROSITE: PS50062; BCL2_FAMILY; 1.
CC      Apoptosis: Alternative splicing.
CC      DOMAIN 59 73 BH3.
CC      FT DOMAIN 98 118 BH1.
CC      FT DOMAIN 150 165 BH2.
CC      SO SEQUENCE 218 AA; 24220 MW; F69DCD70F960192F CRC64;

Query Match 100.0%; Score 81; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 7.9e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLSECLKRIGDELD 16
DB 57 KKLSECLKRIGDELD 72

RESULT 4
ID BAXA_MOUSE STANDARD; PRT; 192 AA.
AC Q07813;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Apoptosis regulator BAX, membrane isoform alpha.
GN BAX.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X DBA/2;
RX MEDLINE=93364978; PubMed=8358790;
RA Olivai Z.N., Milliman C.L., Korsmeyer S.J.;
RT "Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that
RT accelerates programmed cell death.";
RL Cell 74:609-619(1993).
-1- FUNCTION: ACCELERATES PROGRAMED CELL DEATH BY BINDING TO, AND

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CC      ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS
CC      HOMOLOG E1B 19K PROTEIN. INDUCES THE RELEASE OF CYTOCHROME C,
CC      ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS. BAX DEFICIENCY
CC      LEADS TO LYMPHOID HYPERPLASIA AND MALE STERILITY, BECAUSE OF THE
CC      CESSATION OF SPERM PRODUCTION.
CC      -1- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,
CC      E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1.
CC      -1- SUBCELLULAR LOCATION: Membrane-bound.
CC      -1- ALTERNATIVE PRODUCTS: A 21 kDa GAMMA ARE GENERATED BY ALTERNATIVE
CC      SPLICING.
CC      -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
CC      -1- DOMAIN: INTERACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND
CC      BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
CC      WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC      -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOMOLOGY DOMAIN 1 (BH1).
CC      -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOMOLOGY DOMAIN 2 (BH2).
CC      -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOMOLOGY DOMAIN 3 (BH3).
CC      -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: L22472; AAA03622.1; -.
CC      HSSP: Q07817; IMAZ.
CC      MGD: MG1:99702; Bax.
CC      InterPro: IPR002475; BCL2_family.
CC      InterPro: IPR000712; BCL_2.
CC      Pfam: PF00452; Bcl-2; 1.
CC      SMART: SM00337; BCL_1.
CC      PROSITE: PS01080; BH1; 1.
CC      PROSITE: PS01258; BH2; 1.
CC      PROSITE: PS01259; BH3; 1.
CC      PROSITE: PS50062; BCL2_FAMILY; 1.
CC      Apoptosis: Transmembrane; Alternative splicing.
CC      DOMAIN 59 73 BH3.
CC      FT DOMAIN 98 118 BH1.
CC      FT DOMAIN 150 165 BH2.
CC      FT TRANSEM 172 192 POTENTIAL.
CC      SO SEQUENCE 192 AA; 21394 MW; D2E0B3566579FAFF CRC64;

Query Match 96.3%; Score 78; DB 1; Length 192;
Best Local Similarity 93.8%; Pred. No. 2.1e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLSECLKRIGDELD 16
DB 57 KKLSECLKRIGDELD 72

RESULT 5
ID BAXA_RAT STANDARD; PRT; 192 AA.
AC Q63690; Q62995; Q64383;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Apoptosis regulator BAX, membrane isoform alpha.
GN BAX.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96178771; PubMed=8600029;

```

RA Han J., Sabbatini P., Perez D., Rao L., Modha D., White E.;
 RT "The E1B 19K protein blocks apoptosis by interacting with and
 RT inhibiting the p53-inducible and death-promoting Bax protein.";
 RL Genes Dev. 10:461-477(1996).
 RN (2)
 RP SEQUENCE OF 75-192 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=97147318; PubMed=8994223;
 RA Madison D.L., Pfeiffer S.E.;
 RT "Cloning of the 3' end of rat bax-alpha and corresponding
 RT developmental down-regulation in differentiating primary, cultured
 RT oligodendrocytes.";
 RL Neurosci. Lett. 220:183-186(1996).
 RN [3]
 RP SEQUENCE OF 37-169 FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Ovary;
 RX MEDLINE=95129487; PubMed=7828536;
 RA Tilly J.L., Tilly K.L., Kenton M.L., Johnson A.L.;
 RT "Expression of members of the bcl-2 gene family in the immature rat
 RT ovary: equine chorionic gonadotropin-mediated inhibition of granulosa
 RT cell apoptosis is associated with decreased bax and constitutive
 RT bcl-2 and bcl-xl messenger ribonucleic acid levels.";
 RL Endocrinology 136:232-241(1995).
 CC -1- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO, AND
 CC ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS
 CC HOMOLOG E1B 19K PROTEIN. INDUCES THE RELEASE OF CYTOCHROME C,
 CC ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS.
 CC -1- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,
 CC E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1.
 CC -1- SUBCELLULAR LOCATION: Membrane-bound.
 CC -1- ALTERNATIVE PRODUCTS: A 21 kDa MEMBRANE PROTEIN ALPHA AND THE TWO
 CC CYTOPLASMIC PROTEINS BETA AND GAMMA ARE GENERATED BY ALTERNATIVE
 CC SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES, WITH
 CC HIGHEST LEVELS IN THE TESTIS AND OVARY.
 CC -1- DOMAIN: INTACT B3 DOMAIN IS REQUIRED BY BIK, BID, BAX, BAD AND
 CC BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
 CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 1 (BH1).
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 2 (BH2).
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 3 (BH3).
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
 CC -----
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 CC -----
 DR EMBL: U49729; AAC6337.1; -
 DR EMBL: U5184; AAC5298.1; -
 DR EMBL: U32098; AAA75200.1; -
 DR EMBL: U76511; AAC60700.2; -
 DR HSSP: Q07817; 1MAZ.
 DR InterPro: IPR002475; BCL2_family.
 DR InterPro: IPR000712; BCL2.
 DR Pfam: PF00452; BCL2; 1.
 DR SMART: SM00337; BCL; 1.
 DR PROSITE: PS01080; BH1; 1.
 DR PROSITE: PS01258; BH2; 1.
 DR PROSITE: PS01259; BH3; 1.
 DR PROSITE: PS0062; BCL2_FAMILY; 1.
 KW Apoptosis; Transmembrane; Alternative splicing.
 FT DOMAIN 59 73 BH3.
 FT DOMAIN 98 118 BH1.
 FT DOMAIN 150 165 BH2.
 FT TRANSMEM 172 192 POTENTIAL.
 FT CONFLICT 72 72 S -> N (IN REF. 3).
 FT CONFLICT 76 76 L -> M (IN REF. 2).
 FT CONFLICT 126 126 C -> Y (IN REF. 2).

FT CONFLICT 149 149 L -> F (IN REF. 3).
 FT CONFLICT 159 159 D -> E (IN REF. 1).
 SQ SEQUENCE 192 AA; 21350 MM; 7B3CD198B56DF589 CRC64;
 Query Match 96.38; Score 78; DB 1; Length 192;
 Best Local Similarity 93.88; Pred. No. 2,1e-05;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KKLSCLKRIGDELDS 16
 DB 57 KKLSCLKRIGDELDS 72
 RESULT 6
 AACT_DICDI STANDARD; PRT: 862 AA.
 ID AACT_DICDI
 AC P05095;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alpha-actinin, non-muscular (F-actin cross linking protein).
 GN ABPA.
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
 OX NCBI_TaxID=44689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AX2;
 RX MEDLINE=87304850; PubMed=3622778;
 RA Noegel A., Witke W., Schleicher M.;
 RT "Calcium-sensitive non-muscle alpha-actinin contains EF-hand
 RT structures and highly conserved regions.";
 RL FEBS Lett. 221:391-396(1987).
 RN [2]
 RP SEQUENCE OF 92-505 FROM N.A.
 RC STRAIN=AX2;
 RX MEDLINE=86304574; PubMed=3745276;
 RA Witke W., Schleicher M., Lottspeich F., Noegel A.;
 RT "Studies on the transcription, translation, and structure of alpha-
 RT actinin in dictyostelium discoideum.";
 RL J. Cell Biol. 103:969-975(1986).
 CC -1- FUNCTION: F-ACTIN CROSS-LINKING PROTEIN WHICH IS THOUGHT TO ANCHOR
 CC ACTIN TO A VARIETY OF INTRACELLULAR STRUCTURES. THIS IS A BUNDLING
 CC PROTEIN.
 CC -1- SUBUNIT: HOMODIMER, ANTIPARALLEL.
 CC -1- SIMILARITY: CONTAINS 1 ACTIN-BINDING DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 CALPONIN-HOMOLOG (CH) DOMAINS.
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
 CC -1- SIMILARITY: CONTAINS 4 SPECTRIN REPEATS.
 CC -----
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 CC -----
 DR EMBL: Y00689; CAA68685.1; -
 DR EMBL: X04324; CAA27855.1; -
 DR PIR: S00103; FAD0AA.
 DR HSSP: Q01082; 1BKR.
 DR Dictydb: DD01003; abpa.
 DR InterPro: IPR001589; Actinin_act_bind.
 DR InterPro: IPR001715; Calponin_hom.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR002017; Spectrin.
 DR Pfam: PF00307; CH; 2.
 DR Pfam: PF00036; efhand; 2.
 DR Pfam: PF00435; spectrin; 4.
 DR SMART: SM00033; CH; 2.
 DR SMART: SM00054; EFh; 2.

DR SMART; SM00150; SPEC; 3.
 DR PROSITE; PS00019; ACTININ_1; 1.
 DR PROSITE; PS00020; ACTININ_2; 1.
 DR PROSITE; PS00021; CH; 2.
 DR PROSITE; PS00018; EF_HAND; 2.
 KW Actin-binding; Calcium-binding; Repeat.
 FT DOMAIN 1 240 ACTIN-BINDING.
 FT DOMAIN 22 128 CH 1.
 FT DOMAIN 137 240 CH 2.
 FT REPEAT 241 366 SPECTRIN 1.
 FT REPEAT 367 481 SPECTRIN 2.
 FT REPEAT 482 602 SPECTRIN 3.
 FT REPEAT 603 715 SPECTRIN 4.
 FT CA_BIND 743 754 EF_HAND 1 (BY SIMILARITY).
 FT CA_BIND 779 790 EF_HAND 2 (BY SIMILARITY).
 FT CONFLICT 360 360 T -> P (IN REF. 2).
 FT CONFLICT 501 501 I -> T (IN REF. 2).
 SQ SEQUENCE 862 AA; 97598 MW; 15608ADB71213226 CRC64;

Query Match Best Local Similarity 58.0%; Score 47; DB 1; Length 862;
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 KLSCLKRIGDEL 14
 : | | | | | | | | | |
 Db 754 EFSCLKRIGDEL 766

RESULT 7
 ARO8_YEAST STANDARD; PRT; 500 AA.
 ID ARO8_YEAST
 AC P53090;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Aromatic amino acid aminotransferase I (EC 2.6.1.-).
 GN ARO8 OR YGL202W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SIGMA 1278B;
 RX MEDLINE=98151783; PubMed=9491083;
 RA Iragui I., Vissers S., Cartiaux M., Urrestarazu A.;
 RT "Characterisation of Saccharomyces cerevisiae ARO8 and ARO9 genes
 encoding aromatic aminotransferases I and II reveals a new
 Mol. Gen. Genet. 257:238-248(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Bjournson A.J., McReynolds A.D.K., Wright L.F.;
 RT Submitted (May-1996) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: TO YEAST ARO9.
 CC -----
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 CC -----
 DR EMBL; Y13624; CAA73946.1; -;
 DR EMBL; Z72724; CAA96914.1; -;
 DR SGD; S0003170; ARO8.
 KW Transferase; Aminotransferase.
 SQ SEQUENCE 500 AA; 56177 MW; D0D11640D2C560D CRC64;

Query Match

54.3%; Score 44; DB 1; Length 500;

Best Local Similarity 64.3%; Pred. No. 12;
 Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLSCLKRIGDEL 14
 : | | | | | | | | | |
 Db 479 EKLEGLKRIIGDEL 492

RESULT 8
 GRPE_STNP7 STANDARD; PRT; 197 AA.
 ID GRPE_STNP7
 AC Q59984;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE GRPE protein (HSP-70 cofactor) (Fragment).
 GN GRPE.
 OS Synechococcus sp. (strain PCC 7942) (Anaerobically grown R2).
 CC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
 OX NCBI_TaxID=1140;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94257019; PubMed=8198610;
 RA Nimura K., Yoshikawa H., Takahashi H.;
 RT "Identification of dnaK multigene family in Synechococcus sp.
 PCC7942.";
 RL Biochem. Biophys. Res. Commun. 201:466-471(1994).
 CC -1- FUNCTION: STIMULATES, JOINTLY WITH DNMJ, THE APPASE ACTIVITY OF
 DNK. HELPS TO RELEASE ADP FROM DNK THUS ALLOWING DNK TO RECYCLE
 MORE EFFICIENTLY (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE GRPE FAMILY.
 CC -----
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 CC -----
 DR EMBL; D28550; BAA05902.1; -;
 DR HSP; P08372; IDKG.
 DR InterPro; IPR000740; GRPE.
 DR Pfam; PF01025; GRPE; 1.
 DR PROSITE; PS01071; GRPE; 1.
 KW Heat shock; Chaperone.
 FT NON_TER 1
 FT SEQUENCE 197 AA; 21833 MW; FDFPD6FC98BE96E9 CRC64;

Query Match Best Local Similarity 53.1%; Score 43; DB 1; Length 197;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLSCLKRIG 11
 : | | | | | | | | | |
 Db 120 KQVDCIKRIG 130

RESULT 9
 MOBA_METHH STANDARD; PRT; 197 AA.
 ID MOBA_METHH
 AC Q26246;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Probable molybdopter-in-guanine dinucleotide biosynthesis protein A.
 GN MOBA OR MTH143.
 OS Methanobacterium thermoautotrophicum.
 CC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
 CC Methanothermobacter.
 OX NCBI_TaxID=145262;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-DELTA H;
 RX MEDLINE-98037514; PubMed-9371463;
 RA Smith D.R., Doucette-Stamm L.A., Delonghery C., Lee H.-M., Dubois J.,
 RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
 RA Harrison D., Hoang L., Keagle P., Lamm W., Pochler B., Qiu D.,
 RA Spadafora R., Vicore R., Wang Y., Wierzbowski J., Gibson R.,
 RA Jiwani N., Caruso A., Bush D., Sater H., Patwell D., Prabhakar S.,
 RA McDougall S., Shimer G., Goyal A., Pletrovski S., Church G.M.,
 RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
 RT *Complete genome sequence of *Methanobacterium thermoautotrophicum*
 RT deltaH: functional analysis and comparative genomics.*;
 RL J. Bacteriol. 179:7135-7151(1997).
 CC -1- FUNCTION: LINKS A GUANOSINE 5'-PHOSPHATE TO MOLYBDOTERIN (MP)
 CC FORMING MOLYBDOPTERIN GUANINE DINUCLEOTIDE (MGD) (BY SIMILARITY).
 CC -1- PATHWAY: MOLYBDENUM COFACTOR BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE MOBA FAMILY.
 CC -----
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 CC -----
 CC EMBL: AE008003; AAB84649.1; ALT_INIT.
 CC Molybdenum cofactor biosynthesis; GTP-binding; Complete proteome.
 KW SEQUENCE 197 AA; 21556 MW; 6A8D29D2B0AD8619 CRC64;
 SQ

Query Match 53.1%; Score 43; DB 1; Length 197;
 Best Local Similarity 42.9%; Pred. No. 7;
 Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 3 LSECLKRIQDELD 16
 DB 114 MKECFRRLDSCDA 127

RESULT 10
 KAD_ARATH ID KAD_ARATH STANDARD; PRT; 246 AA.
 AC 082514; Q9FWM2;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).
 GN ADK1 OR ATG63400 OR MLE2.3.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID-3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RA Weiers B., Thornburg R.;
 RT *Characterization of the cDNA and gene for the Arabidopsis thaliana
 RT adenylate kinase.*;
 RL (10) Plant Gene Register PCR8-166.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RX MEDLINE-98162728; PubMed-9501997;
 RA Nakamura Y., Sato S., Kaneko T., Kotani H., Asamizu E., Miyajima N.,
 RA Tabata S.;
 RT *Structural analysis of Arabidopsis thaliana chromosome 5. III.
 RT Sequence features of the regions of 1,191,918 bp covered by seventeen
 RT DNA Res. 4:401-414(1997).
 CC -1- FUNCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR

CC MAINTENANCE AND CELL GROWTH.
 CC -1- CATALYTIC ACTIVITY: ATP + AMP = ADP + ADP.
 CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
 CC -----
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 CC -----
 CC EMBL: AF082882; AAC78478.1; -;
 CC EMBL: AB007649; BAB08805.1; -;
 CC HSSP: P07170; IAKY.
 CC Mendel: 33102; Arab.2711.33102.
 CC InterPro: IPR000850; Adenylate_kin.
 CC Pfam: PF00406; adenylatekinase.1.
 CC PRINTS: PR00094; Adenylate_kinase.
 CC ProDom: PD000657; Adenylate_kin.1.
 CC PROSITE: PS00113; ADENYLATE_KINASE; 1.
 CC Transferrase; Kinase; ATP-binding; Multigene family.
 FT NP_BIND 40 48 ATP (BY SIMILARITY).
 FT CONFLICT 144 152 LNFALDDAI -> STLLIMTOS (IN REF. 1).
 SQ SEQUENCE 246 AA; 26932 MW; 659903FBD84B39C7 CRC64;

Query Match 53.1%; Score 43; DB 1; Length 246;
 Best Local Similarity 60.0%; Pred. No. 8.6;
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 KKLSECLKRIQDELD 15
 DB 127 EKLDEMLKRGTEID 141

RESULT 11
 MDH_METFE ID MDH_METFE STANDARD; PRT; 339 AA.
 AC P16142;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Malate/L-sulfolactate dehydrogenase (EC 1.1.1.37) (EC 1.1.1.82).
 GN MDH.
 OS Methanothermobacter feravidus.
 OC Archaea; Euryarchaeota; Methanobacteriales; Methanothermaceae;
 OC Methanothermobacter.
 OX NCBI_TaxID-2180;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-24.
 RC STRAIN-W245 / DSM 2088;
 RX MEDLINE-90235634; PubMed-2110059;
 RA Honka E., Fabry S., Niermann T., Palm P., Hensel R.;
 RT *Properties and primary structure of the L-malate dehydrogenase from
 RT the extremely thermophilic archaeobacterium *Methanothermobacter feravidus*.*;
 RL Eur. J. Biochem. 188:623-632(1990).
 RN [2]
 RP FUNCTION.
 RX MEDLINE-20309698; PubMed-10850983;
 RA Graupner M., Xu H., White R.H.;
 RT *Identification of an archaeal 2-hydroxy acid dehydrogenase catalyzing
 RT reactions involved in coenzyme biosynthesis in methanocorphaea.*;
 RL J. Bacteriol. 182:3688-3692(2000).
 CC -1- FUNCTION: Acts on oxalacetate, sulfolpyruvate but not on pyruvate.
 CC Has a higher selectivity for the coenzyme NADH than for NADPH.
 CC -1- CATALYTIC ACTIVITY: (S)-malate + NAD(P)(+) = oxalacetate +
 CC NAD(P)H.
 CC -1- CATALYTIC ACTIVITY: (R)-sulfolactate + NAD(P)(+) = sulfolpyruvate +
 CC NAD(P)H.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE LDH2/MDH2 OXIDOREDUCTASE FAMILY.


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RT      *Sequence and analysis of chromosome 4 of the plant Arabidopsis
RL      thaliana.
RN      Nature 402:769-777(1999).
RN      [2]
RN      CONCEPTUAL TRANSLATION.
RA      Axelisen K.B.
RA      Unpublished observations (APR-2001).
CC      -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC      -1- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO WRONG EXON
CC      PREDICTIONS FROM THE GENOMIC SEQUENCE. THE PREDICTION MIX UP
CC      CYP71A27 WITH CYP71A28. THERE IS FURTHERMORE A FRAMESHIFT IN THE
CC      GENOMIC SEQUENCE.
CC      -----
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CC      -----
DR      EMBL: AL022224; CAI18249.1; ALT_FRAME.
DR      EMBL: AL161552; CAB79024.1; ALT_FRAME.
DR      InterPro: IPR001128; CYL_P450.
DR      Pfam: PF00067; P450; 1.
DR      PRINTS: PR00385; P450.
DR      PROSITE: PS00086; CYTOCHROME_P450; 1.
KM      Oxidoreductase: Monooxygenase: Transmembrane; Heme: Multigene family.
FT      BINDING 3 23 POTENTIAL.
FT      TRANSMEM 3 23 HEME (BY SIMILARITY).
FT      DOMAIN 164 438 POLY-SER.
FT      SEQUENCE 499 AA; 56990 MW; ASFBZPFI83780B0A CRC64;
SQ
Query Match
Best Local Similarity 50.6%; Score 41; DB 1; Length 499;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
OY      5 ECLKRIQDELDS 16
DB      320 ECKMKRLDEINS 331
RESULT 14
Y380_METJA STANDARD; PRT; 118 AA.
ID      Y380_METJA
AC      057825;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Hypothetical protein M70380.
GN      M70380.
OS      Methanococcus jannaschii.
OC      Archaea: Euryarchaeota; Methanococcales; Methanococcaceae;
OC      Methanococcus
OX      NCBI_TaxID=2190;
RN      (1)
RP      SEQUENCE FROM N.A.
RC      STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
RA      MEDLINE-96337999; PubMed-8688087;
RA      Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA      Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA      Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA      Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA      Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA      Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA      Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA      Klenk H.-P., Fraser G.M., Smith H.O., Woese C.R., Venter J.C.;
RA      Complete genome sequence of the methanogenic archaeon, Methanococcus
RA      jannaschii.
RT      Science 273:1058-1073(1996).
RL      -----
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CC      -----
DR      EMBL: U67467; AAB98086.1;
DR      TIGR: M70095;
KM      Hypothetical protein; Complete proteome.
SQ      SEQUENCE 126 AA; 14709 MW; DA1D24ABDD043E9B CRC64;

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CC      -----
DR      EMBL: U67491; AAB98377.1;
DR      TIGR: M70380;
KM      Hypothetical protein; Complete proteome.
SQ      SEQUENCE 118 AA; 13758 MW; 322C1759E495B1DD CRC64;

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Query Match
Best Local Similarity 49.4%; Score 40; DB 1; Length 118;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
OY      1 KRLECKLRIGD 12
DB      77 KRLEFLREIGD 88
RESULT 15
Y095_METJA STANDARD; PRT; 126 AA.
ID      Y095_METJA
AC      057560;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Hypothetical protein M70095.
GN      M70095.
OS      Methanococcus jannaschii.
OC      Archaea: Euryarchaeota; Methanococcales; Methanococcaceae;
OC      Methanococcus
OX      NCBI_TaxID=2190;
RN      (1)
RP      SEQUENCE FROM N.A.
RC      STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
RA      MEDLINE-96337999; PubMed-8688087;
RA      Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA      Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA      Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA      Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA      Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA      Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA      Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA      Klenk H.-P., Fraser G.M., Smith H.O., Woese C.R., Venter J.C.;
RA      Complete genome sequence of the methanogenic archaeon, Methanococcus
RA      jannaschii.
RT      Science 273:1058-1073(1996).
RL      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch)
CC      -----
DR      EMBL: U67467; AAB98086.1;
DR      TIGR: M70095;
KM      Hypothetical protein; Complete proteome.
SQ      SEQUENCE 126 AA; 14709 MW; DA1D24ABDD043E9B CRC64;

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Query Match
Best Local Similarity 49.4%; Score 40; DB 1; Length 126;
Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
OY      1 KRLECKLRIGDEL 15
DB      54 KEVKELIDKVGDEF 68

```


Fri Sep 20 11:03:15 2002

us-09-544-664-32.rsp

Page 9

Search completed: September 20, 2002, 11:04:34
Job time: 1631 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 20, 2002, 11:03:46 ; Search time 172.19 Seconds,
(without alignments)
16.075 Million cell updates/sec

Title: us-09-544-664-32
Sequence: 1 KKLSECLKRIQDELDS 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_19: *
1: sp.archaea: *
2: sp.bacteria: *
3: sp.fungi: *
4: sp.human: *
5: sp.invertebrate: *
6: sp.mammal: *
7: sp.mhc: *
8: sp.organelle: *
9: sp.phage: *
10: sp.plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp-vertebrate: *
14: sp-unclassified: *
15: sp_rvirus: *
16: sp.bacteriap: *
17: sp-archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	149	6	Q9GMG7
2	81	100.0	164	4	Q9UQD6
3	81	100.0	179	4	Q9NYG7
4	75	92.6	173	11	Q9JXL3
5	69	85.2	221	13	Q98UJ3
6	60	74.1	192	13	Q9I9M4
7	51	63.0	1124	12	Q9DVM1
8	49	60.5	669	17	Q97UJ8
9	46	56.8	488	11	Q99KZ6
10	45	55.6	508	17	Q979F5
11	44	54.3	2376	10	Q9FIN7
12	44	54.3	226	11	Q9CVN5
13	44	54.3	303	11	Q9D9D5
14	43	53.1	72	15	Q9YR06
15	43	53.1	92	16	Q9ZK17
16	43	53.1	169	2	P95332

17	43	53.1	217	17	Q58748	058748 pyrococcus
18	43	53.1	403	5	Q9V608	Q9V608 drosophila
19	43	53.1	527	12	Q9JGP5	Q9JGP5 epizootic h
20	43	53.1	661	17	Q973T7	Q973T7 sulfolobus
21	42.5	52.5	302	17	Q97CJ1	Q97CJ1 thermoplasma
22	42.5	52.5	460	16	Q97LNM	Q97LNM clostridium
23	42	51.9	148	12	Q91TK5	Q91TK5 lupala hep
24	42	51.9	375	10	Q9FRD2	Q9FRD2 oryza sativ
25	42	51.9	256	2	P96145	P96145 uncultured
26	42	51.9	677	2	Q9X878	Q9X878 streptomyces
27	42	51.9	1447	11	Q9OYT2	Q9OYT2 mus musculus
28	42	51.9	1487	11	Q9OYR3	Q9OYR3 mus musculus
29	42	50.6	15	4	Q9OCZ7	Q9OCZ7 homo sapien
30	41	50.6	151	2	Q48800	Q48800 legionella
31	41	50.6	166	5	Q9SV94	Q9SV94 anopheles s
32	41	50.6	285	5	Q9U632	Q9U632 trichomegal
33	41	50.6	286	5	Q27341	Q27341 trichomegal
34	41	50.6	350	5	Q22882	Q22882 caenorhabdi
35	41	50.6	520	3	Q9C1B0	Q9C1B0 gibberella
36	41	50.6	520	3	Q96M90	Q96M90 gibberella
37	41	50.6	520	3	Q96M83	Q96M83 gibberella
38	41	50.6	571	11	Q55160	Q55160 ratius norv
39	41	50.6	662	16	Q98J51	Q98J51 rhizobium 1
40	41	50.6	665	4	Q9H9N3	Q9H9N3 homo sapien
41	41	50.6	670	4	Q9HCL9	Q9HCL9 homo sapien
42	41	50.6	1280	5	Q22554	Q22554 caenorhabdi
43	41	50.6	2138	5	Q9XZK3	Q9XZK3 amoeba prot
44	40	49.4	119	2	Q93SK2	Q93SK2 myxococcus
45	40	49.4	152	9	Q9T0T7	Q9T0T7 bacteriophag

ALIGNMENTS

RESULT 1
ID Q9GMG7 PRELIMINARY; PRT; 149 AA.
AC Q9GMG7;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE BCL2-ASSOCIATED PROTEIN BAX (FRAGMENT).
GN BAX.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
CX NCBI_TaxID:9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Ovary;
RA Murray J.F., Dong Y.B., Leigh A.J., Scaramuzzi R.J., Carter N.D.;
RT "Bax in the sheep ovary".
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF163774; AA98242.1; -
DR HSSP; Q07817; 1AAZ.
DR InterPro; IPR002475; BCL2_family.
DR InterPro; IPR000712; BCL_2.
DR Pfam; PF00452; BCL_2; 1.
DR SMART; SM00337; BCL; 1.
DR PROSITE; PSS0062; BCL2_FAMILY; 1.
DR PROSITE; PSS0080; BHL_1.
FT NON_TER
FT NON_TER
FT SEQUENCE 149 AA; 16917 MW; ABC10CBES64EA2D CRC64;

Query Match 100.0%; Score 81; DB 6; Length 149;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKLSECLKRIQDELDS 16
|||||

Db 29 KKLSECLKRIIGDELDLS 44

RESULT 2

Q9UD06 PRELIMINARY: PRT: 164 AA.

AC 09UD06: 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

DE BAX EPSILON.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCBI_TaxID=9606;

OX NCB1_TaxID=9606;

RN (1)

RP SEQUENCE FROM N.A.

RC TISSUE=BRIN.

RX MEDLINE=99120940; PubMed=9920818;

RA Shi B., Triebe D., Kaji S., Iwata K.K., Bruskin A., Mahajna J.;

RT Identification and characterization of baxepsilon, a novel bax variant missing the BH2 and the transmembrane domains.";

RL Biochem. Biophys. Res. Commun. 254:779-785(1999).

DR EMBL: AF007826; AAD2706.1; -

DR InterPro: IPR002475; BCL2_family.

DR InterPro: IPR000712; BCL_2.

DR Pfam: PF00452; Bcl-2; 1.

DR SMART: SM00337; BCL_1.

DR PROSITE: PS50062; BCL2_FAMILY; 1.

DR PROSITE: PS01080; BH1; 1.

DR PROSITE: PS01259; BH3; 1.

SO SEQUENCE 164 AA; 18129 MW; 12CDB8073EF4C9E CRC64;

QY 1 KKLSECLKRIIGDELDLS 16

Db 57 KKLSECLKRIIGDELDLS 72

Query Match 100.0%; Score 81; DB 4; Length 164;

Best Local Similarity 100.0%; Pred. No. 2.2e-05;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3

ID 09NYG7 PRELIMINARY: PRT: 179 AA.

AC 09NYG7: 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE BAX-SIGMA.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCBI_TaxID=9606;

OX NCB1_TaxID=9606;

RN (1)

RP SEQUENCE FROM N.A.

RX MEDLINE=20237095; PubMed=10772918;

RA Schmitt E., Paquet C., Beauchemin M., Dever-Bertrand J., Bertrand R.;

RT Characterization of bax-sigma, a cell death-inducing isoform of Bax.";

RL Biochem. Biophys. Res. Commun. 270:868-879(2000).

DR EMBL: AF247393; AAF71267.1; -

DR HSSP: Q07817; IMAZ.

DR InterPro: IPR002475; BCL2_family.

DR InterPro: IPR000712; BCL_2.

DR Pfam: PF00452; Bcl-2; 1.

DR SMART: SM00337; BCL_1.

DR PROSITE: PS50062; BCL2_FAMILY; 1.

DR PROSITE: PS01080; BH1; 1.

DR PROSITE: PS01259; BH3; 1.

SO SEQUENCE 179 AA; 19718 MW; 5802B0AC73B2FACE CRC64;

Query Match 100.0%; Score 81; DB 4; Length 179;

Best Local Similarity 100.0%; Pred. No. 2.5e-05;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLSECLKRIIGDELDLS 16

Db 57 KKLSECLKRIIGDELDLS 72

RESULT 4

ID 09UKL3 PRELIMINARY: PRT: 173 AA.

AC 09UKL3: 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE BAX PROTEIN SPLICED VARIANT K.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

NCBI_TaxID=10116;

OX NCB1_TaxID=10116;

RN (1)

RP SEQUENCE FROM N.A.

RC TISSUE=BRIN;

RA Jin K., He X., Greenberg D.A., Simon R.P., Graham S.H.;

RL Submitted (FEB-2000) to the EMBL/Genbank/DBJ databases.

DR EMBL: AF235993; AAF36411.1; -

DR HSSP: Q07817; IMAZ.

DR InterPro: IPR002475; BCL2_family.

DR InterPro: IPR000712; BCL_2.

DR Pfam: PF00452; Bcl-2; 1.

DR SMART: SM00337; BCL_1.

DR PROSITE: PS50062; BCL2_FAMILY; 1.

DR PROSITE: PS01080; BH1; 1.

DR PROSITE: PS01258; BH2; 1.

SO SEQUENCE 173 AA; 19661 MW; F19A45BCF642C34F CRC64;

QY 1 KKLSECLKRIIGDELDLS 16

Db 38 KKLSECLKRIIGDELDN 53

Query Match 92.6%; Score 75; DB 11; Length 173;

Best Local Similarity 87.5%; Pred. No. 0.00022;

Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RESULT 5

ID 098U13 PRELIMINARY: PRT: 221 AA.

AC 098U13: 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE BAX.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

OC Xenopodidae; Xenopus.

NCBI_TaxID=8355;

OX NCB1_TaxID=8355;

RN (1)

RP SEQUENCE FROM N.A.

RX MEDLINE=21107661; PubMed=11158585;

RA Finkelshtein C.V., Lewellyn A.L., Muller J.L.;

RT "The midblastula transition in Xenopus embryos activates multiple RT pathways to prevent apoptosis in response to DNA damage.";

RL Proc. Natl. Acad. Sci. U.S.A. 98:1006-1011(2001).

DR EMBL: AF288809; AAK06406.1; -

DR HSSP: P53563; IAF3.

DR InterPro: IPR002475; BCL2_family.

DR InterPro: IPR000712; BCL_2.

DR Pfam: PF00452; Bcl-2; 1.

RN [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=MAMMARY TUMOR. WAF-TGF ALPHA MODEL. 7 MONTHS OLD, GROSS
 RC TISSUE :
 RC
 RA Strausberg R.;
 RL Submitted (Feb-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC003941; AA03941.1; -
 DR InterPro: IPR000822; Znf-C2H2.
 DR Pfam: PF00096; Zf-C2H2; 9.
 DR SMART: SM00355; Znf-C2H2; 9.
 DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 4.
 DR PROSITE: PS00157; ZINC_FINGER_C2H2_2; 5.
 DR DNA-binding: Metal-binding; Zinc-finger.
 KW SEQUENCE 485 AA; 55678 MW; 52428549C27A2E4F CRC64;

Query Match 56.8%; Score 46; DB 11; Length 485;
 Best Local Similarity 64.3%; Pred. No. 28;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 KLSCLKRIGDELD 15
 DB 461 KCSECLMRGNERD 474

RESULT 10

ID Q979F5 PRELIMINARY; PRT; 508 AA.
 AC Q979F5;
 DT 01-OCT-2001 (TREMBlrel. 18, Created)
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE DNA-DIRECTED RNA POLYMERASE A'.
 GN TVG2333699.
 OS Thermoplasma volcanium.
 OC Archaea; Euryarchaeota; Thermoplasmatales; Thermoplasmaceae;
 OC Thermoplasma.
 OX NCBI_TaxID=50339;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-GSSI / DSM 4299 / JCM 9571;
 RC MEDLINE-20570466; PubMed-11121031;
 RA Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,
 RA Kawashima T., Yamamoto Y., Watanabe K., Yamazaki M., Kanehori K., Kawamoto T.,
 RA Nunoshima T., Yamamoto Y., Arimaki K., Makino K., Suzuki M.,
 RT "Archaeal adaptation to higher temperatures revealed by genomic
 sequence of Thermoplasma volcanium."
 RL Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
 DR EMBL: AP000995; BAB60348.1; -
 DR InterPro: IPR002879; RNA_pol_A2.
 DR Pfam: PF01854; RNA_pol_A2; 1.
 KW DNA-directed RNA polymerase; Complete proteome.
 SO SEQUENCE 508 AA; 56949 MW; 0B17ABCBE0118FE CRC64;

Query Match 55.6%; Score 45; DB 17; Length 508;
 Best Local Similarity 64.3%; Pred. No. 42;
 Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLSCLKRIGDEL 14
 DB 159 KKYREILKRIGEEI 172

RESULT 11

ID Q9FIN7 PRELIMINARY; PRT; 2376 AA.
 AC Q9FIN7;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE GENOMIC DNA, CHROMOSOME 5, TAC CLONE:K16H17.
 OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-COLUMBIA.
 RC MEDLINE-99156233; PubMed-10048488;
 RA Asamizu E., Sato S., Kaneko T., Nakamura Y., Kotani H., Miyajima N.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. VIII.
 RT Sequence features of the regions of 1,081,958 bp covered by seventeen
 RT physically assigned P1 and TAC clones."
 RL DNA Res. 5:379-391(1998).
 DR EMBL: AB016884; BAB11228.1; -
 SO SEQUENCE 2376 AA; 266811 MW; 26612028BDAFCFB6 CRC64;

Query Match 55.6%; Score 45; DB 10; Length 2376;
 Best Local Similarity 71.4%; Pred. No. 2e+02;
 Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 LSECLDRIGREDS 16
 DB 495 LSECLDRIGREDS 508

RESULT 12

ID Q9CVN5 PRELIMINARY; PRT; 226 AA.
 AC Q9CVN5;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE 1700095F04RIK PROTEIN (FRAGMENT).
 GN 1700095F04RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6J; TISSUE-TESTIS;
 RC MEDLINE-21085660; PubMed-11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa H., Nishit K., Kiyosawa H., Kondo S., Yamazaki I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito K.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schiraldi L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein W.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyono-oka K., Wang K.H., Wetzl C., Whitlaker C., Wilming L.,
 RA Wysshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 DR EMBL: AK007251; BAB24916.1; -
 DR MCD; MGI:1914606; 1700095F04RIK.
 FT NON_TER 226 226
 SO SEQUENCE 226 AA; 26797 MW; 90EA1783E4675997 CRC64;

Query Match 54.3%; Score 44; DB 11; Length 226;
 Best Local Similarity 56.2%; Pred. No. 27;
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 20, 2002, 10:35:59 ; Search time 228.86 Seconds

(without alignments)
8,251 Million cell updates/sec

Title: US-09-544-664-57

Sequence: 1 KGVGRQLAIIIGDINR 17

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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1: A.Geneseq_032802.*
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3: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
4: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
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7: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.*
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23: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	85	100.0	17	21	AAAB37057
2	80	94.1	16	20	AAAY05423
3	80	94.1	16	21	AAAB37030
4	80	94.1	16	22	AAAB71977
5	80	94.1	26	21	AAAY63322
6	80	94.1	26	22	AAAB70372
7	80	94.1	27	21	AAAB37004
8	80	94.1	28	17	AAAW6294
9	80	94.1	117	19	AAAW79535
10	80	94.1	141	16	AAAR77880
11	80	94.1	152	16	AAAR77879

12	80	94.1	211	16	AAAR77876
13	80	94.1	211	16	AAAR77877
14	80	94.1	211	17	AAAW03668
15	80	94.1	211	17	AAAW03669
16	80	94.1	211	17	AAAR1451
17	80	94.1	211	19	AAAW79534
18	80	94.1	211	19	AAAY05433
19	78	91.8	16	20	AAAY05424
20	78	91.8	16	20	AAAB37031
21	78	91.8	207	20	AAAB37005
22	78	91.8	208	20	AAAY05432
23	75	88.2	16	21	AAAB37038
24	74	87.1	31	17	AAAW06295
25	69	81.2	15	17	AAAW06302
26	69	81.2	15	22	AAAB5172
27	47.5	55.9	175	21	AAAG08500
28	47.5	55.9	182	21	AAAG08499
29	47.5	55.9	210	21	AAAG08498
30	47.5	55.9	322	21	AAAG32338
31	47.5	55.9	329	21	AAAG32338
32	47.5	55.9	357	21	AAAG32337
33	47	55.3	15	22	AAAB5674
34	47	55.3	165	22	AAAB5668
35	47	55.3	195	22	AAAB5667
36	46	54.1	834	22	AAU34483
37	45	54.1	842	22	AAU34482
38	45	52.9	221	22	AAU38125
39	45	52.9	426	22	AAU381640
40	45	52.9	426	22	AAU35705
41	44.5	52.4	258	21	AAAG55036
42	44.5	52.4	315	21	AAAG11786
43	44.5	52.4	320	21	AAAG33889
44	44.5	52.4	327	21	AAAG33888
45	44.5	52.4	336	21	AAAG11785

ALIGNMENTS

RESULT 1	AAAB37057	standard: peptide: 17 AA.
ID	AAAB37057	
XX	AAAB37057	
AC	AAAB37057	
XX	AAAB37057	
DT	28-FEB-2001	(first entry)
XX	XX	
DE	Bcl2 polypeptide BH3 domain peptide #57.	
XX	XX	
KW	Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;	
KW	cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;	
KW	apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;	
KW	colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;	
KW	melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;	
XX	stroke; myocardial infarction.	
XX	XX	
OS	Homo sapiens.	
XX	XX	
PN	WO200059526-A1.	
PD	12-OCT-2000.	
XX	XX	
PF	06-APR-2000; 2000WO-US09352.	
XX	XX	
PR	07-APR-1999; 99US-0128202.	
XX	XX	
PA	(UYJE-) UNIV JEFFERSON THOMAS.	
XX	XX	
PI	Huang Z, Wang J, Zhang Z, Shan S, Ju Z;	
XX	XX	
DR	WPI; 2000-679325/66.	
XX	XX	
PT	New peptide conjugates for modulating apoptosis or for inhibiting B	

PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for
 PT treating neurodegenerative disorders, stroke, or cancer
 PS Claim 18; Page 20; 74pp; English.

XX The invention relates to a peptide conjugate having the formula:
 CC (R-X)n-peptide where n = 1-10; X = C=O, when the R-X group is attached
 CC to the N-terminus of the peptide, or a side chain of the peptide where
 CC the functional group of the side chain is NH2 or OH; or X = O or NH,
 CC when the R-X group is attached to the C-terminus of the peptide, or a
 CC side chain of the peptide, where the side chain functional group is COOH
 CC or CONH2; and R = 2-Bsc alkyl or alkoxy, 2-14C alkyl/aryl containing one
 CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain
 CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples
 CC of the peptide portion of the conjugate. The peptides represent analogues
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of
 CC the Bcl2 domain of the cell death agonist Bad. The peptide conjugate is
 CC useful for modulating apoptosis in the cells of a subject, or for
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2
 CC function. In particular, the peptide conjugate is useful for treating a
 CC subject afflicted with a cancer characterized by cancer cells that
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric,
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
 CC conjugate is also useful for treating disorders characterized by
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
 XX Sequence 17 AA:
 S0

Query Match 100.0%; Score 85; DB 21; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.9e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KGOVROLAIIIGDDINR 17
 Db 1 KGVYGRQAIIIGDDINR 17

RESULT 2

AA05423
 ID AAY05423 standard; peptide: 16 AA.

XX AC AAY05423:

DT 02-JUL-1999 (first entry)

XX Human BAK BH3 domain.

XX BH3 domain; cell death agonist; bcl homology domain; BCL-2 family;
 KW apoptosis promoter; cancer cell; virus infected cell; inflammation;
 KW autoantibody producing cell; cancer; lymphoproliferative condition;
 KW arthritis; autoimmune disease; therapy.

XX Homo sapiens.

OS

XX W03916787-A1.

XX 08-APR-1999.

XX 22-SEP-1998; 98MO-US19765.

XX 07-OCT-1997; 97US-0946039.

XX 26-SEP-1997; 97US-0060133.

XX (UNITW) UNIV WASHINGTON.

XX Korsmeyer SJ;

DR WPI; 1999-255058/21.

XX Bcl homology domain 3 polypeptide

XX Example 1; Fig 4; 104pp; English.

XX This sequence represents the BH3 domain of human BAK.
 CC The invention relates to a bcl homology domain 3 (BH3 domain),
 CC derived from a proapoptotic member of the BCL-2 family. The
 CC BH3 polypeptide can be used in a method for promoting apoptosis in a
 CC target cell, especially where the cell is a cancer cell a virus infected
 CC cell or an autoantibody producing cell. The BH3 polypeptide can be used
 CC in therapeutic compositions for treating disease including cancer, other
 CC lymphoproliferative conditions, arthritis, inflammation, and autoimmune
 CC diseases, which may result from the down regulation of cell death
 CC regulation.
 XX Sequence 16 AA:
 S0

Query Match 94.1%; Score 80; DB 20; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.4e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GOVGROLAIIIGDDINR 17
 Db 1 GGVYGRQAIIIGDDINR 16

RESULT 3

AA037030
 ID AAB37030 standard; peptide: 16 AA.

XX AC AAB37030:

DT 28-FEB-2001 (first entry)

XX Bcl2 polypeptide BH3 domain peptide #30.

XX Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;
 KW cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;
 KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;
 KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;
 KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
 KW stroke; myocardial infarction.

XX Homo sapiens.

XX W0200059526-A1.

XX 12-OCT-2000.

XX 06-APR-2000; 2000MO-US09352.

XX 07-APR-1999; 99US-0128202.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Huang Z, Wang J, Zhang Z, Shan S, Lu Z;

XX WPI; 2000-679325/66.

XX New peptide conjugates for modulating apoptosis or for inhibiting B
 PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for
 PT treating neurodegenerative disorders, stroke, or cancer

XX Claim 18; Page 18; 74pp; English.

XX The invention relates to a peptide conjugate having the formula:
 CC (R-X)n-peptide where n = 1-10; X = C=O, when the R-X group is attached
 CC to the N-terminus of the peptide, or a side chain of the peptide where
 CC the functional group of the side chain is NH2 or OH; or X = O or NH,
 CC when the R-X group is attached to the C-terminus of the peptide, or a

CC side chain of the peptide, where the side chain functional group is COOH
 CC or CONH₂, and R = 2-18C alkyl or alkoxy, 2-14C alkenyl containing one
 CC or two double bonds, cyclopentyl, cyclohexyl, cycloheptyl optionally
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain
 CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples
 CC of the peptide portion of the conjugate. The peptides represent analogues
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of
 CC the B3 domain of the cell death agonist Bax. The peptide conjugate is
 CC useful for modulating apoptosis in the cells of a subject, or for
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockade of
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2
 CC function. In particular, the peptide conjugate is useful for treating a
 CC subject afflicted with a cancer characterized by cancer cells that
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric,
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
 CC conjugate is also useful for treating disorders characterized by
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.

CC Sequence 16 AA;

Query Match 94.1%; Score 80; DB 21; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.4e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GQVGRQLATIGDDINR 17
 |||||
 DB 1 gvygrqlatigddinr 16

RESULT 4

AAB71977
 ID AAB71977 standard; peptide; 16 AA.

AC AAB71977;

DT 11-MAY-2001 (first entry)

DE Bak B3 peptide.

KW Bak; B3 domain; antiapoptotic; cytostatic; antiapoptotic; apoptosis;
 KM Bcl-2; neoplasia; cancer.

OS Mammalia.

PN WO200114365-A1.

PD 01-MAR-2001.

PF 18-AUG-2000; 2000WO-US22891.

PR 20-AUG-1999; 99US-0149968.

PA (HUTC-) HUTCHINSON CANCER RES CENT FRED.

PI Hockenbery DM, Simon JA, Tsung S;

DR WPI; 2001-244291/25.

PT Novel antiapoptotic derivatives that bind to antiapoptotic Bcl-2 family
 PS protein, useful for modulating the apoptotic state of a cell
 XX Example 6; Page 41; 60pp; English.

CC The present sequence was used in an example illustrating an invention
 CC relating to an antiapoptotic derivative which modulates apoptosis by
 CC binding to a Bcl-2 family protein and preferentially induces apoptosis
 CC in a cell which over-expresses the Bcl-2 family protein. The antiapoptotic
 CC derivative is used in treating an apoptosis-associated disease and for
 CC inducing apoptosis. It is also useful for treating neoplasia and drug

CC resistance. The present sequence binds to the hydrophobic pocket of
 CC Bcl-2. A competitive binding assay was used to determine if the site of
 CC antiapoptotic A3 interaction was the hydrophobic pocket of Bcl-2.

SQ Sequence 16 AA;

Query Match 94.1%; Score 80; DB 22; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.4e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GQVGRQLATIGDDINR 17
 |||||
 DB 1 gvygrqlatigddinr 16

RESULT 5

AAV96322
 ID AAV96322 standard; Peptide; 26 AA.

AC AAV96322;

DT 17-AUG-2000 (first entry)

DE Mammalian Bak Bcl-2 homology domain 3 domain.

KW Mammal; apoptosis; cell death; B3; apoptosis promotion; Bak;
 KM apoptosis inhibition; malignant cell; autoimmune disease.

OS Mammalia.

PN WO200026228-A1.

PD 11-MAY-2000.

PF 28-OCT-1999; 99WO-US25285.

PR 02-NOV-1998; 98US-0184168.

PA (CLON-) CLONTECH LAB INC.

PI Zhu L, Yin X, Chittenden T;

DR WPI; 2000-365560/31.

PT Novel polynucleotide encoding a B3 protein which is useful for
 PS modulating apoptosis, especially in the treatment of cancer and
 PS autoimmune diseases

PS Disclosure; Fig 4; 47pp; English.

CC The present sequence is the mammalian Bak Bcl-2 homology domain 3
 CC (B3) domain, which was used in a sequence alignment with the same
 CC domain of a putative version of the mammalian apoptosis
 CC regulator B3, which was designated B3-ORF2. The B3 protein,
 CC nucleic acids and antibodies are suitable for use in promoting cell
 CC death or for preventing apoptosis in malignant cells and those causing
 CC autoimmune diseases.

SQ Sequence 26 AA;

Query Match 94.1%; Score 80; DB 21; Length 26;
 Best Local Similarity 100.0%; Pred. No. 2.4e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GQVGRQLATIGDDINR 17
 |||||
 DB 3 gvygrqlatigddinr 18

RESULT 6

AAB70372

ID AAB70372 standard; Peptide; 26 AA.
 AC AAB70372;
 XX
 DT 02-MAY-2001 (first entry)
 XX
 DE BAK BH3 consensus peptide sequence SEQ ID NO:5.
 XX
 KM Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;
 XX immunostimulant; neuroprotective; neurotropic; antischismic; Vulnerary;
 XX cytostatic; antiviral; antirheumatic; antinflammatory; wound healing;
 XX immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;
 KM immunodeficiency disease; neurodegenerative disease; viral infection;
 XX ischaemic cell death; reperfusion cell death; arthritis; infertility;
 KM lymphoproliferative condition; Inflammation; autoimmune disease.
 XX
 OS Unidentified.
 XX
 PN MO200110888-A1.
 XX
 PD 15-FEB-2001.
 XX
 PF 30-MAY-2000; 2000MO-US11864.
 XX
 PR 28-MAY-1999; 99US-0136783.
 XX
 PA (APOB-) APOPTOSIS TECHNOLOGY INC.
 XX
 PI Zhou X;
 XX
 DR WP1; 2001-138734/14.
 XX
 PT New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,
 PT useful for screening for candidate compounds which induce or inhibit
 PT apoptosis, comprises amino acid substitutions at Ser118, Ser155 or
 PT Ser113 -
 XX
 PS Example 2; Fig 3a; 157pp; English.
 XX
 XX The present invention describes an isolated or synthetic polypeptide
 CC (1) comprising a less than full length amino acid sequence of a mutant
 CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its
 CC fragment, which contains amino acid substitutions at Ser118 of a human
 CC BAD. Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine
 CC BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective,
 CC neurotropic, antischismic, vulnerary, cytostatic, antiviral,
 CC antirheumatic, antinflammatory and immunosuppressive activities, and
 CC can be used as an apoptosis inducer or inhibitor. BAD polypeptides and
 CC polynucleotides can be used for screening candidate compounds and drugs
 CC for activity that promote cell survival or apoptosis. Other uses include
 CC inducing or inhibiting apoptosis in a cell. Candidate compounds
 CC identified and (mutant) BAD polypeptides are useful in treating
 CC immunodeficiency diseases, neurodegenerative diseases, ischaemic cell
 CC death, reperfusion cell death, wound healing, cancer, viral infections,
 CC lymphoproliferative conditions, arthritis, infertility, inflammation, and
 CC autoimmune diseases. The present sequence represents a Bcl-family member
 CC BH3 domain consensus sequence which is used in an example from the
 CC present invention.
 XX
 XX Sequence 26 AA;
 XX

Query Match 94.1%; Score 80; DB 22; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	2	GGVGRQLAIIGDDINR	17
Db	3	ggvgrqlaaiigddinr	18

RESULT
AAB37004

ID	AA037004 standard; peptide: 27 AA.
XX	
AC	AA037004:
XX	
DT	28-FEB-2001 (first entry)
XX	
DE	Bcl2 polypeptide BH3 domain peptide #4.
XX	
KW	Cytostatic; neuroprotective; anti-HIV; virocidic; cerebroprotective;
KW	cardiac; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;
KW	apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;
KW	colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;
KW	metastoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
KW	stroke; myocardial infarction.
XX	
OS	Homo sapiens.
XX	
PN	W0200059526-A1.
XX	
PD	12-OCT-2000.
XX	
PF	06-APR-2000; 2000MO-US09352.
XX	
PR	07-APR-1999; 99US-0128202.
XX	
PA	(UYJE-) UNIV JEFFERSON THOMAS.
XX	
PI	Huang Z, Wang J, Zhang Z, Shan S, Lu Z;
XX	
DR	WPI; 2000-679325/66.
XX	
PT	New peptide conjugates for modulating apoptosis or for inhibiting B
PT	cell lymphoma/leukemia 2 (bcl-2) function, especially useful for
PT	treating neurodegenerative disorders, stroke, or cancer -
XX	
PS	Claim 18; Page 17; 74pp: English.

The invention relates to a peptide conjugate having the formula: (R-X)-peptide where n = 1-10; X = CO-, when the R-X group is attached to the N-terminus of the peptide, or a side chain of the peptide where the functional group of the side chain is NH₂ or OH; or X = O or NH, when the R-X group is attached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain functional group is COOH or CONH₂; and R = 2-18C alkyl or alkoxy, 2-14C alkylaryl containing one or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, phenyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples of the peptide portion of the conjugate. The peptides represent analogues of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of the B33 domain of the cell death agonist Bad. The peptide conjugate is useful for modulating apoptosis in the cells of a subject, or for reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of apoptosis in cancer cells. It is also useful for inhibiting Bcl-2 function. In particular, the peptide conjugate is useful for treating a subject afflicted with a cancer characterized by cancer cells that express Bcl-2. The cancer includes prostate, colorectal, gastric, non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is also useful for treating disorders characterized by increased apoptosis, e.g., neurodegenerative disorders, acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction.

Query Match	94.18;	Score 80;	DB 21;	Length 27;
Best Local Similarity	100.08;	Pred. No. 2.5e-07;		
Matches	16;	Conservative	0;	Indels 0;
		Mismatches	0;	Gaps 0;

```
QY      2 GQVGRQLAIGDDINR 17
          |||||
Db      6 qvqgrqlalggddinr 21
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RESULT      8
AAW06294
ID   AAW06294 standard; Peptide: 28 AA.
XX
AC   AAW06294;
XX
DT   29-JUL-1997 (first entry)
XX
DE   GD domain region for Bak amino acid residues 67-94.
XX
KW   Apoptosis; follicular lymphoma; tumour; p53; antibody.
XX
OS   Synthetic.
XX
PN   MO9635951-A1.
XX
PD   14-NOV-1996.
XX
PF   06-MAY-1996; 96MO-US06122.
XX
PR   12-MAY-1995; 95US-0440391.
XX
PA   (IMMU-) IMMUNOGEN INC.
XX
PI   Chittenden TD, Lutz RJ;
XX
DR   WPI: 1996-518805/51.
XX
N-PSDB: AAT42428.
XX
PT   Peptide(s) comprising GD domains - have similar activities to wild
PT   type Bak, and cause cellular apoptosis for treatment of viral
PT   infection
XX
PS   Claim 2; Page 52; 69pp; English.
XX
CC   The term GD domain refers to a protein domain first identified in
CC   Bak and shown to be essential for the interaction of Bak with Bcl-x(L)
CC   and for Bak's cell killing function; and to peptides and/or molecules
CC   capable of mimicking its structure and/or function. The present sequence
CC   represents a GD domain corresponding to amino acid residues 67-94 of
CC   Bak. An antibody raised against a GD domain may be used to screen a
CC   cDNA expression library for clones comprising cDNA inserts encoding
CC   immunocrossreactive proteins. Truncated GD domain peptides have been
CC   shown to maintain the protein binding and cell killing function
CC   exhibited by wild type Bak. These molecules may induce apoptosis in
CC   tumour cell. These peptides act independently of p53 status. Bak or
CC   GD domain mimetics that inhibit Bcl-2 may be selectively toxic to
CC   certain tumours, e.g. follicular lymphoma, which depend on high levels
CC   of Bcl-2 for their continued growth and survival. GD domain mimetics
CC   may also be used for combating viral infections by causing apoptosis
CC   of infected cells.
XX
SQ   Sequence 28 AA:

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```

Query Match      94.1%; Score 80; DB 17; Length 28;
Best Local Similarity 100.0%; Pred. No. 2,6e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY   2 GOVGRQLAIIIGDDINR 17
    |||
DB   6 gvgvgrqlaIIIGDDINR 21

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RESULT      9
AAW79535
ID   AAW79535 standard; Protein: 117 AA.
XX
AC   AAW79535;
XX
DT   11-JAN-1999 (first entry)

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```

XX   Truncated Bak polypeptide Bak-delta2-TM.
XX
KW   Bak; bak binding protein; BBP; bbbpd-1; bbbpd-2; Bcl-2; apoptosis;
KW   cell death; cancer; lymphoma; neurodegeneration; heart disease;
KW   cell proliferation; infection; human; therapy; diagnosis.
XX
OS   Homo sapiens.
XX
PN   WO9841626-A1.
XX
PD   24-SEP-1998.
XX
PF   03-MAR-1998; 98MO-US04079.
XX
PR   09-JAN-1998; 98US-0071097.
XX
PR   20-MAR-1997; 97US-0041328.
XX
PA   (LXRB-) LXR BIOTECHNOLOGY INC.
XX
PI   Barr PJ, Fitzpatrick PA, Gibson HL, Kiefer MC;
XX
DR   WPI: 1998-521220/44.
XX
PT   New Bak-binding protein and related nucleic acid, vectors,
PT   transformed cells and antibodies - are useful for modulation of
PT   apoptosis in cancer, neuro-degeneration etc., also peptide fragments
PT   of Bak that interact with the protein
XX
PS   Example 1; Page 53; 77pp; English.
XX
CC   This is the amino acid sequence of Bak-delta2-TM, a truncated
CC   polypeptide comprising amino acids 71-187 of Bak (see AAW79534).
CC   A nucleotide sequence encoding Bak-delta2-TM was obtained from
CC   cDNA by PCR and cloned as an in-frame fusion to the GAL4-DNA
CC   binding domain in vector pAS2-1. The construct was used in a
CC   two-hybrid screen of human heart cDNA for the identification of
CC   clones encoding Bak binding proteins. The invention relates to a
CC   novel Bak binding protein (BBP, see AAW79537), the gene encoding BBP
CC   (see AAW61499), methods for detecting substances that alter the
CC   specific binding between Bak and BBP, as well as diagnostic and
CC   therapeutic methods utilising BBP.
XX
SQ   Sequence 117 AA:

```

```

Query Match      94.1%; Score 80; DB 19; Length 117;
Best Local Similarity 100.0%; Pred. No. 1,3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY   2 GOVGRQLAIIIGDDINR 17
    |||
DB   2 gvgvgrqlaIIIGDDINR 17

```

```

RESULT      10
AAR77880
ID   AAR77880 standard; Protein: 141 AA.
XX
AC   AAR77880;
XX
DT   21-NOV-1995 (first entry)
XX
DE   Human Cdn-1(71-211).
XX
KW   Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
KW   autoimmune disease; reperfusion injury; hepatitis; osteoporosis;
KW   shock; lymphoma; eczema.
XX
OS   Homo sapiens.
XX
PN   WO9515084-A.
XX

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PD 08-JUN-1995.
XX
XX 30-NOV-1994; 94WO-US13930.
XX
XX 07-OCT-1994; 94US-0320157.
PR 30-NOV-1993; 93US-0160067.
XX
XX (LXRB-) LXR BIOTECHNOLOGY INC.
XX
XX Barr PJ, Kiefer MC;
XX
XX WPI; 1995-215106/28.
XX
XX New nucleic acid sequences encoding Cdn apoptosis modulators - and
XX related vectors, transformed cells, proteins and antibodies, useful
XX or diagnosis and treatment e.g. of HIV infection, reperfusion injury
XX etc.
XX
XX Disclosure; Fig.11; 66pp; English.
XX
XX Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in
XX increased cell survival in response to anti-Fas-mediated apoptosis.
XX Deletion of the N-terminal 70 amino acids of Cdn-1 improved this
XX activity, suggesting that small, truncated Cdn-1 molecules may be
XX potent therapeutics.
XX
XX Sequence 141 AA:

Query Match 94.1%; Score 80; DB 16; Length 141;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GGVGROLAIGDDINR 17
   |||||
Db 2 ggygrqlaigddinr 17

RESULT 11
AAR77879
ID AAR77879 standard; Protein; 152 AA.
XX
XX AAR77879;
AC
XX
XX 21-NOV-1995 (first entry)
DT
XX
XX Human Cdn-1(60-211).
DE
XX
XX Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
XX autoimmune disease; reperfusion injury; hepatitis, osteoporosis;
XX shock; lymphoma; eczema.
XX
XX Homo sapiens.
OS
XX
XX WO9515084-A.
PN
XX
XX 08-JUN-1995.
PD
XX
XX 30-NOV-1994; 94WO-US13930.
PF
XX
XX 07-OCT-1994; 94US-0320157.
PR 30-NOV-1993; 93US-0160067.
XX
XX (LXRB-) LXR BIOTECHNOLOGY INC.
XX
XX Barr PJ, Kiefer MC;
XX
XX WPI; 1995-215106/28.
XX
XX New nucleic acid sequences encoding Cdn apoptosis modulators - and
XX related vectors, transformed cells, proteins and antibodies, useful
XX or diagnosis and treatment e.g. of HIV infection, reperfusion injury
XX etc.
XX
XX .

```

```

XX
XX Disclosure; Fig.11; 66pp; English.
XX
XX Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in
XX increased cell survival in response to anti-Fas-mediated apoptosis.
XX Deletion of the N-terminal 59 amino acids of Cdn-1 only slightly
XX decreased this activity, suggesting that small, truncated Cdn-1
XX molecules may be potent therapeutics.
XX
XX Sequence 152 AA:

Query Match 94.1%; Score 80; DB 16; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GGVGROLAIGDDINR 17
   |||||
Db 13 ggygrqlaigddinr 28

RESULT 12
AAR77876
ID AAR77876 standard; Protein; 211 AA.
XX
XX AAR77876;
AC
XX
XX 21-NOV-1995 (first entry)
DT
XX
XX Human Cdn-1.
DE
XX
XX Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
XX autoimmune disease; reperfusion injury; hepatitis, osteoporosis;
XX shock; lymphoma; eczema.
XX
XX Homo sapiens.
OS
XX
XX WO9515084-A.
PN
XX
XX 08-JUN-1995.
PD
XX
XX 30-NOV-1994; 94WO-US13930.
PF
XX
XX 07-OCT-1994; 94US-0320157.
PR 30-NOV-1993; 93US-0160067.
XX
XX (LXRB-) LXR BIOTECHNOLOGY INC.
XX
XX Barr PJ, Kiefer MC;
XX
XX WPI; 1995-215106/28.
XX
XX N-PSDB; AAO95492.
DR
XX
XX New nucleic acid sequences encoding Cdn apoptosis modulators - and
XX related vectors, transformed cells, proteins and antibodies, useful
XX or diagnosis and treatment e.g. of HIV infection, reperfusion injury
XX etc.
XX
XX Disclosure; Fig.3A-B; 66pp; English.
XX
XX Cdn-1 cDNA was isolated from a human heart cDNA library using a
XX previously isolated clone as probe. Recombinant Cdn-1 was produced
XX in Sf9 and human colon adenocarcinoma H729 cells. Expression of
XX Cdn-1 in WI-L2 lymphoblastoid cells resulted in increased cell
XX survival in response to anti-Fas-mediated apoptosis.
XX
XX Sequence 211 AA:

Query Match 94.1%; Score 80; DB 16; Length 211;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2 GOVGRQLAIIIGDDINR 17
 |||||||
 Db 72 gvgvgrqlaiigddlnr 87

RESULT 13

AAW03668
 ID AAR77877 standard; Protein; 211 AA.
 XX AAR77877;
 AC
 XX
 XX 21-NOV-1995 (first entry)
 DT
 XX
 DE Human Cdn-2.

XX Cdn-2; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
 KM autoimmune disease; reperfusion injury; hepatitis; osteoporosis;
 KW shock; lymphoma; eczema.

XX Homo sapiens.
 OS
 XX MO9515084-A.
 PN
 XX 08-JUN-1995.
 PD
 XX 30-NOV-1994; 94MO-US13930.
 PE
 XX 07-OCT-1994; 94US-0320157.
 PR
 XX 30-NOV-1993; 93US-0160067.
 PA (LXRB-) LXR BIOTECHNOLOGY INC.
 XX
 PI Barr PJ, Kiefer MC;
 XX
 DR WPI; 1995-215106/28.
 DR N-PSDB; AA035493.
 XX
 PT New nucleic acid sequences encoding Cdn apoptosis modulators - and
 PT related vectors, transformed cells, proteins and antibodies, useful
 PT or diagnosis and treatment e.g. of HIV infection, reperfusion injury
 PT etc.
 XX
 PS Disclosure; Fig. 5D-E; 66pp; English.
 XX
 CC Cdn-2 cDNA was isolated from a human placental genomic library
 CC using a 950 bp fragment of Cdn-1 cDNA. Expression of Cdn-2
 CC in mouse progenitor B-cell FL5.12 cells decreased IL-3-induced
 CC apoptosis. The Cdn-2 protein displayed 97% amino acid identity
 CC with Cdn-1 (AAR77876).
 XX
 XX
 SQ Sequence 211 AA;

Query Match 94.1%; Score 80; DB 16; Length 211;
 Best Local Similarity 100.0%; Pred. No. 2.5e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GOVGRQLAIIIGDDINR 17
 |||||||
 Db 72 gvgvgrqlaiigddlnr 87

RESULT 14

AAW03668
 ID AAW03668 standard; Protein; 211 AA.
 XX
 XX AAW03668;
 AC
 XX
 XX 22-FEB-1997 (first entry)
 DT
 XX
 DE Bak protein.

XX Human; Bak; apoptosis; latency; virus replication;
 KW

KW Epstein-Barr virus; BHRL; fusion protein; epitope tag;
 KW drug screening; co-precipitation; ELISA; immunosay; antibody;
 KW protein interactive trapping; virucide; antitumour; diagnostic.

XX Homo sapiens.
 OS
 XX MO9633416-A1.
 PN
 XX 24-OCT-1996.
 PD
 XX 19-APR-1996; 96MO-US05639.
 PE
 XX 20-APR-1995; 95US-0426529.
 PR
 XX (LXRB-) LXR BIOTECHNOLOGY INC.
 PA
 XX
 PI Barr PJ, Kiefer MC;
 XX
 DR WPI; 1996-485886/48.
 DR N-PSDB; AAT42138.

PT Screening for anti-viral agents - by detecting the ability of an
 PT agent to disrupt the interaction of a Bak protein and a viral
 PT protein
 XX

PS Disclosure; fig 1; 24pp; English.

XX This Bak protein sequence represents a bcl-1 homologue which
 CC interacts with Epstein-Barr virus (EBV) early lytic cycle BHRL
 CC protein, and is capable of modulating apoptosis. The protein may
 CC be used in complete or partial form, or as an epitope tag fusion
 CC protein, in a new virucide drug screening method, which involves
 CC combination of Bak protein and a viral protein (e.g. EBV BHRL).
 CC exposure to a test compound, and monitoring for disruption of the
 CC interaction, e.g. by co-precipitation, protein interactive trapping
 CC or ELISA. Interaction of Bak and viral proteins allows viral
 CC replication or latency in the absence of apoptosis. Compounds which
 CC inhibit the interaction may be used as virucide, antitumour or
 CC diagnostic agents.
 XX
 XX
 SQ Sequence 211 AA;

Query Match 94.1%; Score 80; DB 17; Length 211;
 Best Local Similarity 100.0%; Pred. No. 2.5e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GOVGRQLAIIIGDDINR 17
 |||||||
 Db 72 gvgvgrqlaiigddlnr 87

RESULT 15

AAW03669
 ID AAW03669 standard; Protein; 211 AA.
 XX
 XX AAW03669;
 AC
 XX
 XX 22-FEB-1997 (first entry)
 DT
 XX
 DE Bak-2 protein.

XX Human; Bak-2; apoptosis; latency; virus replication;
 KW Epstein-Barr virus; BHRL; fusion protein; epitope tag;
 KW drug screening; co-precipitation; ELISA; immunosay; antibody;
 KW protein interactive trapping; virucide; antitumour; diagnostic.

XX Homo sapiens.
 OS
 XX MO9633416-A1.
 PN
 XX 24-OCT-1996.
 PD
 XX

PF 19-APR-1996; 96MO-US05639.

XX 20-APR-1995; 95US-0426529.

XX (LXRB-) LXR BIOTECHNOLOGY INC.

XX Barr PJ, Kiefer MC;

XX WPI: 1996-485886/48.

DR N-PSDB; AAT42139.

XX Screening for anti-viral agents - by detecting the ability of an
PT agent to disrupt the interaction of a Bak protein and a viral
PT protein

PS Disclosure; Fig 2; 24pp; English.

XX This Bak-2 protein sequence represents a bcl-1 homologue which
CC interacts with Epstein-Barr virus (EBV) early lytic cycle BHRF1
CC protein, and is capable of modulating apoptosis. The protein may
CC be used in complete or partial form, or as an epitope tag fusion.
CC protein, in a new virucide drug screening method, which involves
CC combination of Bak-2 protein and a viral protein (e.g. EBV BHRF1),
CC exposure to a test compound, and monitoring for disruption of the
CC interaction, e.g. by co-precipitation. Protein interaction trapping
CC or ELISA. Interaction of Bak-2 and viral proteins allows viral
CC replication or latency in the absence of apoptosis. Compounds which
CC inhibit the interaction may be used as virucide, antitumour or
CC diagnostic agents.

XX Sequence 211 AA;

Query Match 94.1%; Score 80; DB 17; Length 211;

Best Local Similarity 100.0%; Pred. No. 2.5e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGVGRQLAIIIGDDINR 17

|||||

Db 72 gvgvgrqlaigddinr 87

Search completed: September 20, 2002, 10:35:59
Job time: 427 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 20, 2002, 10:37:21 : Search time 75.64 Seconds
(without alignments)
5.490 Million cell updates/sec

Title: US-09-544-664-57

Perfect score: 85

Sequence: 1 KGOVROLAIIIGDDINR 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	80	94.1	19	4	US-09-236-385A-35
2	80	94.1	20	4	US-09-236-385A-36
3	80	94.1	28	1	US-08-440-391-2
4	80	94.1	28	1	US-08-440-391-18
5	80	94.1	28	2	US-08-908-597A-2
6	80	94.1	28	2	US-08-908-597A-18
7	80	94.1	28	4	US-09-236-385A-2
8	80	94.1	28	4	US-09-236-385A-18
9	80	94.1	28	5	PCT-US96-06122-2
10	80	94.1	28	5	PCT-US96-06122-18
11	80	94.1	36	1	US-08-440-391-14
12	80	94.1	36	2	US-08-908-597A-14
13	80	94.1	36	5	PCT-US96-06122-14
14	80	94.1	141	1	US-08-471-058-23
15	80	94.1	152	1	US-08-471-058-22
16	80	94.1	210	3	US-08-471-057-12
17	80	94.1	211	1	US-08-321-071A-16
18	80	94.1	211	1	US-08-471-058-7
19	80	94.1	211	1	US-08-471-058-9
20	80	94.1	211	1	US-08-471-058-10
21	80	94.1	211	1	US-08-471-058-11
22	80	94.1	211	2	US-08-944-530-2
23	80	94.1	211	2	US-08-944-530-4
24	80	94.1	211	3	US-08-471-057-7
25	80	94.1	211	3	US-08-471-057-9
26	80	94.1	211	3	US-08-471-057-10
27	80	94.1	211	3	US-08-471-057-10

28	80	94.1	211	3	US-08-471-057-11	Sequence 11, Appl
29	74	87.1	15	4	US-09-236-385A-37	Sequence 37, Appl
30	74	87.1	31	1	US-08-440-391-3	Sequence 3, Appl
31	74	87.1	31	1	US-08-440-391-16	Sequence 16, Appl
32	74	87.1	31	2	US-08-908-597A-3	Sequence 3, Appl
33	74	87.1	31	2	US-08-908-597A-16	Sequence 16, Appl
34	74	87.1	31	4	US-09-236-385A-3	Sequence 3, Appl
35	74	87.1	31	4	US-09-236-385A-16	Sequence 16, Appl
36	74	87.1	31	5	PCT-US96-06122-3	Sequence 3, Appl
37	74	87.1	31	5	PCT-US96-06122-16	Sequence 16, Appl
38	69	81.2	15	1	US-08-440-391-10	Sequence 10, Appl
39	69	81.2	15	1	US-08-908-597A-10	Sequence 10, Appl
40	69	81.2	15	2	US-08-908-597A-20	Sequence 20, Appl
41	69	81.2	15	2	US-09-236-385A-10	Sequence 10, Appl
42	69	81.2	15	4	US-09-236-385A-20	Sequence 20, Appl
43	69	81.2	15	4	US-09-236-385A-38	Sequence 38, Appl
44	69	81.2	15	4	PCT-US96-06122-10	Sequence 10, Appl
45	69	81.2	15	5	PCT-US96-06122-10	Sequence 10, Appl

ALIGNMENTS

```

RESULT 1
US-09-236-385A-35
Sequence 35, Application US/09236385A
Patent No. 6221615
GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.; and
LUTZ, Robert J.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/236,385A
FILING DATE: 25-Jan-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
(C) ATTORNEY DOCKET NO. 104322.147CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8484
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-09-236-385A-35
Query Match 94.1%; Score 80; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 GGOVROLAIIIGDDINR 17
DB 2 GGOVROLAIIIGDDINR 17

```

RESULT 2
US-09-236-385A-36
Sequence 36, Application US/09236385A
Patent No. 6221615
GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.; and
LUTZ, Robert J.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/236,385A
FILING DATE: 25-Jan-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
(C) ATTORNEY DOCKET NO. 104322.147CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 36
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 36
US-09-236-385A-36
Query Match 94.1%; Score 80; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 GOVROLAIIIGDDINR 17
Db 3 GOVROLAIIIGDDINR 18
RESULT 3
US-08-440-391-2
Sequence 2, Application US/08440391
Patent No. 5656725
GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.; and
LUTZ, Robert J.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,391
FILING DATE: 12-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.147
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-440-391-2
Query Match 94.1%; Score 80; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.9e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 GOVROLAIIIGDDINR 17
Db 6 GOVROLAIIIGDDINR 21
RESULT 4
US-08-440-391-18
Sequence 18, Application US/08440391
Patent No. 5656725
GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.; and
LUTZ, Robert J.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,391
FILING DATE: 12-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.147
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-440-391-18
Query Match 94.1%; Score 80; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.9e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GOVROLAIIIGDDINR 17
Db 6 GOVROLAIIIGDDINR 21

RESULT 5

US-08-908-597A-2
; Sequence 2, Application us/08908597A
; Patent No. 5863795

GENERAL INFORMATION:

APPLICANT: CHITTENDEN, Thomas D.; and
APPLICANT: LOTZ, Robert J.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/908.597A

FILING DATE:

CLASSIFICATION: 530
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/440.391
FILING DATE: 12-MAY-1995

ATTORNEY/AGENT INFORMATION:

NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.147
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-908-597A-2

Query Match

Best Local Similarity 94.1%; Score 80; DB 2; Length 28;
Pred. No. 5.9e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GOVROLAIIIGDDINR 17
Db 6 GOVROLAIIIGDDINR 21

RESULT 6

US-08-908-597A-18
; Sequence 18, Application us/08908597A
; Patent No. 5863795

GENERAL INFORMATION:

APPLICANT: CHITTENDEN, Thomas D.; and
APPLICANT: LOTZ, Robert J.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington

STATE: D.C.

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/908.597A
FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/440.391
FILING DATE: 12-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.147
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-908-597A-18

Query Match

Best Local Similarity 94.1%; Score 80; DB 2; Length 28;
Pred. No. 5.9e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GOVROLAIIIGDDINR 17
Db 6 GOVROLAIIIGDDINR 21

RESULT 7

US-09-236-385A-2
; Sequence 2, Application us/09236385A
; Patent No. 6221615

GENERAL INFORMATION:

APPLICANT: CHITTENDEN, Thomas D.; and
APPLICANT: LOTZ, Robert J.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
STATE: D.C.
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/236.385A
FILING DATE: 25-Jan-1999

CLASSIFICATION: <unknown>

ATTORNEY/AGENT INFORMATION:

NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
TELECOMMUNICATION INFORMATION: (C) ATTORNEY DOCKET NO. 104322.147CIP
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 28 amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 2
US-09-236-385A-2

Query Match 94.1%; Score 80; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.9e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GOVGR0LATIIGDDINR 17
|||||
Db 6 GOVGR0LATIIGDDINR 21

RESULT 8
US-09-236-385A-18
Sequence 18, Application US/09236385A
Patent No. 6221615
GENERAL INFORMATION:

APPLICANT: CHITTENDEN, Thomas D.; and
LUTZ, Robert J.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS

NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESSES:

ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/236,385A
FILING DATE: 25-Jan-1999

CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073

TELECOMMUNICATION INFORMATION:
(C) ATTORNEY DOCKET NO. 104322.147CIP
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 28 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-236-385A-18

Query Match 94.1%; Score 80; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.9e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GOVGR0LATIIGDDINR 17
|||||
Db 6 GOVGR0LATIIGDDINR 21

RESULT 9
PCT-US96-06122-2
Sequence 2, Application PC/TUS9606122
GENERAL INFORMATION:
APPLICANT: IMMUNOGEN, INC.

TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS
WHICH MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESSES:

ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/06122

FILING DATE: HERewith

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/440,391

FILING DATE: 12-MAY-1995

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073

REFERENCE/DOCKET NUMBER: 104322.147PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-942-8400

TELEFAX: 202-942-8484

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 28 amino acid

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

PCT-US96-06122-2

Query Match 94.1%; Score 80; DB 5; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.9e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GOVGR0LATIIGDDINR 17
|||||
Db 6 GOVGR0LATIIGDDINR 21

RESULT 10
PCT-US96-06122-18
Sequence 18, Application PC/TUS9606122

GENERAL INFORMATION:

APPLICANT: IMMUNOGEN, INC.

TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS
WHICH MODULATE APOPTOSIS

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Hale and Dorr

STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/06122

FILING DATE: HERewith

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/440,391

FILING DATE: 12-MAY-1995

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.147PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US96-06122-18

Query Match 94.1%; Score 80; DB 5; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.9e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GOVGROLAIIGDDINR 17
|||||
Db 6 GOVGROLAIIGDDINR 21

RESULT 11
US-08-440-391-14
Sequence 14, Application US/08440391
Patent No. 5656725
GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.; and
APPLICANT: LUTZ, Robert J.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,391
FILING DATE: 12-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.147
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-440-391-14

Query Match 94.1%; Score 80; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 7.9e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 GOVGROLAIIGDDINR 17
|||||

Db 8 GOVGROLAIIGDDINR 23

RESULT 12
US-08-908-597A-14
Sequence 14, Application US/08908597A
Patent No. 5863795
GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.; and
APPLICANT: LUTZ, Robert J.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/908,597A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/440,391
FILING DATE: 12-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.147
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 36
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-908-597A-14

Query Match 94.1%; Score 80; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 7.9e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GOVGROLAIIGDDINR 17
|||||
Db 8 GOVGROLAIIGDDINR 23

RESULT 13
US-09-236-385A-14
Sequence 14, Application US/09236385A
Patent No. 6221615
GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.; and
APPLICANT: LUTZ, Robert J.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/236,385A
FILING DATE: 25-Jan-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
(C) ATTORNEY DOCKET NO. 104322.147CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-236-385A-14

Query Match 94.1%; Score 80; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 7,9e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GOVGRQALIIIGDDINR 17
DB 8 GOVGRQALIIIGDDINR 23
|||||

RESULT 14
PCT-US96-06122-14
Sequence 14, Application PC/WTUS9606122
GENERAL INFORMATION:
APPLICANT: IMMUNOGEN, INC.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS
TITLE OF INVENTION: WHICH MODULE APOPTOSIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/06122
FILING DATE: HEREMITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/440,391
FILING DATE: 12-MAY-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.147PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8484
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: peptide
PCT-US96-06122-14

Query Match 94.1%; Score 80; DB 5; Length 36;
Best Local Similarity 100.0%; Pred. No. 7,9e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GOVGRQALIIIGDDINR 17
DB 8 GOVGRQALIIIGDDINR 23
|||||

RESULT 15
US-08-471-058-23
Sequence 23, Application US/08471058
Patent No. 5770443
GENERAL INFORMATION:
APPLICANT: Kieffer, Michael C.
APPLICANT: Bart, Phillip J.
TITLE OF INVENTION: NOVEL APOPTOSIS MODULATING
TITLE OF INVENTION: PROTEINS, DNA ENCODING THE PROTEINS AND METHODS OF USE
TITLE OF INVENTION: THEROF
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,058
FILING DATE: 06-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/320,157
FILING DATE: 07-OCT-1994
APPLICATION NUMBER: 08/160,067
FILING DATE: 30-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20007.12
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-471-058-23

Query Match 94.1%; Score 80; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GOVGRQALIIIGDDINR 17
DB 2 GOVGRQALIIIGDDINR 17
|||||

Search completed: September 20, 2002, 10:37:21

Fri Sep 20 11:03:21 2002

us-09-544-664-57.ra1

Page 7

Job time: 409 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 20, 2002, 10:39:13 ; Search time 95.59 Seconds

(without alignments)
17.089 Million cell updates/sec

Title: US-09-544-664-57

Sequence: 1 KQVGRQLATIGDDINR 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

1: PIR-71:*
2: PIR:*
3: PIR:*
4: PIR:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	80	94.1	211	2	S58873
2	80	94.1	211	2	S58873
3	47.5	55.9	357	2	T06508
4	46	54.1	833	2	AE0564
5	46	54.1	834	1	C64779
6	46	54.1	834	2	A90696
7	46	54.1	834	2	E85546
8	46	54.1	834	2	H82104
9	46	54.1	1226	2	S44824
10	46	52.9	263	2	F89890
11	45	52.9	426	2	S58684
12	45	52.9	426	2	H71967
13	45	52.4	355	2	H84643
14	44.5	51.8	258	2	H75027
15	44	51.8	261	2	B71213
16	44	51.8	593	2	S75352
17	44	51.8	693	2	G82618
18	44	51.8	803	1	E70041
19	43.5	51.2	532	2	JN0084
20	43	50.6	444	2	JQ1185
21	43	50.6	446	2	T03267
22	43	50.6	446	2	T03267
23	43	50.6	447	2	G86940
24	43	50.6	475	2	T48031
25	43	50.6	664	2	D96633
26	43	50.6	770	2	T23999
27	43	50.6	827	2	B95969
28	42	49.4	356	2	S71460
29	42	49.4	356	2	A53433

30	42	49.4	575	2	I59327	olfactory cyclic n
31	42	49.4	826	2	D95330	Actp copper transp
32	41	48.2	70	2	H71313	hypothetical prote
33	41	48.2	251	2	T44678	chemotaxis protein
34	41	48.2	383	2	S76964	hypothetical prote
35	41	48.2	447	2	T13091	probable minor cap
36	41	48.2	530	2	C72291	methyl-accepting c
37	41	48.2	539	2	F72288	methyl-accepting c
38	41	48.2	539	2	S22342	Chaperonin Hsp60 -
39	41	48.2	566	2	A72254	methyl-accepting c
40	41	48.2	570	2	H97244	membrane associate
41	41	48.2	642	2	F84172	ABC transport prot
42	41	48.2	654	2	F71298	probable methyl-ac
43	41	48.2	656	2	A72428	methyl-accepting c
44	41	48.2	656	2	E72379	methyl-accepting c
45	41	48.2	661	2	G72316	methyl-accepting c

ALIGNMENTS

RESULT 1

S58873

Bak protein - human
N:Alternate names: Bcl-2 homolog; cdc-1 protein

C:Species: Homo sapiens (man)

C:Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 08-Oct-1999

C:Accession: S58873; S58872; S58874

R:Chittenden, T.; Harrington, E.A.; O'Connor, R.; Flemington, C.; Lutz, R.J.; Evan, G

Nature 374, 733-736, 1995

A:Title: Induction of apoptosis by the Bcl-2 homologue Bak.

A:Reference number: S58873; MUID:95231653

A:Accession: S58873

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-211 <CHI>

A:Cross-references: EMBL:U23765; NID:G758797; PIDD:AAA93066.1; PID:G758798

R:Kiefer, M.C.; Brauer, M.J.; Powers, V.C.; Wu, J.D.; Umansky, S.R.; Tomei, L.D.; Bar

Nature 374, 736-739, 1995

A:Title: Modulation of apoptosis by the widely distributed Bcl-2 homologue Bak.

A:Reference number: S58874; MUID:95231654

A:Accession: S58874

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-211 <KIE>

A:Cross-references: EMBL:U16811; NID:G595923; PIDD:AAA74466.1; PID:G595924

C:Gene: GDB:BAK

A:Cross-references: GDB:635887

Query Match 94.1% Score 80; DB 2; Length 211;

Best Local Similarity 100.0%; Pred. No. 5.4e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GQVGRQLATIGDDINR 17

DB 72 GQVGRQLATIGDDINR 87

RESULT 2

S58875

cdn-2 protein - human
C:Species: Homo sapiens (man)

C:Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 21-Jul-2000
C:Accession: S58875
R:Kleider, M.C., Brauer, M.J.: Powers, V.C.: Wu, J.J.: Umansky, S.R.: Tomei, L.D.: Barr,
Nature 374, 736-739, 1995
A:Title: Modulation of apoptosis by the widely distributed Bcl-2 homologue Bak.
A:Reference number: S58874; MUID:95231654
A:Accession: S58875
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-211 <KB>
A:Cross-references: EMBL:U16112; NID:9595925; PION:AA47467.1; PID:9595926
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1994

Query Match 94.18; Score 80; DB 2; Length 211;
Best Local Similarity 100.0%; Pred. No. 5.4e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0;
Gaps 0.

```

OY      2 GOVGRQLAIIGDDINR 17
        |||||
Db      72 GOVGRQLAIIIGDDINR 87

```

RESULT 3
T06308
Protein phosphatase 2C homolog F11C18.60 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 30-Apr-1999 #sequence=revision 30-Apr-1999 #text-change 15-Jun-2001
C:Accession: T06308
R:Bevan, M.; Terry, N.; Ardiles, W.; Buyschaert, C.; Desseville, R.; De Clerck, R.; De
ewes, H.W.; Mayer, K.F.X.; Schueler, C.
submitted to the Protein Sequence Database, April 1999
#Reference number: Z15589

Query Match	55.98;	Score 47.5;	DB 2;	Length 357;
Best Local Similarity	55.68;	Pred. NO. 3.2;		
Matches 10;	Conservative 5;	Mismatches 2;	Indels 1;	Gaps 1

```
QY      1 KQVC-RQLATIGDDINR 17
        :|| | | :|| :|| | | :
Db      103 QGQRGWRELAVLGDKINK 120
```

RESULT 4
 AE0564
 H+/K+-exchanging ATPase (EC 3.6.1.36) - *Salmonella enterica* subsp. *enterica* serovar Typh
 C:Species: *Salmonella enterica* subsp. *enterica* serovar Typh
 A:Note: This species has also been called *Salmonella typhi*
 C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
 C:Accession: AE0564
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher
 lb, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
 S.; Moule, S.; O'Garra, P.
 Nature 413, 848-852, 2001
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
 A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov
 A:Reference number: AB0502; PMID:11677608
 A:Accession: AE0564
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-833 <PAR>
 A:Cross-references: GB:AL513382; PID:CAD04983.1; PID:g16501768; GSPDF:GN00176

C:Genetics: A:Gene: STY0544
C:Superfamily: Bacillus probable copper-transporting ATPase yvqX: ATPase nucleotide-b-
C:Keywords: hydrolase

Query Match	54.18;	Score 46;	DB 2;	Length 833;
Best Local Similarity	66.78;	Pred. No. 15;		
Matches	8;	Conservative	3;	Mismatches 1; Indels 0; Gaps 0;

```
Qy      5 GRQLATIGDDIN 16  
      111:1:11 11  
Db      711 GRQVAMVGDGIN 722
```

RESULT 5
C64779
probable copper-transporting ATPase (EC 3.6.1.-) - Escherichia coli
C:Species: Escherichia coli
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 11-Jan-2000
C:Accession: C64779
R:Blattner, F., Plunkett III, G., Bloch, C.A., Perna, N.T., Burland, V., Riley, M.,
A.: Rose, D., Mau, B., Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
#:Reference number: A64720: MUID:97426617

A:Cross-references: GB:AE000154; GB:U00096; NID:g1786683; PION:AA073586.1; PID:g178666
A:Experimental source: strain K-12, substrain M61655
A:Genetics:
A:Gene: ynfB
A:Superfamily: Bacillus probable copper-transporting ATPase ynfK; ATPase nucleotide-b-
C:Keywords: ATP; copper binding; hydrolase; ion transport; metal binding; phosphotric
F:9-8/Domain: heavy-metal-associated homology <HM1>
F:105-134/Domain: heavy-metal-associated homology <HM2>
F:189-205/Domain: transmembrane #status predicted <TM1>
F:218-234/Domain: transmembrane #status predicted <TM2>
F:224-568/Domain: ATPase transduction domain homology <ATP>
F:438-454/Domain: transmembrane #status predicted <TM3>
F:468-484/Domain: transmembrane #status predicted <TM4>
F:631-647/Domain: transmembrane #status predicted <TM5>
F:664-785/Domain: ATPase nucleotide-binding domain homology <ATN>
F:806-892/Domain: transmembrane #status predicted <TM6>
F:108,110,113/Binding site: copper (met, Cys, Cys) #status predicted
F:523/Active site:Asp (aspartylphosphate intermediate) #status predicted

Query Match	54.1%;	Score 46;	DB 1;	length 834;
Best Local Similarity	66.7%;	Pred. NO. 15;		
Matches	8;	Conservative	3;	Mismatches 1; Indels 0; Gaps 0

```

OY      5 GRQLATIGDDIN 16
         |||:|:| | |
Db      712 GRQVAMVGDCIN 723

```

RESULT 6
A90696
Cu(1)-translocation P-type ATPase [imported] - *Escherichia coli* (strain O157:H7, subspecies: *Escherichia coli*)
C|Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C|Accession: A90696
R|Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.; Gasawara, N.; Yasunaga, T.; Kuhnara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A|Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and genome analysis of a closely related strain
A|Reference number: A99629; MUID:21156231; PMID:11258796
A|Accession: A90696
A|Status: preliminary
A|Molecule type: DNA

A:Residues: 1-834 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA033960.1; PID:q13359994; GSPDB:GN00154
A:Experimental source: strain 0157:H7, substrain RMD 0509952
C:Genetics:
A:Gene: EC0537
C:Superfamily: Bacillus probable copper-transporting ATPase yvqX; ATPase nucleotide-bind

Query Match 54.1%; Score 46; DB 2; Length 834;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 5 GROLAIIIGDIN 16
|||::|||
Db 712 GQVAMVGDGIN 723

RESULT 7
E85546
probable ATPase ybar [imported] - Escherichia coli (strain 0157:H7, substrain EDL933)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: E85546
R:Perina, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Iller, L.; Grobeck, E.J.; Davis, N.W.; Lam, A.; Dimalanta, E.; Potamoudis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: E85546
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-834 <STO>
A:Cross-references: GB:AE005174; NID:q12513357; PIDN:AG54833.1; GSPDB:GN00145; UMGF:206
A:Experimental source: strain 0157:H7, substrain EDL933
C:Genetics:
A:Gene: ybar
C:Superfamily: Bacillus probable copper-transporting ATPase yvqX; ATPase nucleotide-bind

Query Match 54.1%; Score 46; DB 2; Length 834;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 5 GROLAIIIGDIN 16
|||::|||
Db 712 GQVAMVGDGIN 723

RESULT 8
H82104
cation transport ATPase, El-E2 family VC2215 [imported] - Vibrio cholerae (strain N16961)
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: H82104
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
Chadson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoti, I.; Sellers, F.
I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833
A:Accession: H82104
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-915 <HEI>
A:Cross-references: GB:AE004293; GB:AE003852; NID:g9656766; PIDN:AA95339.1; GSPDB:GN001
A:Experimental source: serogroup O1; strain N16961, biotype El Tor
C:Genetics:
A:Gene: VC2215
A:Map position: 1
C:Superfamily: Bacillus probable copper-transporting ATPase yvqX; ATPase nucleotide-bind

Query Match 54.1%; Score 46; DB 2; Length 915;

Best Local Similarity 64.3%; Pred. No. 17;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 3 QVGRVAMIGDIN 16
|||::|||
Db 786 QOGRVAMIGDIN 799

RESULT 9
S44824
F54F2.1 protein - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 23-Mar-2001
C:Accession: S44824
R:Anderson, K.
submitted to the EMBL Data Library, September 1993
A:Description: Sequence of the C. elegans cosmid F54F2.
A:Reference number: S44817
A:Accession: S44824
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1226 <AND>
A:Cross-references: EMBL:L23645; NID:g388603; PID:g388605
C:Genetics:
A:Introns: 58/2; 137/3; 179/1; 316/2; 393/1; 551/3; 597/2; 662/2; 899/3; 1178/3
C:Keywords: cytoskeleton; transmembrane protein

Query Match 54.1%; Score 46; DB 2; Length 1226;
Best Local Similarity 53.8%; Pred. No. 23;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 2 GQVGRVAMIGDIN 14
|||::|||
Db 359 GVFGKQIAVAGD 371

RESULT 10
F89890
conserved hypothetical protein SA1030 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: F89890
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; O
ma, A.; Mizutani-Oi, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaiho, C.; Sekimizu, K.
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: F89890
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-263 <KUR>
A:Cross-references: GB:BA000018; PID:q13700986; PIDN:BA042282.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA1030

Query Match 52.9%; Score 45; DB 2; Length 263;
Best Local Similarity 75.0%; Pred. No. 6.1;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 KGQVGRVAMIG 12
|||::|||
Db 250 KGQVGRVAMIG 261

RESULT 11
S58684
phosphopyruvate hydratase (EC 4.2.1.11) - Helicobacter pylori (strains 26695 and othe
N:Alternate names: enolase
C:Species: Helicobacter pylori

C>Date: 29-Nov-1995 #sequence_revision 17-Sep-1997 #text_change 22-Jun-1999
 C:Accession: B64539; S58684
 R:Tomb, J.F.; White, O.; Kervlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.; Nature 388, 539-547, 1997
 A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
 A:Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.
 A:Reference number: A64520; MUID:97394467
 A:Accession: B64539
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-426 <TOM>
 A:Cross-references: GB:AE000536; GB:AE000511; NID:g2313230; PIDN:AAD07219.1; PID:g231323
 A:Experimental source: Strain 26695
 R:Schmitt, W.; Odenbreit, S.; Heuermann, D.; Haas, R.
 Mol. Gen. Genet. 248, 563-572, 1995
 A:Title: Cloning of the *Helicobacter pylori* recA gene and functional characterization of
 A:Reference number: S58683; MUID:96027928
 A:Accession: S58684
 A:Molecule type: DNA
 A:Residues: 1-25, 1', 27-68 <SCH>
 A:Cross-references: EMBL:Z35478
 C:Genetics:
 A:Gene: HP0154
 C:Function:
 A:Description: catalyzes the reversible dehydration of 2-phospho-D-glyceric acid to phosphoglycerate
 A:Pathway: glycolysis
 C:Superfamily: enolase
 C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase; magnesium
 F:42/Binding site: magnesium 2 (Ser) #status predicted
 F:205,338/Active site: Glu, Lys #status predicted
 F:242,286,313/Binding site: magnesium 1 (Asp, Glu, Asp) #status predicted

Query Match 52.9%; Score 45; DB 2; Length 426;
 Best Local Similarity 46.2%; Pred. No. 10;
 Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

OY 3 OVGROLAIIIGDDI 15
 :||||:||||:
 Db 303 ELGRQIQLVGDDL 315

RESULT 12
 H71967
 enolase - *Helicobacter pylori* (strain J99)
 C:Species: *Helicobacter pylori*
 A:Variety: strain J99
 C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 22-Jun-1999
 C:Accession: H71967
 R:Alm, R.A.; Ling, L.S.L.; Molr, D.T.; King, B.L.; Brown, E.D.; Dolg, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jlang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
 A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric pathogen *Helicobacter pylori*.
 A:Reference number: A71800; MUID:99120557
 A:Accession: H71967
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-426 <ARN>
 A:Cross-references: GB:AE001453; GB:AE001439; NID:g4154651; PIDN:AAD05723.1; PID:g415465
 A:Experimental source: strain J99
 C:Genetics:
 A:Gene: eno
 A:Superfamily: enolase

Query Match 52.9%; Score 45; DB 2; Length 426;
 Best Local Similarity 46.2%; Pred. No. 10;
 Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

OY 3 OVGROLAIIIGDDI 15
 :||||:||||:

Db 303 ELGRQIQLVGDDL 315

RESULT 13
 H84643
 probable protein phosphatase 2C [imported] - *Arabidopsis thaliana*
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)
 C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 15-Jun-2001
 C:Accession: H84643
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Beilto, M.I.; Town, C.D.; Fujii, C.Y.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, J.; Nielsen, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
 A:Reference number: A84420; MUID:20083487
 A:Accession: H84643
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-355 <STO>
 A:Cross-references: GB:AE002093; NID:g4559345; PIDN:AAD23006.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: At2g25070
 A:Map position: 2
 C:Superfamily: human phosphoprotein phosphatase 1A

Query Match 52.4%; Score 44.5; DB 2; Length 355;
 Best Local Similarity 50.0%; Pred. No. 10;
 Matches 9; Conservative 6; Mismatches 2; Indels 1; Gaps 1;

OY 1 KGQVG-RQLAIIIGDDINR 17
 :|||:||||:||||:
 Db 103 QGQGRGRELAVLGDKNMK 120

RESULT 14
 H75027
 sy-v-acapase proteolipid PAB1189 - *Pyrococcus abyssi* (strain Orsay)
 C:Species: *Pyrococcus abyssi*
 C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
 C:Accession: H75027
 R:anonymous, Genoscope
 submitted to the EMBL Data Library, July 1999
 A:Description: *Pyrococcus abyssi* genome sequence: insights into archaeal chromosome s
 A:Reference number: A75001
 A:Accession: H75027
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-258 <RAW>
 A:Cross-references: GB:AJ248288; GB:AL096836; NID:g5458960; PIDN:CAB50662.1; PID:e151
 A:Experimental source: strain Orsay
 C:Genetics:
 A:Gene: PAB1189

Query Match 51.8%; Score 44; DB 2; Length 258;
 Best Local Similarity 43.8%; Pred. No. 8.8;
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 2 GQVGRQIAIIIGDDINR 17
 :|||:||||:||||:
 Db 122 GEAGRGFAVADDIR 137

RESULT 15
 B71213
 probable chemoreceptor protein - *Pyrococcus horikoshii*
 C:Species: *Pyrococcus horikoshii*
 C>Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000
 C:Accession: B71213
 R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Halkawa, Y.; Hino, Y.; Yamamoto, S.; Se M.; Onfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kishida, N.; Ogu DNA Res. 5, 55-76, 1998

A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
A:Reference number: A71000; MUID:98344137
A:Accession: B71213
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-261 <KAM>
A:Cross-references: GB:AP000007; NID:g3236134; PIDN:BAA31097.1; PID:g3258414
A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PH1970

Query Match 51.8%; Score 44; DB 2; Length 261;
Best Local Similarity 43.8%; Pred. No. 8.9;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 2 GQVGRQALITGDDINR 17
| : | | : : | : | |
Db 125 GEAGRGFAVVADEIR 140

Search completed: September 20, 2002, 10:39:13
Job time: 485 sec

GenCore version 4.5
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OK protein - protein search, using sw model

Run on: September 20, 2002, 11:04:35 ; Search time 44.99 Seconds
(without alignments) 14.631 Million cell updates/sec

Title: US-09-544-664-57

Sequence: 1 KGVGRQLATIGDDINR 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	80	94.1	211 1 BAK2_HUMAN	Q13014 homo sapien
2	80	94.1	211 1 BAK_HUMAN	Q16811 homo sapien
3	78	91.8	208 1 BAK_MOUSE	Q08734 mus muscula
4	46	54.1	834 1 ATC0_ECOLI	Q59385 escherichia
5	46	54.1	1226 1 PAT2_CAEEL	P34446 caenorhabd1
6	45	52.9	263 1 YLMD_STRAU	Q92ha4 staphylococ
7	45	52.9	426 1 ENO_HELPJ	Q92ms6 helicobacte
8	45	52.9	426 1 ENO_HELPJ	P48385 helicobacte
9	44	51.8	803 1 ATCU_BACSU	Q32320 bacillus su
10	43.5	51.2	532 1 CRT1_APHSP	P21134 aphanocearsa
11	43	50.6	444 1 ENO_LYCES	P26300 lycopersico
12	43	50.6	446 1 ENO2_MAIZE	Q42895 zea mays (m
13	43	50.6	446 1 ENO_ORYSA	Q42891 oryza sativ
14	43	50.6	770 1 YRN9_CAEEL	Q09609 caenorhabd1
15	43	50.6	827 1 ATC2_RHIME	P58342 rhizobium m
16	43	50.6	827 1 ATC2_RHIME	Q945x3 rhizobium m
17	42	49.4	575 1 CNGX_RAT	Q64559 rattus norv
18	42	49.4	826 1 ATC1_RHIME	P58341 rhizobium m
19	41	48.2	70 1 Y35_TREPA	O83346 treponema p
20	41	48.2	499 1 CPN1_MESAU	P97720 mesocricetu
21	41	48.2	539 1 CH60_CLOPE	P26821 clostridium
22	41	48.2	682 1 PILJ_PSEAE	P42257 pseudomonas
23	41	48.2	759 1 PARC_CAVCA	O54478 caulobacter
24	40	47.1	290 1 STX_APICA	O16932 aplysia cal
25	40	47.1	428 1 ENO_PYRHO	O59603 pyrococcus
26	40	47.1	446 1 ENO1_MAIZE	P26301 zea mays (m
27	40	47.1	665 1 CNG_DROME	Q24278 drosophila
28	40	47.1	4344 1 DYHC_EMEENI	P45444 emesicella
29	40	47.1	4349 1 DYHC_FUSSO	P78716 fusarium so
30	40	47.1	4367 1 VAF2_NEICR	P45443 neurospora
31	39	45.9	124 1 VAF2_DROME	O94113 drosophila
32	39	45.9	211 1 CRB3_CHICK	P55165 gallus gall
33	39	45.9	252 1 YD05_PYRAB	Q94yb5 pyrococcus

ALIGNMENTS

RESULT 1	ID	BAK2_HUMAN	STANDARD:	PRT:	211 AA.
AC	Q13014	BAK2_HUMAN			
DT	01-NOV-1997	(Rel. 35, Created)			
DT	01-NOV-1997	(Rel. 35, Last sequence update)			
DT	16-OCT-2001	(Rel. 40, Last annotation update)			
DE	Bcl-2 homologous antagonist/killer 2 (Apoptosis regulator BAK-2).				
GN	BCL2L7P1 OR BAK2.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=95231654; PubMed=7715731;				
RA	Kiefer M.C., Brauer M.J., Powers V.C., Wu J.J., Umansky S.R.,				
RA	Tomei L.D., Barr P.J.;				
RT	Modulation of apoptosis by the widely distributed Bcl-2 homologue				
RT	Bak."				
RL	Nature 374:736-739(1995).				
CC	- FUNCTION: IN THE PRESENCE OF AN APPROPRIATE STIMULUS, ACCELERATES				
CC	PROGRAMED CELL DEATH BY BINDING TO, AND ANTAGONIZING THE A				
CC	REPRESSOR BCL-2 OR ITS ADENOVIRUS HOMOLOG E1B 19K PROTEIN.				
CC	- SUPUNIT: FORMS HETERODIMERS WITH BCL-2, E1B 19K PROTEIN, AND BCL-				
CC	X(L).				
CC	- SUBCELLULAR LOCATION: Membrane-associated (Potential).				
CC	- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES, WITH				
CC	HIGHEST LEVELS IN THE HEART AND SKELETAL MUSCLE.				
CC	- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND				
CC	BAK FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION				
CC	WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.				
CC	APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.				
CC	- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 1 (BH1).				
CC	- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 2 (BH2).				
CC	- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 3 (BH3).				
CC	- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.				
CC	- CAUTION: THIS COULD BE THE PRODUCT OF A PSEUDOGENE.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL: U16812; AAA74467.1; -.				
DR	HSSP: Q16611; IBL.				
DR	InterPro: IPR002475; BCL2_family.				
DR	InterPro: IPR007112; Bcl-2.				
DR	Pfam: PF00452; Bcl-2; 1.				
DR	SMART: SM00337; BCL: 1.				
DR	PROSITE: PS01080; BH1; 1.				
DR	PROSITE: PS01258; BH2; 1.				
DR	PROSITE: PS01259; BH3; 1.				

```

DR PROSITE: PS50062; BCL2_FAMILY; 1.
KW Apoptosis; Transmembrane.
FT DOMAIN 74 88 BH3.
FT DOMAIN 117 136 BH1.
FT DOMAIN 169 184 BH2.
FT TRANSMEM 188 205 POTENTIAL.
SQ SEQUENCE 211 AA: 23411 MW: 7038756CADCC1D3 CRC64:

Query Match          94.1%; Score 80; DB 1; Length 211;
Best Local Similarity 100.0%; Pred. No. 7.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 GOVROLA1IGDDINR 17
Db 72 GOVROLA1IGDDINR 87

RESULT 2
BAK_HUMAN STANDARD; PRT; 211 AA.
ID BAK_HUMAN
AC 016611; Q92533;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Bcl-2 homologous antagonist/killer (Apoptosis regulator BAK).
GN BAK1 OR BAK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=R-cell;
RX MEDLINE=95231652; PubMed=7715729;
RA Farrow S.N., White J.H.M., Martinou I., Raven T., Pun K.-T.,
RA Grisham C.J., Martinou J.C., Brown R.;
RT "Cloning of a bcl-2 homologue by interaction with adenovirus E1B
RT 19K.";
RL Nature 374:731-733(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95231653; PubMed=7715730;
RA Chitenden T., Harrington E.A., O'Connor R., Flemington C., Lutz R.J.,
RA Evan G.I., Guild B.C.;
RT "Induction of apoptosis by the Bcl-2 homologue Bak.";
RL Nature 374:733-736(1995).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=95231654; PubMed=7715731;
RA Kiefer M.C., Brauer M.J., Powers V.C., Wu J.J., Umansky S.R.,
RA Tomei L.D., Barr P.J.;
RT "Modulation of apoptosis by the widely distributed Bcl-2 homologue
RT Bak.";
RL Nature 374:736-739(1995).
RN [4]
RP SEQUENCE FROM N.A.
RA Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 96-206 FROM N.A.
RA Eguchi H., Hayashi S.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [6]
RP MUTAGENESIS AND FUNCTION OF BH3 DOMAIN.
RX MEDLINE=96091131; PubMed=8521816;
RA Chitenden T., Flemington C., Houghton A.B., Ebb R.G., Gallo G.J.,
RA Elangovan B., Chinnadurai G., Lutz R.J.;
RT "A conserved domain in Bak, distinct from BH1 and BH2, mediates cell
RT death and protein binding functions.";
RL EMBO J. 14:5589-5596(1995).
RN [7]
RP STRUCTURE BY NMR OF 72-87.

```

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RX MEDLINE=97172562; PubMed=9020082;
RA Sattler M., Liang H., Nettesheim D., Meadows R.P., Harlan J.E.,
RA Eberstadt M., Koch H.S., Shuker S.B., Chang B.S., Minn A.J.,
RA Thompson C.B., Fesik S.W.;
RT Structure of Bcl-xL-Bak peptide complex: recognition between
RT regulators of apoptosis.";
RL Science 275:983-986(1997).
CC -1- FUNCTION: IN THE PRESENCE OF AN APPROPRIATE STIMULUS, ACCELERATES
CC PROGRAMED CELL DEATH BY BINDING TO, AND ANTAGONIZING THE A
CC REPRESSOR BCL-2 OR ITS ADENOVIRUS HOMOLOG E1B 19K PROTEIN.
CC -1- SUBUNIT: FORMS HETERODIMERS WITH BCL-2, E1B 19K PROTEIN, AND BCL-
CC X(L).
CC -1- SUBCELLULAR LOCATION: Membrane-bound (Potential).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES, WITH
CC HIGHEST LEVELS IN THE HEART AND SKELETAL MUSCLE.
CC -1- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND
CC BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC -1- SIMILARITY: MEMBERS OF THE BCL-2 FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
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CC -----
DR EMBL: X84213; CAA58997.1; -
DR EMBL: U23765; AAA93066.1; -
DR EMBL: U16811; AAA74466.1; -
DR EMBL: Z93017; CAB65626.1; -
DR EMBL: D88397; BAA13606.1; -
DR EMBL: D88396; BAA13606.1; JOINED.
DR PDB: 1BXL; 29-OCT-97.
DR MIM: 600516; -
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; BCL-2.
DR Pfam: PR00452; BCL-2; 1.
DR SMART: SM00337; BCL.1.
DR PROSITE: PS01080; BH1.1.
DR PROSITE: PS01258; BH2.1.
DR PROSITE: PS01259; BH3.1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
KW Apoptosis; Transmembrane; 3D-structure.
FT DOMAIN 74 88 BH3.
FT DOMAIN 117 136 BH1.
FT DOMAIN 169 184 BH2.
FT TRANSMEM 188 205 POTENTIAL.
SQ SEQUENCE 211 AA: 23409 MW: A2200FE72A46D04E CRC64:

Query Match          94.1%; Score 80; DB 1; Length 211;
Best Local Similarity 100.0%; Pred. No. 7.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 GOVROLA1IGDDINR 17
Db 72 GOVROLA1IGDDINR 87

RESULT 3
BAK_MOUSE STANDARD; PRT; 208 AA.
ID BAK_MOUSE
AC 008734;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Bcl-2 homologous antagonist/killer (Apoptosis regulator BAK).

```


GN BAK1 OR BAK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SWISS: TISSUE-Liver;
 RX MEDLINE=97446138; PubMed=9299236;
 RA Ullrich E., Kaufmann-Zeh A., Hueber A.O., Williamson J.,
 RA Chittenden T., Ma A., Evan G.I.;
 RT "Gene structure, cDNA sequence, and expression of murine Bak, a
 RT proapoptotic Bcl-2 family member.";
 RL Genomics 44:195-200(1997).
 CC -1- FUNCTION: IN THE PRESENCE OF AN APPROPRIATE STIMULUS, ACCELERATES
 CC PROGRAMED CELL DEATH BY BINDING TO, AND ANTAGONIZING THE A
 CC REPRESSOR BCL-2 OR ITS ADENOVIRUS HOMOLOG ELB 19K PROTEIN (BY
 CC SIMILARITY).
 CC -1- SUBUNIT: FORMS HETERODIMERS WITH BCL-2, ELB 19K PROTEIN, AND BCL-
 CC X(L) (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Membrane-associated (potential).
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED.
 CC -1- DOMAIN: INTRACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND
 CC BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
 CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
 CC APOPTOTIC MEMBERS OF THE BCL-2 FAMILY (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 1 (BH1).
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 2 (BH2).
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 HOMOLOG DOMAIN 3 (BH3).
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
 CC -----
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 CC -----
 DR EMBL: Y13231; CAA73684.1; -
 DR HSP: Q16611; IBLX.
 DR MGD: MGI:1097161; BAK1.
 DR InterPro: IPR002475; BCL2_family.
 DR InterPro: IPR000712; BCL_2.
 DR Pfam: PF00452; BCL-2; 1.
 DR SMART: SM00337; BCL; 1.
 DR PROSITE: PS01080; BH1; 1.
 DR PROSITE: PS01258; BH2; 1.
 DR PROSITE: PS01259; BH3; 1.
 DR PROSITE: PS50062; BCL2_FAMILY; 1.
 KW Apoptosis; Transmembrane.
 FT DOMAIN 71 85 BH3.
 FT DOMAIN 114 133 BH1.
 FT DOMAIN 166 181 BH2.
 FT TRANSMEM 185 202 POTENTIAL.
 SQ SEQUENCE 208 AA; 23300 MM; DAFCLIB160C523C9 CRC64;

Query Match 91.8%; Score 78; DB 1; Length 208;
 Best Local Similarity 93.8%; Pred. No. 1.6e-05;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGVGRLAIGDDINR 17
 |||||:|||||
 DB 69 GGVGRLALIGDDINR 84

RESULT 4
 ATCU_ECOLI STANDARD; PRT; 834 AA.
 AC 059385; P78245;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-MAR-2002 (Rel. 41, last annotation update)
 GN Probable copper-transporting ATPase (EC 3.6.3.4).
 DE YBAR OR B0484.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RA Das S., Chuang E., Vulpe C., Goldman J., Gitschler J.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Roberts D., Allen E., Araujo R., Aparicio A., Chung E., Davis K.,
 RA Duncan M., Federspiel N., Hyman R., Kaiman S., Komp C., Kurd O.,
 RA Lew H., Lin D., Nemeth A., Oefner P., Schramm S., Davis R.W.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: INVOLVED IN COPPER TRANSPORT.
 CC -1- CATALYTIC ACTIVITY: ATP + H(2)O -> ADP + ORTHOPHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).
 CC -1- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
 CC (EI-E2 ATPASES). SUBFAMILY IB.
 CC -1- SIMILARITY: CONTAINS 2 HMA DOMAINS.
 CC -----
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 CC -----
 DR EMBL: U58330; AAB02268.1; -
 DR EMBL: AE000154; AAC73586.1; -
 DR EMBL: U82664; AAB40238.1; -
 DR HSP: P04129; IAFI.
 DR Ecogene: EG33246; Ybar.
 DR InterPro: IPR001757; E1-E2_ATPase.
 DR InterPro: IPR001934; HMA.
 DR InterPro: IPR001454; Hydrolyase.
 DR Pfam: PF00122; E1-E2_ATPase; 1.
 DR Pfam: PF00403; HMA; 2.
 DR Pfam: PF00702; Hydrolyase; 1.
 DR PRINTS: PR00119; CATALYPASE.
 DR PROSITE: PS00154; ATPASE_E1_E2; 1.
 DR PROSITE: PS01047; HMA_1; 1.
 DR PROSITE: PS50846; HMA_2; 2.
 KW Hydrolyase; Transmembrane; Phosphorylation; ATP-binding; Copper;
 KW Metal-binding; Repeat; Complete proteome.
 FT TRANSMEM 187 207 POTENTIAL.
 FT TRANSMEM 218 236 POTENTIAL.
 FT TRANSMEM 254 274 POTENTIAL.
 FT TRANSMEM 284 304 POTENTIAL.
 FT TRANSMEM 438 458 POTENTIAL.
 FT TRANSMEM 464 484 POTENTIAL.
 FT TRANSMEM 485 505 POTENTIAL.
 FT TRANSMEM 627 647 POTENTIAL.
 FT TRANSMEM 733 753 POTENTIAL.
 FT TRANSMEM 779 799 POTENTIAL.
 FT TRANSMEM 801 821 POTENTIAL.
 FT DOMAIN 4 65 HMA 1.
 FT DOMAIN 100 163 HMA 2.

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FT METAL 110 110 COPPER (POTENTIAL).
FT METAL 113 113 COPPER (POTENTIAL).
FT MOD.RES 523 523 PHOSPHORYLATION (PROBABLE).
FT CONFLICT 162 181 EATEDAKRERQOETRAVAT ->
FT CONFLICT 508 508 KRLKMLTMAASAKRPPSLA (IN REF. 1).
FT CONFLICT 576 576 A -> R (IN REF. 1).
FT CONFLICT 576 576 Q -> R (IN REF. 1).
SQ SEQUENCE 834 AA; 87873 MW; CF84A1BFE208E6F6 CRC64;

Query Match 54.1%; Score 46; DB 1; Length 834;
Best Local Similarity 66.7%; Pred. No. 9.2;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 5 GROLAIGDIDIN 16
| | | | | | | |
DB 712 GROVANVGDCIN 723

RESULT 5
PAT2_CAEEL STANDARD; PRT: 1226 AA.
AC P34446:
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Integrin alpha pat-2 precursor.
GN PAT-2 OR F54F2.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Feloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE-94150718; PubMed-7906398;
RA Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laisler N.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
RA Sims M., Smaildon N., Smith A., Smith M., Sonhammer E., Staden K.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterston R., Watson A., Weinstock L., Wilkinson-Spratt J.,
RA Woldman P.;
RA *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RA elegans.*;
RT Nature 368:32-38(1994).
RL
CC -1- FUNCTION: POSSIBLE ROLE IN CELL-CELL INTERACTIONS (BY SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA PAT-2
CC ASSOCIATES WITH BETA PAT-3.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.
CC -1- SIMILARITY: CONTAINS 7 FG-GAP REPEATS.
CC
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CC -----
CC EMBL: L23645; AAK26134.1; .
CC PIR: S44824; S44824.
CC HSSP: P1215; 1ABX.
CC Wormpep: F54F2.1; CE00194.
CC InterPro: IPR000413; Integrin_alpha.
CC Pfam: PF00357; Integrin_A; 1.
CC PRINTS: PRO185; INTEGRINA.

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DR SMART: SM00191; Int.alpha; 5.
DR PROSITE: PS00242; INTEGRIN_ALPHA; 1.
KW Integrin: Cell adhesion; Receptor; Glycoprotein; Transmembrane;
KW Signal; Repeat.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 1226 INTEGRIN ALPHA PAT-2.
FT DOMAIN 26 1154 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1155 1177 POTENTIAL.
FT DOMAIN 1178 1226 CYTOPLASMIC (POTENTIAL).
FT REPEAT 40 103 FG-GAP 1.
FT REPEAT 120 172 FG-GAP 2.
FT REPEAT 189 243 FG-GAP 3.
FT REPEAT 244 297 FG-GAP 4.
FT REPEAT 300 372 FG-GAP 5.
FT REPEAT 373 433 FG-GAP 6.
FT REPEAT 437 485 FG-GAP 7.
FT CARBOHYD 108 108 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 679 679 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 775 775 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 819 819 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1226 AA; 135939 MW; B9169AU75B88901D CRC64;

Query Match 54.1%; Score 46; DB 1; Length 1226;
Best Local Similarity 53.8%; Pred. No. 14;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 2 GOVGROLAIGDD 14
| | | | | | | |
DB 359 GVGKQIAVVGDD 371

RESULT 6
YLMD_STAUA STANDARD; PRT: 263 AA.
ID YLMD_STAUA
AC Q9ZHA4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 30.1 kDa protein in ftsz 3 region.
GN YLMD.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 14154;
RX MEDLINE-99061199; PubMed-9846742;
RA Massida O., Anderluzzi D., Friedli L., Feger G.;
RT "Unconventional organization of the division and cell wall gene
RT cluster of Streptococcus pneumoniae.";
RL Microbiology 144:3069-3078(1998).
CC -1- SIMILARITY: BELONGS TO THE UPF0124 FAMILY.
CC
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CC -----
CC EMBL: AF068904; AAC95459.1; .
CC InterPro: IPR003730; DUF152.
CC Pfam: PF02578; DUF152; 1.
CC Hypothetical protein
SQ SEQUENCE 263 AA; 30097 MW; 76A0DA0BFC62AD CRC64;

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Query Match 52.9%; Score 45; DB 1; Length 263;
 Best Local Similarity 75.0%; Pred. No. 4;
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 KQVGRGLATIG 12
 DB 250 KQVGRGLATIG 261

RESULT 7

ENO_HELPJ STANDARD; PRT; 426 AA.

AC Q9ZMS6; 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase).
 GN ENO OR HP0142.
 OS Helicobacter pylori J99 (Campylobacter pylori J99).
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
 OC Helicobacter.
 OX NCBI_TaxID=85963;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99120557; PubMed=9923682;
 RA Alm R.A., Ling L.S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
 RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
 RA Tummino P.J., Carnuso A., Uria-Nickelsen M., Mills D.M., Ives C.,
 RA Gibson R., Merberg D., Mills S.D., Jiang O., Taylor D.E., Voyis G.F.,
 RA Trust T.J.;
 RT "Genomic sequence comparison of two unrelated isolates of the human
 RT gastric pathogen Helicobacter pylori.";
 RL Nature 397:176-180(1999).
 CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate + phosphoenolpyruvate +
 H(2)O.
 CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
 THE DIMER (BY SIMILARITY).
 CC -1- PATHWAY: GLYCOLYSIS.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
 CC -----
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 CC -----
 CC DR EMBL; AE001453; AAD05723.1; -;
 DR HSSP; P00924; 4ENL.
 DR InterPro; IPR000941; Enolase.
 DR Pfam; PF00113; enolase.1.
 DR PRINTS; PR00148; ENOLASE.
 DR ProDom; PD000902; Enolase.1.
 DR PROSITE; PS00164; ENOLASE.1.
 KW Lyase; Glycolysis; Magnesium; Complete proteome.
 FT ACT_SITE 155 155 BY SIMILARITY.
 FT METAL 242 242 MAGNESIUM (BY SIMILARITY).
 FT METAL 286 286 MAGNESIUM (BY SIMILARITY).
 FT METAL 313 313 MAGNESIUM (BY SIMILARITY).
 SO SEQUENCE 426 AA; 46654 MW; EDFA73EA8EB7BEE CRC64;

Query Match 52.9%; Score 45; DB 1; Length 426;
 Best Local Similarity 46.2%; Pred. No. 6;
 Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

OY 3 OVRGLATIGDDI 15
 DB 303 FLGRGLATIGDDI 315

RESULT 8

ENO_HELPJ STANDARD; PRT; 426 AA.

AC P48285; 01-FEB-1996 (Rel. 33, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase).
 GN ENO OR HP0154.
 OS Helicobacter pylori (Campylobacter pylori).
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
 OC Helicobacter.
 OX NCBI_TaxID=210;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=26695 / ATCC 700392;
 RX MEDLINE=97394467; PubMed=9252185;
 RA Tomb J.-F., White O., Kervatage A.R., Clayton R.A., Sutton G.G.,
 RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
 RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
 RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
 RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
 RA Berg D.E., Cooney J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
 RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Matthey L., Wallin E.,
 RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
 RA Venter J.C.;
 RT "The complete genome sequence of the gastric pathogen Helicobacter
 RT pylori.";
 RL Nature 388:539-547(1997).
 RN [2]
 RP SEQUENCE OF 1-178 FROM N.A.
 RC STRAIN=ATCC 53726 / 84-183;
 RX MEDLINE=95286262; PubMed=7768597;
 RA Thompson S.A., Blaser M.J.;
 RT "Isolation of the Helicobacter pylori recA gene and involvement of
 RT the recA region in resistance to low pH.";
 RL Infect. Immun. 63:2185-2193(1995).
 CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate + phosphoenolpyruvate +
 H(2)O.
 CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
 THE DIMER (BY SIMILARITY).
 CC -1- PATHWAY: GLYCOLYSIS.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
 CC -----
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 CC -----
 CC DR EMBL; AE000536; AAD07219.1; -;
 DR EMBL; U13756; AAC43380.1; -;
 DR HSSP; P00924; 4ENL.
 DR TIGR; HP0154; -;
 DR InterPro; IPR000941; Enolase.
 DR Pfam; PF00113; enolase.1.
 DR PRINTS; PR00148; ENOLASE.
 DR ProDom; PD000902; Enolase.1.
 DR PROSITE; PS00164; ENOLASE.1.
 KW Lyase; Glycolysis; Magnesium; Complete proteome.
 FT ACT_SITE 155 155 BY SIMILARITY.
 FT METAL 242 242 MAGNESIUM (BY SIMILARITY).
 FT METAL 286 286 MAGNESIUM (BY SIMILARITY).
 FT METAL 313 313 MAGNESIUM (BY SIMILARITY).
 FT CONFLICT 26 26 V -> I (IN REF. 2).
 FT CONFLICT 85 85 I -> T (IN REF. 2).

SQ SEQUENCE 426 AA; 46534 MW; 7B7A0B87A5DFB398 CRC64;
 Query Match
 Best Local Similarity 46.2%; Score 45; DB 1; Length 426;
 Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
 OY 3 OVERQIATIGDDI 15
 Db 303 ELGRQIQLVGDLL 315
 RESULT 9
 ATCU_BACSU STANDARD; PRT; 803 AA.
 AC 032220;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Potential copper-transporting ATPase (EC 3.6.3.4).
 GN YV6X.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 CC Bacillus/Staphylococcus group; Bacillus.
 CX NCBI_TaxID=1423;
 OX [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=168;
 RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: INVOLVED IN COPPER TRANSPORT (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: ATP + H(2)O -> ADP + ORTHOPHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
 CC (EL-E2 ATPASES). SUBFAMILY 1B.
 CC -1- SIMILARITY: CONTAINS 2 HMA DOMAINS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: Z99121; CAB15355.1; -
 DR HSSP: P04129; IAF3.
 DR Subtilist; BG14106; YV9X.
 DR InterPro: IPR001366; Cad_ATPase.
 DR InterPro: IPR000579; Cat_P_ATPase.
 DR InterPro: IPR001756; Cu_ATPase.
 DR InterPro: IPR001877; El-E2_ATPase.
 DR InterPro: IPR001802; HG_scaVenger.
 DR InterPro: IPR001544; HMA.
 DR InterPro: IPR001454; Hydrolase.
 DR pfam: PF00403; HMA_2.
 DR pfam: PF00702; Hydrolase; 1.
 DR pfam: PF00940; CATATPASE.
 DR PRINTS: PR00941; CATATPASE.
 DR PRINTS: PR00943; CDATPASE.
 DR PRINTS: PR00942; CUATPASE.
 DR PRINTS: PR00946; HGSCAVENGER.
 DR PROSITE: PS00154; ATPASE_EL_E2; 1.
 DR PROSITE: PS01047; HMA_1; 2.
 DR PROSITE: PS00846; HMA_2; 2.
 DR Hydrolase; Transmembrane; Phosphorylation; Magnesium; ATP-binding;
 KW Metal-binding; Copper; Repeat; Complete proteome.
 FT TRANSMEM 163 183 POTENTIAL.
 FT TRANSMEM 197 217 POTENTIAL.
 FT TRANSMEM 229 249 POTENTIAL.

FT TRANSMEM 260 280 POTENTIAL.
 FT TRANSMEM 416 436 POTENTIAL.
 FT TRANSMEM 448 468 POTENTIAL.
 FT TRANSMEM 610 630 POTENTIAL.
 FT TRANSMEM 704 724 POTENTIAL.
 FT TRANSMEM 767 787 POTENTIAL.
 FT DOMAIN 7 73 HMA 1.
 FT METAL 75 141 HMA 2.
 FT METAL 17 17 COPPER (POTENTIAL).
 FT METAL 20 20 COPPER (POTENTIAL).
 FT METAL 85 85 COPPER (POTENTIAL).
 FT METAL 88 88 COPPER (POTENTIAL).
 FT MOD_RES 500 500 PHOSPHORYLATION (BY SIMILARITY).
 FT METAL 699 699 MAGNESIUM (BY SIMILARITY).
 FT METAL 703 703 MAGNESIUM (BY SIMILARITY).
 SQ SEQUENCE 803 AA; 86024 MW; D9C8DA5D40326C6B CRC64;

Query Match
 Best Local Similarity 51.8%; Score 44; DB 1; Length 803;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 5 GROLATIGDIN 16
 Db 691 GROTAMVGDGIN 702

RESULT 10
 CRTI_APHSP STANDARD; PRT; 532 AA.
 ID CRTI_APHSP
 AC P21134;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Phytoene dehydrogenase (EC 1.14.99.-) (Phytoene desaturase).
 GN CRTI.
 OS Aphanocephala sp.
 OC Bacteria; Cyanobacteria; Chroococcales; Aphanocephala.
 CX NCBI_TaxID=1120;
 OX [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=PCC 6714;
 RC MEDLINE=90382685; PubMed=2119326;
 RA Schmidt A., Sandmann G.;
 RT Cloning and nucleotide sequence of the crtI gene encoding phytoene
 RT dehydrogenase from the cyanobacterium Aphanocephala PCC6714.?
 RL Gene 91:113-117(1990).
 CC -1- FUNCTION: THIS ENZYME CONVERTS PHYTOENE INTO ZETA-CAROTENE VIA THE
 CC INTERMEDIARY OF PHYTOFLUENE BY THE SYMMETRICAL INTRODUCTION OF TWO
 CC DOUBLE BONDS AT THE C-11 AND C-11' POSITIONS OF PHYTOENE.
 CC DOUBBLE BONDS AT THE C-11 AND C-11' POSITIONS OF PHYTOENE.
 CC -1- COFACTOR: NAD, NADP, OR FAD (PROBABLE).
 CC -1- PATHWAY: CAROTENOID BIOSYNTHESIS.
 CC -1- SIMILARITY: BELONGS TO THE PHYTOENE DEHYDROGENASE FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M55647; AAA62573.1; -
 DR PIR: JN0084; JN0084.
 DR Carotenoid biosynthesis; Oxidoreductase; FAD; Flavoprotein; NAD.
 KW NP_BIND 22 49 FAD (ADP PART) (POTENTIAL).
 FT NP_BIND 22 49
 SQ SEQUENCE 532 AA; 56754 MW; 06296C65A914B19F CRC64;

Query Match
 Best Local Similarity 51.2%; Score 43.5; DB 1; Length 532;
 Matches 9; Conservative 5; Mismatches 2; Indels 3; Gaps 1;

OY 2 GVGROLATIGDDI 17
 DB 141 GGTGRLQLETFEGDYHR 159

RESULT 11

ENO_LYCSES STANDARD: PRT; 444 AA.
 ID ENO_LYCSES
 AC P26300;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase).
 GN PGH1.
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4081;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. SUPERSONIC;
 RX MEDLINE=93044507; PubMed=1841726;
 RA van der Straeten D., Rodrigues-Pousada R.A., Goodman H.M.,
 RA van Montagu M.;
 RT "Plant enolase: gene structure, expression, and evolution.";
 RL Plant Cell 3:719-735(1991).
 CC -1 CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate + H(2)O.
 CC -1 COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
 CC -1 PATHWAY: GLYCOLYSIS.
 CC -1 SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1 SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1 SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
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 CC EMBL: X58108; CAA4115.1; -
 DR PIR: J01185; J01185.
 DR HSSP: P56252; 1PDZ.
 DR Mendel: 611; LYCES:Pgh1.2.
 DR InterPro: IPR000941; Enolase.
 DR Pfam: PF00113; enolase.1.
 DR PRINTS: PR00148; ENOLASE.1.
 DR PRODOM: PD000902; Enolase.1.
 DR PROSITE: PS00164; ENOLASE.1.
 DR Lyase; Glycolysis; Magnesium.1.
 FT ACT_SITE 163 163 BY SIMILARITY.
 FT METAL 250 250 MAGNESIUM (BY SIMILARITY).
 FT METAL 300 300 MAGNESIUM (BY SIMILARITY).
 FT METAL 327 327 MAGNESIUM (BY SIMILARITY).
 SO SEQUENCE 444 AA; 47798 MW; 73C384181ED620AD CRC64;

Query Match 50.6%; Score 43; DB 1; Length 444;
 Best Local Similarity 46.2%; Pred. No. 14;
 Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 3 GVGROLATIGDDI 15
 DB 317 EIGEGVQIVGDDL 329

RESULT 12
 ENO2_MAIZE

ID ENO2_MAIZE STANDARD; PRT; 446 AA.
 AC P42835;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Enolase 2 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 2).
 GN ENO2.
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
 OC Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. B73; TISSUP=Root;
 RX MEDLINE=99063764; PubMed=9847102;
 RA Lal S.K., Lee C., Sachs M.M.;
 RT "Differential regulation of enolase during anaerobiosis in maize.";
 RL Plant Physiol. 118:1285-1293(1998).
 CC -1 CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate + H(2)O.
 CC -1 COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
 CC -1 PATHWAY: GLYCOLYSIS.
 CC -1 SUBUNIT: HOMODIMER.
 CC -1 SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1 SIMILARITY: BELONGS TO THE ENOLASE FAMILY.

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 CC EMBL: U17973; AAD04187.1; -
 DR HSSP: P56252; 1PDZ.
 DR MaizeDB: 30060; -
 DR Mendel: 16623; Zeama:Pgh1:16623.
 DR InterPro: IPR000941; Enolase.
 DR Pfam: PF00113; enolase.1.
 DR PRINTS: PR00148; ENOLASE.1.
 DR PRODOM: PD000902; Enolase.1.
 DR PROSITE: PS00164; ENOLASE.1.
 DR Lyase; Glycolysis; Magnesium; Multigene family.
 FT ACT_SITE 164 164 BY SIMILARITY.
 FT METAL 251 251 MAGNESIUM (BY SIMILARITY).
 FT METAL 302 302 MAGNESIUM (BY SIMILARITY).
 FT METAL 329 329 MAGNESIUM (BY SIMILARITY).
 SO SEQUENCE 446 AA; 48162 MW; DC27708CF92F850 CRC64;

Query Match 50.6%; Score 43; DB 1; Length 446;
 Best Local Similarity 46.2%; Pred. No. 14;
 Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 3 GVGROLATIGDDI 15
 DB 319 EIGEGVQIVGDDL 331

RESULT 13
 ENO_ORYSA STANDARD; PRT; 446 AA.
 ID ENO_ORYSA
 AC Q42971;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) (OSEI).
 OS Oryza sativa (Rice).

CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 CC Euphorbiaceae; Oryzaeae; Oryza.
 CC NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, TAINUNG 67; TISSUE=Seed;
 RA Hsling Y.-I.C., Tsao C.-W., Hsieh J.-S., Chen Z.-Y., Shu T.-F.,
 RA Chow T.-Y.;
 RT "A rice early embryogenesis-specific enolase cDNA";
 RL (in) Plant Gene Register PGR95-084.
 CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate -> phosphoenolpyruvate +
 H₂O.
 CC -1- COPACITOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
 THE DIMER.
 CC -1- PATHWAY: GLYCOLYSIS.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: EXPRESSED DURING EARLY EMBRYOGENESIS.
 CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
 CC -----
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 or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: U09450; AAC49173.1; -
 CC HSSP: P56252; IPD2.
 CC InterPro: IPR000941; Enolase.
 CC DR Pfam: PF00113; enolase; 1.
 CC DR PRINTS: PR00148; ENOLASE.
 CC DR Prodom: PD000902; Enolase; 1.
 CC DR PROSITE: PS00164; ENOLASE; 1.
 CC KM Lyase; Glycolysis; Magnesium.
 CC FT ACT SITE 164 164 BY SIMILARITY.
 CC FT METAL 251 251 MAGNESIUM (BY SIMILARITY).
 CC FT METAL 302 302 MAGNESIUM (BY SIMILARITY).
 CC FT METAL 329 329 MAGNESIUM (BY SIMILARITY).
 CC FT SEQUENCE 446 AA; 47986 MW; FECD81319246D477 CRC64;
 SQ
 Query Match 50.6%; Score 43; DB 1; Length 446;
 Best Local Similarity 46.2%; Pred. No. 14;
 Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 OY 3 OYGR0LATIIGDDI 15
 DB 319 EIGEOVQIVGDDI 331
 RESULT 14
 YRN9_CAEEL STANDARD: PRT: 770 AA.
 AC Q09609;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Hypothetical 84.2 kDa protein R07B1.9 in chromosome X.
 GN R07B1.9
 OS Caenorhabditis elegans.
 CC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 CC Rhabditidae; Peloderinae; Caenorhabditis.
 CC NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Kershav J.;
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
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 CC -----
 CC EMBL: Z48621; CAA8546.1; -
 CC WormRep: R07B1.9; CE01635.
 CC KW Hypothetical protein.
 CC SEQUENCE 770 AA; 84235 MW; 42EA80C594ACBBDB8 CRC64;
 SQ
 Query Match 50.6%; Score 43; DB 1; Length 770;
 Best Local Similarity 56.2%; Pred. No. 26;
 Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 OY 2 OYGR0LATIIGDDI 17
 DB 738 GQPGQSPANVDDPNR 753
 RESULT 15
 ATC2_RHIME STANDARD: PRT: 827 AA.
 ID ATC2_RHIME
 AC P58342;
 DT 01-MAR-2002 (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Copper-transporting ATPase 2 (PC 3.6.3.4).
 GN ACTP2 OR ACTU2 OR RB1018 OR SMC21578.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 CC Plasmid pSymB (megaplasmid 2).
 CC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 CC Rhizobiaceae; Sinorhizobium.
 CC NCBI_TaxID=382;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021.
 RX MEDLINE=2136508; PubMed=11481431;
 RA Finan T.M., Weidner S., Wong K., Buhmester J., Chain P.,
 RA Vordolter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,
 RA Golding B., Puehler A.;
 RT "The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-
 RT fixing endosymbiont Sinorhizobium meliloti".
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
 CC -1- FUNCTION: INVOLVED IN COPPER TRANSPORT (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: ATP + H₂O -> ADP + ORTHOPHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
 (F1-F2 ATPASES), SUPRASILY IB.
 CC -1- SIMILARITY: CONTAINS 2 HMA DOMAINS.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: AL603645; CAC49418.1; -
 CC DR PROSITE: PS00154; ATPASE_E1_E2; 1.
 CC DR PROSITE: PS01047; HMA_1; 2.
 CC DR PROSITE: PS00846; HMA_2; 2.
 CC KM Hydrolyase; Transmembrane; Phosphorylation; Magnesium; ATP-binding;
 CC Metal-binding; Copper; Repeat; Plasmid; Complete proteome.
 CC FT TRANSMEM 174 194 POTENTIAL.
 CC FT TRANSMEM 210 230 POTENTIAL.
 CC FT TRANSMEM 246 266 POTENTIAL.
 CC FT TRANSMEM 271 291 POTENTIAL.
 CC FT TRANSMEM 430 450 POTENTIAL.
 CC FT TRANSMEM 458 478 POTENTIAL.

FT	TRANSMEM	771	793	POTENTIAL.
FT	TRANSMEM	797	819	POTENTIAL.
FT	DOMAIN	16	81	HMA 1.
FT	DOMAIN	83	149	HMA 2.
FT	METAL	26	26	COPPER (POTENTIAL).
FT	METAL	29	29	COPPER (POTENTIAL).
FT	METAL	93	93	COPPER (POTENTIAL).
FT	METAL	96	96	COPPER (POTENTIAL).
FT	MOD_RES	515	515	PHOSPHORYLATION (BY SIMILARITY).
FT	METAL	714	714	MAGNESIUM (BY SIMILARITY).
FT	METAL	718	718	MAGNESIUM (BY SIMILARITY).
SO	SEQUENCE	827 AA:	85861 MW:	A3DBDFDD1315FCB CRC64;

Query Match 50.68; Score 43; DB 1; Length 827;
 Best Local Similarity 64.38; Pred. No. 28;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 3 QVGRQLAIGDDIN 16
 Db 704 QGSRGVAFIGDSIN 717

Search completed: September 20, 2002, 11:04:35
 Job time: 1632 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 20, 2002, 11:03:48 ; Search time 172.19 Seconds
(without alignments)
17.079 Million cell updates/sec

Title: US-09-544-664-57

Sequence: 1 KGQVGRQLAITGDDINR 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_19:*

- 1: sp._archaea:*
- 2: sp._bacteria:*
- 3: sp._fungi:*
- 4: sp._human:*
- 5: sp._invertebrate:*
- 6: sp._mammal:*
- 7: sp._mhc:*
- 8: sp._organelle:*
- 9: sp._phage:*
- 10: sp._plant:*
- 11: sp._rodent:*
- 12: sp._virus:*
- 13: sp._vertebrate:*
- 14: sp._unclassified:*
- 15: sp._virus:*
- 16: sp._bacteriophage:*
- 17: sp._archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	80	94.1	80	6	077738	077738 sus scrofa
2	79	92.9	103	6	09M7S6	09M7S6 ovis aries
3	78	91.8	151	11	091WXS	091WXS mus musculus
4	78	91.8	209	11	091XO59	091XO59 ratius norv
5	47.5	55.9	357	10	09S253	09S253 arabidopsis
6	46	54.1	915	16	09KPZ7	09KPZ7 vibrio chol
7	45	52.9	263	16	099US8	099US8 staphylococ
8	44.5	52.4	355	10	081716	081716 arabidopsis
9	44	51.8	258	17	09UXV1	09UXV1 pyrococcus
10	44	51.8	261	17	057733	057733 pyrococcus
11	44	51.8	556	10	09LHL6	09LHL6 arabidopsis
12	44	51.8	593	16	P73239	P73239 synechocyst
13	44	51.8	608	10	09FG35	09FG35 arabidopsis
14	44	51.8	693	16	09PC32	09PC32 xylella fas
15	43	50.6	421	16	098KM2	098KM2 rhizobium l
16	43	50.6	447	16	09CD42	09CD42 mycobacteri

17	43	50.6	475	10	Q9LZQ1	Q9LZQ1 arabidopsis
18	43	50.6	664	10	Q22716	Q22716 arabidopsis
19	42	49.4	158	11	Q925D2	Q925D2 ratius norv
20	42	49.4	170	10	Q94208	Q94208 oryza sativ
21	42	49.4	356	4	Q14558	Q14558 homo sapien
22	42	49.4	356	4	Q96H06	Q96H06 homo sapien
23	42	49.4	356	11	Q61468	Q61468 ratius norv
24	42	49.4	356	11	Q9D0M1	Q9D0M1 mus musculu
25	42	49.4	369	4	Q60256	Q60256 homo sapien
26	42	49.4	369	11	Q08618	Q08618 ratius norv
27	42	49.4	383	5	Q95WA9	Q95WA9 tetrahymena
28	42	49.4	552	5	Q967Y5	Q967Y5 musca domes
29	42	49.4	733	16	Q99YGS	Q99YGS streptococ
30	42	49.4	898	5	Q9WIS3	Q9WIS3 drosophila
31	42	49.4	952	5	Q97198	Q97198 leishmania
32	41	48.2	102	10	Q9AR96	Q9AR96 linum usita
33	41	48.2	102	10	Q9AR95	Q9AR95 linum usita
34	41	48.2	251	1	Q06508	Q06508 desulfuroco
35	41	48.2	383	16	P74756	P74756 synechocyst
36	41	48.2	447	9	Q64320	Q64320 bacterioph
37	41	48.2	530	16	Q9XOM7	Q9XOM7 thermotoga
38	41	48.2	539	16	Q9XON0	Q9XON0 thermotoga
39	41	48.2	566	16	Q9XIE2	Q9XIE2 thermotoga
40	41	48.2	570	16	Q97FD7	Q97FD7 clostridium
41	41	48.2	577	2	Q53050	Q53050 leptospirill
42	41	48.2	614	5	Q9BLI1	Q9BLI1 saturnia ja
43	41	48.2	642	17	Q9HS07	Q9HS07 halobacteri
44	41	48.2	644	2	Q52777	Q52777 treponema p
45	41	48.2	654	16	Q83646	Q83646 treponema p

ALIGNMENTS

RESULT 1

ID 077738 PRELIMINARY; PRT: 80 AA.

AC 077738;

DT 01-NOV-1998 (TREMBLrel. 08, Created)

DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE BAK PROTEIN (FRAGMENT).

GN BAK.

OS Sus scrofa (pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.

OX NCBI_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RA Batlling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;

RT Expression of Apoptosis-associated genes in hibernating and stunned

RT myocardium of pig.

RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL: AJ001204; CAA04598.1; -

DR HSSP: O16611; 1BXL.

DR InterPro: IPR002475; BCL2_family.

DR InterPro: IPR000712; BCL2.

DR Pfam: PF00452; Bcl-2; 1.

DR SMART: SM00357; BCL_1.

DR PROSITE: PS50062; BCL2_FAMILY; 1.

DR PROSITE: PS01259; BH3; 1.

FT NON_TER 1

FT NON_TER 1

FT NON_TER 1

SEQUENCE 80 AA: 8818 MW: FDIAF83BD7D59C86 CRC64:

Query Match 94.1%; Score 80; DB 6; Length 80;
Best Local Similarity 100.0%; Pred. No. 8.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GQVGRQLAITGDDINR 17
DB 23 GQVGRQLAITGDDINR 38

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RESULT 2
ID 09MZS6 PRELIMINARY: PRT: 163 AA.
AC 09MZS6;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, last sequence update)
DE 01-DEC-2001 (TREMblrel. 19, last annotation update)
DE BAK PROTEIN (FRAGMENT).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Kuminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxId=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Ovary;
RA Murray J.F., Dong Y.B., Leigh A.J., Scaramuzzi R.J., Carter N.D.;
RT Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF164518; AAF89533.1; -.
DR HSSP: Q16611; 1BXL.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; BCL2.
DR Pfam: PF00452; Bcl-2; 1.
DR SMART: SM00337; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
FT NON_TER 1
FT NON_TER 163
SQ SEQUENCE 163 AA: 18039 MW: FB35E8A8C53AD5B CRC64:

Query Match 92.9%; Score 79; DB 6; Length 163;
Best Local Similarity 93.8%; Pred. No. 2.6e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 GOVROLAIGDDINR 17
DB 31 GOVROLAIGDDINR 46

RESULT 3
ID 091WX5 PRELIMINARY: PRT: 151 AA.
AC 091WX5;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, last sequence update)
DE 01-DEC-2001 (TREMblrel. 19, last annotation update)
DE N-BAK1.
GN BAK1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MRI; TISSUE=NEURONAL;
RX MEDLINE=2138300; PubMed=11278671;
RA Sun Y.F., Yu L.Y., Saarna M., Timusk T., Arumae U.;
RT "Neuron-specific Bcl-2 homolog 3 domain-only splice variant of Bak 1s
anti-apoptotic in neurons, but pro-apoptotic in non-neuronal cells.";
RL EMBL: AF402617; AAL01876.1; -.
SQ SEQUENCE 151 AA: 16402 MW: 18C13BFF86E4F33B CRC64:

Query Match 91.8%; Score 78; DB 11; Length 151;
Best Local Similarity 93.8%; Pred. No. 3.6e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY 2 GOVROLAIGDDINR 17
DB 70 GOVROLAIGDDINR 85

RESULT 4
ID 09JK59 PRELIMINARY: PRT: 209 AA.
AC 09JK59;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, last sequence update)
DE 01-DEC-2001 (TREMblrel. 19, last annotation update)
DE BAK PROTEIN.
GN BAK.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RA Itoh T., Itoh A., Pleasure D.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF259504; AAF71760.1; -.
DR HSSP: Q16611; 1BXL.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; BCL2.
DR Pfam: PF00452; Bcl-2; 1.
DR SMART: SM00337; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
SQ SEQUENCE 209 AA: 23153 MW: 2493B814B1972421 CRC64:

Query Match 91.8%; Score 78; DB 11; Length 209;
Best Local Similarity 93.8%; Pred. No. 5.1e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 GOVROLAIGDDINR 17
DB 70 GOVROLAIGDDINR 85

RESULT 5
ID 09S253 PRELIMINARY: PRT: 357 AA.
AC 09S253;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, last sequence update)
DE 01-DEC-2001 (TREMblrel. 19, last annotation update)
DE PROTEIN PHOSPHATASE 2C-LIKE PROTEIN (AT4G31860/F11C18_60).
GN F11C18.60 OR AT4G31860.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxId=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Terry N., Ardles W., Buyschaert C., Dasseville R.,
RA De Clerck R., De Keyser A., Neyt P., Kouze P., Van Den Daele H.,
RA Villarroel R., Gieles J., Van Montagu M., Hohnleisel J., Mewes H.W.,
RA Mayer K.F.X., Schellier C.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.

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RA Terry N., Ardiles W., Buyschaert C., Daseville R., De Clerck R.,
 RA De Keyser A., Neyt P., Kouze P., Van Den Daele H., Villaroel R.,
 RA Gielen J., Van Montagu M., Nemes H.W., Lemcke K., Mayer K.F.X.,
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RA SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.-J., Koesema E., Meyers M.C., Banh J.,
 RA Bowser L., Garinaci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
 RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
 RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
 RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
 RA Yamanura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
 RA Becker J.R.,
 RT "Arabidopsis cDNA clones."
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL049607; CAB40756.1; -
 DR EMBL; AL161579; CAB79904.1; -
 DR EMBL; AY057611; AAL14406.1; -
 DR HSSP; P35813; 1A60.
 DR InterPro: IPR000222; PP2C.
 DR InterPro: IPR001932; PP2C_domain.
 DR Pfam; PF00481; PP2C_2.
 DR SMART; SM00332; PP2C; 1.
 DR SMART; SM00331; PP2C_SIG; 1.
 DR PROSITE; PS01032; PP2C; 1.
 SQ SEQUENCE 357 AA; 39203 MW; 98EE1A09818CA0D3 CRC64;

Query Match 55.9%; Score 47.5; DB 10; Length 357;
 Best Local Similarity 55.6%; Pred. No. 10;
 Matches 10; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 1 KGQV-RQLATIGDINR 17
 Db 103 QGQGRKRLAVLDGDKNK 120

RESULT 6
 Q9KPZ7 PRELIMINARY; PRT; 915 AA.
 AC Q9KPZ7;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE CATION TRANSPORT ATPASE, E1-E2 FAMILY.
 GN VC2215.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
 NCBI_TaxID=666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-EL TOR N16961 / SEROTYPE O1;
 RX MEDLINE-20406833; PubMed-10952301;
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
 RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 RA Gill S.R., Nelson K.E., Read T.D., Tettein H., Richardson D.,
 RA Ermiolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
 RA McDonald L., Uterback T., Fleischmann R.D., Nierman W.C., White O.,
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 Fraser C.M.,
 RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
 cholerae."
 RL Nature 406:477-483(2000).
 DR EMBL; AE004293; AAF95359.1; -
 DR HSSP; P04129; 1AFJ.
 DR TIGR; VC2215; -
 DR InterPro: IPR001757; Cat_P_ATPase.
 DR InterPro: IPR001757; E1-E2_ATPase.

DR InterPro: IPR001802; HG_scavenger.
 DR InterPro: IPR001934; HMA.
 DR InterPro: IPR001454; Hydrolase.
 DR InterPro: IPR000150; Hypothet_cof.
 DR Pfam; PF00122; E1-E2_ATPase; 1.
 DR Pfam; PF00403; HMA; 3.
 DR Pfam; PF00702; Hydrolase; 1.
 DR PRINTS; PR00119; CATPATPASE.
 DR PRINTS; PR00940; CATPATPASE.
 DR PRINTS; PR00946; HGSCAVENGER.
 DR PROSITE; PS00154; ATPASE_E1_E2; UNKNOWN_1.
 DR PROSITE; PS01229; COE_2; UNKNOWN_1.
 DR PROSITE; PS01047; HMA; 1.
 KW Complete proteome.
 SQ SEQUENCE 915 AA; 97311 MW; 2F31EE2640AD0D20 CRC64;

Query Match 54.1%; Score 46; DB 16; Length 915;
 Best Local Similarity 64.3%; Pred. No. 52;
 Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 QVGRQLATIGDIN 16
 Db 786 QGQGRKRLAVLDGDKNK 799

RESULT 7
 Q990S8 PRELIMINARY; PRT; 263 AA.
 AC Q990S8;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE HYPOTHETICAL PROTEIN SA1030 (HYPOTHETICAL PROTEIN SAV1187).
 GN SA1030 OR SAV1187.
 OS Staphylococcus aureus (strain N315), and
 OS Staphylococcus aureus (strain Mu50).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Staphylococcus.
 NCBI_TaxID=158879; 158878;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES-S aureus (strain N315), and S. aureus (strain Mu50);
 RX MEDLINE-21311952; PubMed-11418146;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iano J.-Q., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Ul Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekizawa K., Hiraoka H., Kohara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiratake S.,
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus."
 RL Lancet 357:1225-1240(2001).
 DR EMBL; AP003132; BAB4282.1; -
 DR EMBL; AP003361; BAB57349.1; -
 DR InterPro: IPR003730; DUF152.
 DR Pfam; PF02578; DUF152; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 263 AA; 30257 MW; 7AB013BD94EB07F9 CRC64;

Query Match 52.9%; Score 45; DB 16; Length 263;
 Best Local Similarity 75.0%; Pred. No. 19;
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 KGQVGRQLATIG 12
 Db 250 KGQGRKRLAVLDGDKNK 261

RESULT 8
 O81716

ID 081716 PRELIMINARY: PRT: 355 AA.
 AC 081716.
 DT 01-NOV-1998 (TRENBLREL. 08, Created)
 DT 01-NOV-1998 (TRENBLREL. 08, last sequence update)
 DT 01-DEC-2001 (TRENBLREL. 19, last annotation update)
 DE HYPOHETICAL 39.4 KDA PROTEIN.
 GN AT2G25070.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_Taxid=3702;
 RX MEDLINE=20083487; PubMed=16117197.
 RA LIN X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
 RA Buell C.R., Ketchum K.A., Lee J.C., Ronning C.M., Koo H.J., Moffat K.S.,
 RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
 RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
 RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
 RA Salzberg S.L., Fraser C.M., Venter J.C.;
 RA "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 thaliana".
 RT Nature 402:761-768(1999).
 RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Pham P.K., Banh J., Dale J.M., Goldsmith A.D.,
 RA Jiang P.X., Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M.,
 RA Yamamura Y., Fu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R.,
 RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawaji J., Kim C., Koeseke E., Lam B., Lin J., Meyers M.C., Miranda M.,
 RA Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,
 RA Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W.,
 RA Ecker J.R., Theologis A.;
 RA "Full length cDNA of gene F77C12.1/At2G25070 (GI:4559345).";
 RT Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
 RL EMBL: AC065585; MADS2006.1; -;
 RA EMBL: AF030873; MAK92810.1; -;
 DR HSSP: P35813; 1A6Q.
 DR InterPro: IPR000222; PP2C.
 DR InterPro: IPR001932; PP2C_domain.
 DR Pfam: PF00481; PP2C; 2.
 DR SMART: SM00332; PP2C; 1.
 DR SMART: SM00331; PP2C-StG; 1.
 DR PROSITE: PS01032; PP2C; 1.
 KW Hypothetical Protein.
 SQ SEQUENCE 355 AA: 39354 MW: CAD638796203C746 CRC64;

Query Match 52.4%; Score 44.5; DB 10; Length 355;
 Best Local Similarity 50.0%; Pred. No. 32;
 Matches 9; Conservative 6; Mismatches 2; Indels 1; Gaps 1;

OY 1 KQGVG-ROLAIIIGDDINR 17
 DB 103 QGGRGRELAVLGDKNK 120
 ID 09UXV1 PRELIMINARY: PRT: 258 AA.
 AC 09UXV1.
 DT 01-MAY-2000 (TRENBLREL. 13, Created)
 DT 01-MAY-2000 (TRENBLREL. 13, last sequence update)
 DT 01-DEC-2001 (TRENBLREL. 19, last annotation update)
 DE SY V-ATPase PROTEOLIPID.

GN PA81189.
 OS Pyrococcus abyssi.
 OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
 OX NCBI_TaxID=29292;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ORSAY;
 RA Hellig R.;
 RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
 structure and evolution."
 RT Submitted (JUL-1999) to the EMBL/Genbank/DBJ databases.
 RL EMBL: AJ248288; CAB50662.1; -;
 DR EMBL: AJ248288; CAB50662.1; -;
 DR InterPro: IPR004089; Chemotaxis_transducer.
 DR InterPro: IPR004090; Me-chemotaxis.
 DR Pfam: PF00015; MCPsignal; 1.
 DR PRINTS: PR00260; CHEMTRNSDCR.
 DR SMART: SM00283; MA; 1.
 KW Complete proteome.
 SQ SEQUENCE 258 AA: 29033 MW: EDEB44AC4B515112 CRC64;

Query Match 51.8%; Score 44; DB 17; Length 258;
 Best Local Similarity 43.8%; Pred. No. 27;
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 2 GQVGRQLAIIIGDDINR 17
 DB 122 GQGRGFAVVADEIR 137
 ID 057733 PRELIMINARY: PRT: 261 AA.
 AC 057733.
 DT 01-AUG-1998 (TRENBLREL. 07, Created)
 DT 01-AUG-1998 (TRENBLREL. 07, last sequence update)
 DT 01-DEC-2001 (TRENBLREL. 19, last annotation update)
 DE 261AA LONG HYPOHETICAL CHEMORECEPTOR PROTEIN.
 GN PH1970.
 OS Pyrococcus horikoshii.
 OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
 OX NCBI_TaxID=53953;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OTS;
 RX MEDLINE=98344137; PubMed=9679194;
 RA Kawarabayashi Y., Sawada M., Horikawa H., Hatake Y., Hino Y.,
 RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
 RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
 RA Funahashi T., Tanaka T., Kudo Y., Yamazaki J., Kushiida N., Oguchi A.,
 RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
 RA Maechli Y., Shizuya H., Kikuchi H.;
 RA "Complete sequence and gene organization of the genome of a hyper-
 thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
 RT DNA Res. 5:55-76(1998).
 RL EMBL: AP000007; BAA31097.1; -;
 DR InterPro: IPR004089; Chemotaxis_transducer.
 DR Pfam: PF00015; MCPsignal; 1.
 DR SMART: SM00283; MA; 1.
 KW Complete proteome.
 SQ SEQUENCE 261 AA: 29234 MW: 2FD6C7CC08223D46 CRC64;

Query Match 51.8%; Score 44; DB 17; Length 261;
 Best Local Similarity 43.8%; Pred. No. 27;
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 2 GQVGRQLAIIIGDDINR 17
 DB 125 GQGRGFAVVADEIR 140
 ID 057733 PRELIMINARY: PRT: 261 AA.
 AC 057733.
 DT 01-AUG-1998 (TRENBLREL. 07, Created)
 DT 01-AUG-1998 (TRENBLREL. 07, last sequence update)
 DT 01-DEC-2001 (TRENBLREL. 19, last annotation update)
 DE 261AA LONG HYPOHETICAL CHEMORECEPTOR PROTEIN.
 GN PH1970.
 OS Pyrococcus horikoshii.
 OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
 OX NCBI_TaxID=53953;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OTS;
 RX MEDLINE=98344137; PubMed=9679194;
 RA Kawarabayashi Y., Sawada M., Horikawa H., Hatake Y., Hino Y.,
 RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
 RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
 RA Funahashi T., Tanaka T., Kudo Y., Yamazaki J., Kushiida N., Oguchi A.,
 RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
 RA Maechli Y., Shizuya H., Kikuchi H.;
 RA "Complete sequence and gene organization of the genome of a hyper-
 thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
 RT DNA Res. 5:55-76(1998).
 RL EMBL: AP000007; BAA31097.1; -;
 DR InterPro: IPR004089; Chemotaxis_transducer.
 DR Pfam: PF00015; MCPsignal; 1.
 DR SMART: SM00283; MA; 1.
 KW Complete proteome.
 SQ SEQUENCE 261 AA: 29234 MW: 2FD6C7CC08223D46 CRC64;

09LHL6
ID 09LHL6 PRELIMINARY; PRT; 556 AA.
AC 09LHL6;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE GB|AA|30301.1 (HYPOTHEICAL 63.0 KDA PROTEIN).
GN T21B4.12.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Nakamura Y.;
RX PubMed=10907853;
RA Nakamura Y.;
RT *Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the regions of 4,251,695 bp covered by ninety P1,
RT TAC and BAC clones.";
RL DNA Res. 7:217-221(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=21016720; PubMed=11130713;
RA Salanoubat M., Lemcke K., Rieger M., Ansoorge W., Unsel M.,
RA Fatmann B., Valle G., Bloeker H., Perez-Alonso M., Obermayer B.,
RA Deisyony M., Bouly M., Grivell L.A., Mache R., Puigdomenech P.,
RA De Simone V., Choisme N., Artiguenave F., Robert C., Brottier P.,
RA Wincker P., Cattolico L., Weissensbach J., Saurin W., Queller F.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wurmbach E., Drzenek H., Erfle H., Jordan N., Bangert S.,
RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppi S., Simionati B.,
RA Conrad A., Hohnischer K., Kauer G., Loehner T.-H., Nordiek G.,
RA Reichelt J., Scharte M., Schoen O., Barges M., Terol J., Climent J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwelder B., Duchemin D.,
RA Cooke R., Laurie M., Berger-Liauro C., Purnelle B., Masuy D.,
RA de Haan M., Maarse A.C., Alcaraz J.-P., Collet A., Casacuberta E.,
RA Monfort A., Argitlou A., Flores M., Liguori R., Vitale D.,
RA Mannhaupt G., Haese D., Schoof H., Rudd S., Zaccaria P., Meves H.-W.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Walts A., Ulterback T., Fujii C.Y., Shea T.P.,
RA Cressy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA Pai G., Miltischer J., Sellers P., Gill J.E., Feldblum T.V.,
RA Preuss D., Lin X., Niernan W.C., Salzberg S.L., White O., Venter J.C.,
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsuno M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shimp S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
RT *Sequence and analysis of chromosome 3 of the plant Arabidopsis
thaliana.";
RT Nature 408:820-822(2000).
DR EMBL: AP002040; BAB03118.1;
DR EMBL: AC069473; AAG51057.1;
KM Hypothetical protein.
SO SEQUENCE 556 AA; 63004 MW; F697359ABBB7213F CRC64;

Query Match 51.8%; Score 44; DB 10; Length 556;
Best Local Similarity 53.8%; Pred. No. 64;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 5 GROLATIGDDINR 17
DB 262 GRLRFVGDSDINR 274

RESULT 12
ID P73239 PRELIMINARY; PRT; 593 AA.
AC P73239;
DT 01-FEB-1997 (TReMBLrel. 02, Created)
DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE ABC TRANSPORTER.
GN SUR2019.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirosewa M., Sugita M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimp S., Takeuchi C., Wada T., Watanabe A., Yasuda M.,
RA Tabata S.;
RT *Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
CC -1- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
(ABC TRANSPORTERS).
CC EMBL: D90904; BAA17266.1;
DR InterPro: IPR003593; AAA.
DR InterPro: IPR001140; ABC_transporter_tmnm.
DR InterPro: IPR003439; ABC_transporter.
DR InterPro: IPR001687; ATP_GTP_A.
DR Pfam: PF00664; ABC_membrane; 1.
DR Pfam: PF00005; ABC_tran; 1.
DR SMART: SM00382; AAA; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
DR ATP-binding; Complete proteome; Transport.
SO SEQUENCE 593 AA; 65761 MW; DA48CE3D0EDAC69 CRC64;

Query Match 51.8%; Score 44; DB 16; Length 593;
Best Local Similarity 61.5%; Pred. No. 69;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 5 GROLATIGDDINR 17
DB 128 GRLMALINDINQ 140

RESULT 13
ID 09FG35 PRELIMINARY; PRT; 608 AA.
AC 09FG35;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE EMB|CAB82953.1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Kotani H.,
RA Tabata S.;
RT *Structural analysis of Arabidopsis thaliana chromosome 5. XI.";
RT Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP002032; BAB09804.1;
DR InterPro: IPR000531; TonB_boxC.
DR PROSITE: PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.

SEQUENCE 608 AA: 67925 MW: 7595DF42E697586C CRC64;

Query Match

Best Local Similarity 51.8%; Score 44; DB 10; Length 608;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 5 GROLAIIIGDDINR 17
Db 321 GRLVPGVDSINR 333

RESULT 14

OC 09PC32 PRELIMINARY; PRT; 693 AA.
ID 09PC32
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DE PLUS BIOGENESIS PROTEIN.
GN XE1953.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xylella
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9A5C;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
Alvaranga R., Alves L.M.C., Araya J.E., Bala G.S., Baptista C.S.,
Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Brianna M.R.S.,
Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
Colombo C., Colombo C., Costa F.E., Costa M.C.R., Costa Neto C.M.,
Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
Facchini A.P., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
Fraga J.S., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
Gavril M., Goldman G.H., Junqueira M.L., Kemper E.L., Kitajima J.P.,
Ho P.L., Homelagel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
Machado M.A., Madella A.M.B.N., Madella H.M.F., Martino C.L.,
Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
Nhani A.Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
de Oliveira B.R., Pereira G.A.G., Pereira H.A.Jr., Pesquero J.B.,
Quaglini R.B., Roberto P.C., Rodrigues V., de Rosa A.J.M.,
de Rosa V.E.Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A.Jr.,
da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
de Souza A.P., Terezzi M.F., Truffi D., Tsai S.M., Tsunako M.H.,
Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
Zago M.A., Zatz M., Zeldanis J., Setubal J.C.;
RT "the genome sequence of the plant pathogen Xylella fastidiosa";
RL Nature 406:151-159(2000).
DR EMBL: AE004014; AAF84755.1; -;
DR HSSP: P02942; 1007.
DR InterPro: IPR004089; Chemotaxis_transducer.
DR InterPro: IPR004090; Me_chemotaxis.
DR Pfam: PF00015; MCPsignal; 1.
DR PRINTS: PR00260; CHEMTRNSDUCR.
DR SMART: SM00283; MA; 1.
KW Complete proteome.
SQ SEQUENCE 693 AA: 74235 MW: EAD48C73BF573D80 CRC64;

Query Match 51.8%; Score 44; DB 16; Length 693;
Best Local Similarity 43.8%; Pred. No. 82;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
OY 2 GCGVRLAIIIGDDINR 17

Db 550 GCGRGFAIVADVEQR 565

RESULT 15

OY 098KM2 PRELIMINARY; PRT; 421 AA.
ID 098KM2
DT 01-OCT-2001 (TEMBLrel. 18, Created)
DT 01-OCT-2001 (TEMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TEMBLrel. 18, Last annotation update)
DE PROBABLE FAD-DEPENDENT MONOOXYGENASE.
GN ML1411.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti";
RL DNA Res. 7:331-338(2000).
DR EMBL: AP002997; BAB48792.1; -;
DR InterPro: IPR000759; Adnrx_reductase.
DR InterPro: IPR001327; FAD_pyridox.
DR InterPro: IPR000733; Flavo_monooxygenase.
DR InterPro: IPR002938; Mox_FAD_binding.
DR InterPro: IPR00205; NAD_binding.
DR InterPro: IPR001103; Pyridine_redox.
DR InterPro: IPR003042; Rng_mnoxygenase.
DR Pfam: PF01494; FAD_binding_3; 1.
DR Pfam: PF01360; Monooxygenase; 1.
DR PRINTS: PR00419; ADXRDASE.
DR PRINTS: PR00368; FADPR.
DR PRINTS: PR00411; PNDROTASE1.
DR PRINTS: PR00469; PNDROTASE1.
DR PRINTS: PR00420; RINGMONOXGNASE.
KW Monooxygenase; Complete proteome.
SQ SEQUENCE 421 AA: 45340 MW: 2B1E71C87476F1E CRC64;

Query Match 50.6%; Score 43; DB 16; Length 421;
Best Local Similarity 80.0%; Pred. No. 68;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 4 GCGRLAIIIGD 13
Db 294 GCGRLAIIIGD 303

Search completed: September 20, 2002, 11:03:48
Job time: 1665 sec

GenCore version 4.5
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OK protein - protein search, using sw model

Run on: September 20, 2002, 10:35:56 ; Search time 228.86 Seconds
(without alignments)
13.104 Million cell updates/sec

Title: US-09-544-664-6
Perfect score: 135
Sequence: 1 QDASTKTLSECLKRGIDELDSNMEIQR 27

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	135	100.0	27	21	AAB37006 Bcl2 polypeptide B
2	135	100.0	78	21	AAV70818 Human neutrophil
3	135	100.0	131	21	AAV34149 Human truncated Ba
4	135	100.0	192	16	AAV71406 Human Bax protein
5	135	100.0	192	20	AAV34150 Human wild-type Ba
6	135	100.0	192	20	AAV05435 Human BAX protein
7	135	100.0	192	20	AAV87804 A human Bcl-2 asso
8	135	100.0	192	20	AAV87809 Human Bcl-2 asso
9	135	100.0	192	21	AAV70827 Human BAX alpha pr
10	135	100.0	192	21	AAV69202 Amino acid sequenc
11	135	100.0	192	22	AAB74121 Human bcl-2 associ

12	135	100.0	192	22	AAB74126 Human bcl-2 associ
13	135	100.0	192	22	AAB48286 Human Bax protein
14	135	100.0	192	22	AAB35129 Human Bax. Homo s
15	135	100.0	192	22	AAB50539 Human Bax protein
16	135	100.0	197	21	AAV78512 Truncated Bax amin
17	135	100.0	221	18	AAV10688 Bax omega protein,
18	135	100.0	331	20	AAV39263 Coding region of c
19	132	97.8	27	21	AAV37007 Bcl2 polypeptide B
20	132	97.8	78	21	AAV70819 Mouse neutrophil
21	132	97.8	192	16	AAV71407 Mouse Bax protein
22	132	97.8	192	20	AAV05434 Mouse BAX protein
23	132	97.8	192	20	AAV87805 Murine Bcl-2 assoc
24	132	97.8	192	20	AAV70828 Murine Bcl-2 assoc
25	132	97.8	192	21	AAV70828 Murine Bcl-2 assoc
26	132	97.8	192	22	AAV74125 Murine bcl-2 assoc
27	132	97.8	192	22	AAV74125 Murine bcl-2 assoc
28	132	97.8	192	22	AAV35128 Murine Bax. Mus s
29	130	96.3	26	17	AAV06298 GD domain region f
30	130	96.3	34	20	AAV05430 Human BAX BH3 doma
31	120	88.9	24	20	AAV05411 Human BAX BH3 doma
32	120	88.9	26	21	AAV96532 Mammalian Bax Bcl-
33	120	88.9	26	21	AAV70822 BAX BH3 consensus
34	117	86.7	24	21	AAV70824 Mouse neutrophil
35	95	70.4	70	21	AAV70816 Mouse neutrophil
36	92	68.1	70	21	AAV70817 Mouse neutrophil
37	89	65.9	70	21	AAV70820 Human neutrophil
38	89	65.9	78	21	AAV70822 Human neutrophil
39	86	63.7	70	21	AAV70821 Mouse neutrophil
40	86	63.7	78	21	AAV70823 Mouse neutrophil
41	82	60.7	24	20	AAV05418 Mouse BAX BH3 doma
42	81	60.0	16	21	AAV37032 Bcl2 polypeptide B
43	78	57.8	16	20	AAV05426 Mouse BAX BH3 doma
44	78	57.8	16	21	AAB37033 Bcl2 polypeptide B
45	77	57.0	15	17	AAV06296 GD domain region f

ALIGNMENTS

RESULT 1
ID AAB37006 standard; peptide: 27 AA.
XX AAB37006:
XX
AC AAB37006:
XX
DT 28-FEB-2001 (first entry)
XX
XX Bcl2 polypeptide BH3 domain peptide #6.
XX
XX Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;
KW cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;
KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;
KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;
KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
KW stroke; myocardial infarction.
XX
XX Homo sapiens.
OS
XX
XX PN WO200059526-A1.
XX PD 12-OCT-2000.
XX
XX 06-APR-2000; 2000WO-US09352.
XX PF 07-APR-1999; 99US-0128202.
XX PR (UYJE-) UNIV JEFFERSON THOMAS.
XX PA
XX PI Huang Z, Wang J, Zhang Z, Shan S, Lu Z;
XX DR WPI, 2000-679325/66.
XX PT New peptide conjugates for modulating apoptosis or for inhibiting B

PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for
 PT treating neurodegenerative disorders, stroke, or cancer
 PS Claim 18: Page 17: 74pp: English.

XX The invention relates to a peptide conjugate having the formula:
 CC (R-X)n-peptide where n = 1-10; X = C=O, when the R-X group is attached
 CC to the N-terminus of the peptide, or a side chain of the peptide where
 CC the functional group of the side chain is NH₂ or OH; or X = O or NH,
 CC when the R-X group is attached to the C-terminus of the peptide, or a
 CC side chain of the peptide, where the side chain functional group is COOH
 CC or CONH₂; and R = 2-18C alkyl or alkoxy, 2-14C alkylphenyl optionally
 CC or two double bonds, cyclohexyl, cyclopentyl, cyclohexyl optionally
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain
 CC alkyl group, or benzyl. The peptides AB37001-B37058 represent examples
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of
 CC the Bcl-2 domain of the cell death agonist Bad. The peptide conjugate is
 CC useful for modulating apoptosis in the cells of a subject, or for
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2
 CC function. In particular, the peptide conjugate is useful for treating a
 CC subject afflicted with a cancer characterized by cancer cells that
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric, or
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
 CC conjugate is also useful for treating disorders characterized by
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.

XX Sequence 27 AA:

Query Match 100.0%; Score 135; DB 21; Length 27;
 Best Local Similarity 100.0%; Pred. No. 1.1e-12;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QDASTKKLSECLKRIQDELDNSMELQ 27
 Db 1 qdastkklseclkrigeldnsmeIdr 27

RESULT 2

AAV70818
 ID AAV70818 standard; Protein: 78 AA.

AC AAV70818:

DT 31-JUL-2000 (first entry)

DE Human neuroprotective truncated BAX protein, tBAX78.

XX Human; truncated BAX protein; tBAX78; BAX alpha; Bcl-2 family;
 KW neuron; anti-apoptotic; cerebroprotective; neuroprotective;
 KW apoptosis; treatment; neurodegenerative disease; peripheral nerve injury;
 KM spinal cord injury; head trauma; stroke.

XX Homo sapiens.

OS Key Location/Qualifiers
 XX Region 1..58
 FT /note="N-terminal region of BAX alpha"
 FT 59..73
 FT /label=BH3_domain

PN WO200023083-A1.

PD 27-APR-2000.

PF 22-OCT-1999; 99WO-US24747.

PR 22-OCT-1998; 98US-0177315.

XX (UNIV) UNIV WASHINGTON.

XX Johnson EM, Easton R;

XX WPI; 2000-339513/29.

XX Truncated BAX polypeptides useful for preventing apoptosis of neurons
 PT for the treatment of nervous system disorders -

PS Claim 4: Page 33: 43pp: English.

XX The present sequence is a specifically claimed truncated BAX protein
 CC tBAX78 which inhibits neuronal apoptosis induced by trophic factor
 CC deprivation. The protein consists of first 78 amino acids of human
 CC BAX alpha, that includes the N-terminal region and BH3
 CC domain. It lacks the BH1, BH2 and C-terminal transmembrane domains of
 CC the full-length BAX alpha. The tBAX protein lacking only the
 CC transmembrane domain has been shown to have anti-apoptotic activity.
 CC The present sequence is used to treat diseases associated with neuronal
 CC apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury,
 CC spinal cord injury, head trauma and stroke.

XX Sequence 78 AA:

Query Match 100.0%; Score 135; DB 21; Length 78;
 Best Local Similarity 100.0%; Pred. No. 3.1e-12;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QDASTKKLSECLKRIQDELDNSMELQ 27
 Db 52 qdastkklseclkrigeldnsmeIdr 78

RESULT 3

AAV34149
 ID AAV34149 standard; Protein: 131 AA.

AC AAV34149:

DT 30-NOV-1999 (first entry)

DE Human truncated Bax protein.

XX Apoptosis; adenovirus; dimeric; Bcl-2; p53; cancer; gene therapy.

XX Homo sapiens.

OS Key Location/Qualifiers
 XX Domain 59..101
 FT /note="Portion of BH3 domain essential for dimerisation"

PN WO9946371-A2.

PD 16-SEP-1999.

PF 11-MAR-1999; 99WO-US05359.

PR 11-MAR-1998; 98US-0077541.

PS (TEXA) UNIV TEXAS SYSTEM.

XX McDowell TJ, Swisher SG, Fang B, Bruckheimer EM, Sarkiss MG;

XX JI L, Roth JA;

XX WPI; 1999-551404/46.

XX N-P-SDB; AA219763.

XX New adenovirus vectors, used for killing or inhibiting the growth of
 PT cells and for treating cancers -
 PS Claim 26: Page 148-149; 151pp: English.

XX This sequence represents a human truncated Bax protein. The cDNA
CC contains a single base deletion relative to the wild-type (AA219764),
CC causing a frameshift which leads to translation of a premature stop
CC codon, resulting in a truncated protein. However, the domain responsible
CC for its function is still present in the truncated protein. Bax (Bcl-2
CC associated x protein) is a proapoptotic member of the Bcl-2 gene family.
CC Bax functions as a primary response gene in the p53-regulated apoptotic
CC pathway. The Bax gene promoter has 4 p53 binding sites and the
CC expression of Bax is upregulated at the transcriptional level by p53, and
CC Bax mRNA and protein expression have been shown to increase following
CC induction of p53. Bax protein can function as a homodimer, or it can
CC heterodimerise with other Bcl-2 gene family members such as the
CC antiapoptotic protein Bcl-2. Heterodimerisation of Bcl-2 family members
CC provides a means of controlling cell death via the "rheostat" model. This
CC model suggests that the relative amounts of Bcl-2 and Bax determine the
CC susceptibility of a cell to undergo apoptosis. If Bcl-2 is in excess,
CC Bcl-2/Bax heterodimers predominate and cell death is inhibited. If Bax is
CC in excess, however, Bax homodimers predominate and the cell becomes
CC susceptible to apoptosis following exposure to an apoptotic stimulus.
CC Additionally, Bax can function in its monomeric form to accelerate cell
CC death. Use of novel adenoviral vectors containing this Bax gene may
CC augment and complement wild-type p53 gene therapy, which induces a G1
CC cell cycle arrest and/or apoptosis in malignant cells carrying p53
CC mutations. In addition, Bax overexpression could provide the apoptotic
CC effect of p53 without the need for p53 itself.

50 Sequence 131 AA;

Query Match	100.0%;	Score 135;	DB 20;	Length 131;
Best Local Similarity	100.0%;	Pred. No. 5.3e-12;		
Matches 27; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

```
QY      1 QDASTKKIIECLKRIIGDELDSNMELQR 27
        |||||
Db      52 qdasttkliscclkrigdelldsmelqr 78
```

RESULT	4
AAR71406	
ID	AAR71406 standard; Protein; 192 AA

XX Methods for producing and identifying mutant bcl-2 proteins -
PT that lack death repressor activity and/or lacks binding to Bax
XX
PS Disclosure; Fig 3; 133pp; English.

This sequence represents human Bax protein. Bax is a protein which is associated with the human bcl-2 alpha and beta proteins, the sequences of which are given in [BAR71404-05](#) respectively. bcl-2 is encoded by a proto-oncogene and is capable of inhibiting apoptosis in many hematopoietic cell systems. bcl-2 is a 26 kD membrane-associated cytoplasmic protein and is thought to function by enhancing the survival of hematopoietic cells of B and T origins rather than directly promoting proliferation of these cell types. bcl-2 has not been shown to directly promote cell cycle progression nor does it necessarily alter the dose response to limiting concentrations of IL-3. bcl-2 has been shown to form heterodimers with this 21 kD protein, Bax. Overexpressed Bax accelerates apoptotic cell death induced by cytokine deprivation in an IL-3 dependent cell line, and it also acts to counter the death repressor activity of bcl-2. Therefore, the ratio between bcl-2 and Bax determines cell survival or death following an apoptotic stimulus. The invention gives a mutant form of bcl-2 in which there is at least one amino acid substitution or deletion in the BH1 or BH2 domains. This makes the mutant protein substantially incapable of binding Bax and/or incapable of death repressor activity. Down regulation of bcl-2 is useful in cancer therapy, controlling hyperplasias and eliminating self-reactive clones in autoimmunity by favouring death effector molecules. Up regulating bcl-2 is beneficial in treatment and diagnosis of immuno-deficiency diseases, including AIDS and neurodegenerative and ischaemic cell death.

Query Match	100.0%;	Score 135;	DB 16;	Length 192;
Best Local Similarity	100.0%;	Pred. No. 7,9e-12;		
Matches 27; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

```
OY      1 QDASTKLSSECLKRIGDELDSDNMELÖR 27
        |||||
DB      52 qdastklseclkrigeldsdnmelgr 78
```

RESULT	5
AAV34150	
ID	AAV34150 standard; Protein; 192 AA

FH	Key	Location/Qualifiers
FT	Domain	59..101
FT		/note="Portion of BH3 domain essential for dimerisation"

PN	MO9946371-A2.	
XX		
PD	16-SFP-1999.	
XX		
PF	11-MAR-1999;	99WO-0505359
XX		
PR	11-MAR-1998;	98US-0077541
XX		
PA	(TEXA) UNIV TEXAS SYSTEM.	
XX		
PI	McDonnell TJ, Swisher SG,	
SI	JL, Roth JA;	

XX WPI: 1999-551404/46.
 DR N-PSDB: AAZ19764.
 XX
 PT New adenovirus vectors, used for killing or inhibiting the growth of
 PT cells and for treating cancers -
 PS
 XX Disclosure: Page 149-150; 151pp; English.
 CC This sequence represents human wild-type Bax protein. A naturally
 CC occurring mutant protein (AAV34149) was also isolated. Bax (Bcl-2
 CC associated x protein) is a proapoptotic member of the Bcl-2 gene family.
 CC Bax functions as a primary response gene in the p53-regulated apoptotic
 CC pathway. The Bax gene promoter has 4 p53 binding sites and the
 CC expression of Bax is upregulated at the transcriptional level by p53, and
 CC Bax mRNA and protein expression have been shown to increase following
 CC induction of p53. Bax protein can function as a homodimer, or it can
 CC heterodimerize with other Bcl-2 gene family members such as the
 CC antiapoptotic protein Bcl-2. Heterodimerisation of Bcl-2 family members
 CC provides a means of controlling cell death via the "rheostat" model. This
 CC model suggests that the relative amounts of Bcl-2 and Bax determine the
 CC susceptibility of a cell to undergo apoptosis. If Bcl-2 is in excess, the
 CC Bcl-2/Bax heterodimers predominate and cell death is inhibited. If Bax is
 CC in excess, however, Bax homodimers predominate and the cell becomes
 CC susceptible to apoptosis following exposure to an apoptotic stimulus.
 CC Additionally, Bax can function in its monomeric form to accelerate cell
 CC death. Use of novel adenoviral vectors containing the Bax gene may
 CC augment and complement wild-type p53 gene therapy, which induces a G1
 CC cell cycle arrest and/or apoptosis in malignant cells carrying p53
 CC mutations. In addition, Bax overexpression could provide the apoptotic
 CC effect of p53 without the need for p53 itself.
 CC
 XX Sequence 192 AA:
 SQ
 Query Match 100.0%; Score 135; DB 20; Length 192;
 Best Local Similarity 100.0%; Pred. No. 7.9e-12;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 QDASTKKLSECLKRIQDELDSNMEIQR 27
 ||||||||||||||||||||||||||||
 Db 52 qdastkklseclkrigdeldsnmeiqr 78
 RESULT 6
 AAY05435
 ID AAY05435 standard; peptide: 192 AA.
 AC AAY05435;
 XX
 DT 02-JUL-1999 (first entry)
 XX
 DE Human BAX protein sequence.
 XX
 KW BH3 domain; cell death agonist; bcl homology domain; BCL-2 family;
 KW apoptosis promoter; cancer cell; virus infected cell; inflammation;
 KW autoantibody producing cell; cancer; lymphoproliferative condition;
 KW arthritis; autoimmune disease; therapy.
 XX
 OS Homo sapiens.
 XX
 PN MO9916787-A1.
 XX
 PD 08-APR-1999.
 XX
 PF 22-SEP-1998; 98WO-US19765.
 XX
 PR 07-OCT-1997; 97US-0946039.
 PR 26-SEP-1997; 97US-0060133.
 XX
 PA (UNIW) UNIV WASHINGTON.
 XX
 PI Korsmeyer SJ;

XX WPI: 1999-255058/21.
 DR Bcl homology domain 3 polypeptide
 XX
 PT
 XX
 PS Disclosure: Fig 21c; 104pp; English.
 CC This sequence represents the human BAX protein.
 CC The invention relates to a bcl homology domain 3 (BH3 domain),
 CC derived from a proapoptotic member of the BCL-2 family. The
 CC BH3 polypeptide can be used in a method for promoting apoptosis in a
 CC target cell, especially where the cell is a cancer cell a virus infected
 CC cell or an autoantibody producing cell. The BH3 polypeptide can be used
 CC in therapeutic compositions for treating disease including cancer, other
 CC lymphoproliferative conditions, arthritis, inflammation, and autoimmune
 CC diseases, which may result from the down regulation of cell death
 CC regulation.
 CC
 XX Sequence 192 AA:
 SQ
 Query Match 100.0%; Score 135; DB 20; Length 192;
 Best Local Similarity 100.0%; Pred. No. 7.9e-12;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 QDASTKKLSECLKRIQDELDSNMEIQR 27
 ||||||||||||||||||||||||||||
 Db 52 qdastkklseclkrigdeldsnmeiqr 78
 RESULT 7
 AAW87804
 ID AAW87804 standard; Protein: 192 AA.
 AC AAW87804;
 XX
 DT 10-MAR-1999 (first entry)
 XX
 DE A human Bcl-2 associated protein designated Bax.
 XX
 KW Human; Bcl-2 associated protein; Bax; bcl-2; antibody; modulator;
 KW bcl-2-related function; apoptosis.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 97..118 "BH1 domain"
 FT 146..168
 FT 168..192 "BH2 domain"
 XX
 PN US5856171-A.
 XX
 PD 05-JAN-1999.
 XX
 PF 10-NOV-1994; 94US-0337646.
 XX
 PR 10-NOV-1994; 94US-0337646.
 PR 26-AUG-1993; 93US-0112208.
 PR 25-MAY-1994; 94US-0248819.
 XX
 PA (UNIW) UNIV WASHINGTON.
 XX
 PI Korsmeyer SJ;
 XX
 DR WPI: 1999-105119/09.
 DR N-PSDB: AAW84005.
 XX
 PT DNA composition encoding bcl-2 two-hybrid and reporter system - for
 PT identifying modulators of bcl-2 function
 XX
 XX Example 1: Columns 71-74; 105pp; English.
 XX

CC The present sequence represents a human Bcl-2 associated protein
 CC designated Bax. The Bax protein is used in a composition which
 CC comprises a bcl-2 family member polypeptide, a naturally occurring
 CC Bax polypeptide and an antibody that binds to the Bax polypeptide.
 CC The composition is used to identify modulators of bcl-2-related
 CC function, e.g. substances that inhibit binding of Bax to bcl-2,
 CC which would be potentially useful as drugs for modulating
 CC apoptosis.

XX
 XX
 SQ Sequence 192 AA;

Query Match 100.0%; Score 135; DB 20; Length 192;
 Best Local Similarity 100.0%; Pred. No. 7.9e-12;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ODASTKKLSKRIKIGDELDSNMELOR 27
 ||||||||||||||||||||
 Db 52 qdastkksicrkrigdeldsnmelqr 78

RESULT 8

AAW87809
 ID AAW87809 standard; Protein: 192 AA.

AAW87809;

10-MAR-1999 (first entry)

A human Bcl-2 associated protein designated Bax.

Human: Bcl-2 associated protein; Bax; bcl-2; antibody; modulator;
 bcl-2-related function; apoptosis.

OS Homo sapiens.

US5856171-A.

05-JAN-1999.

10-NOV-1994; 94US-0337646.

10-NOV-1994; 94US-0337646.

26-AUG-1993; 93US-0112208.

25-MAY-1994; 94US-0248819.

(UNIM) UNIV WASHINGTON.

Korismeyer SJ;

WPI; 1999-105119/09.

DNA composition encoding bcl-2 two-hybrid and reporter system - for
 identifying modulators of bcl-2 function

Example 7; Fig 7; 105pp; English.

CC The present sequence represents a human Bcl-2 associated protein
 CC designated Bax. The Bax protein is used in a composition which
 CC comprises a bcl-2 family member polypeptide, a naturally occurring
 CC Bax polypeptide and an antibody that binds to the Bax polypeptide.
 CC The composition is used to identify modulators of bcl-2-related
 CC function, e.g. substances that inhibit binding of Bax to bcl-2,
 CC which would be potentially useful as drugs for modulating
 CC apoptosis.

XX
 XX
 SQ Sequence 192 AA;

Query Match 100.0%; Score 135; DB 20; Length 192;
 Best Local Similarity 100.0%; Pred. No. 7.9e-12;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ODASTKKLSKRIKIGDELDSNMELOR 27
 ||||||||||||||||||||
 Db 52 qdastkksicrkrigdeldsnmelqr 78

RESULT 9

AAV70827
 ID AAV70827 standard; Protein: 192 AA.

AAV70827;

31-JUL-2000 (first entry)

Human BAX alpha protein.

Human: truncated BAX protein; tBAX; BAX alpha; BCL-2 family; head trauma;
 neuron; anti-apoptotic; cerebroprotective; neuroprotective; neuroactive;
 apoptosis; treatment; neurodegenerative disease; peripheral nerve injury;
 spinal cord injury; stroke; pro-apoptotic; PCD; programmed cell death.

OS Homo sapiens.

Key Location/Qualifiers

Region /label= N-terminal_region

Domain /label= BH3_domain

Domain /label= BH1_domain

Domain /label= BH2_domain

Domain /label= Transmembrane_domain

WO200023083-A1.

27-APR-2000.

22-OCT-1999; 99WO-US24747.

22-OCT-1998; 98US-0177315.

(UNIM) UNIV WASHINGTON.

Johnson EM, Easton R;

WPI; 2000-339513/29.

Truncated BAX polypeptides useful for preventing apoptosis of neurons
 for the treatment of nervous system disorders -

Disclosure: Page 35-36; 43pp; English.

CC The present sequence is a human BAX alpha protein, a pro-apoptotic
 CC protein which is a member of BCL-2 family of proteins that are involved
 CC in regulation of neuronal programmed cell death. The patent discloses
 CC specific truncated proteins derived from BAX alpha which inhibit neuronal
 CC apoptosis induced by trophic factor deprivation. The anti-apoptotic
 CC truncated BAX (tBAX) proteins include tBAX70, tBAX78 and their mutants.
 CC These proteins contain the N-terminal region and at least a portion of
 CC the BH3 domain of BAX alpha and lack the BH1, BH2 and C-terminal
 CC transmembrane domains. The tBAX protein lacking only the
 CC transmembrane domain has been shown to have anti-apoptotic activity.
 CC The tBAX proteins are used to treat diseases associated with neuronal
 CC apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury,
 CC spinal cord injury, head trauma and stroke.

XX
 XX
 SQ Sequence 192 AA;

Query Match 100.0%; Score 135; DB 21; Length 192;
 Best Local Similarity 100.0%; Pred. No. 7.9e-12;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 QDASTKRLSECLKRIgDELdSNMELQR 27
 Db 52 qdastkrlseclkrigdeldsnmeiqr 78

RESULT 10

AAV69202
 ID AAV69202 standard; peptide; 192 AA.

XX AAV69202;

AC 30-MAY-2000 (first entry)

XX Amino acid sequence of the human Bax protein.

DE Pro-apoptotic peptide; Bax; BH3 domain; channel inducer; transport;

XX cytochrome C transport; mitochondria; apoptosis; ion selectivity;

KM anti-apoptotic BCL-2 family member; neoplasia; Epstein Barr virus;

KW African swine fever virus; adenovirus; lymphoproliferative condition;

KM cancer; arthritis; Crohn's disease; inflammation; autoimmune disease;

KW immunodeficiency; senescence; neurodegenerative disease;

KM reperfusion cell death; infertility; wound.

XX Homo sapiens.

OS

XX WO200006187-A2.

PN 10-FEB-2000.

PD 30-JUL-1999; 99WO-US17276.

XX 31-JUL-1998; 98US-0127048.

PR (UNIW) UNIV WASHINGTON.

XX Korsmeyer SJ, Schlesinger PH;

XX WPI; 2000-195193/17.

XX Modulating apoptosis in cells by modulating channel ion selectivity for

PT transport of cytochrome C -

XX Disclosure: Page 34; 57pp; English.

XX The present sequence represents the Bax protein. A pro-apoptotic

CC peptide can be derived from the BH3 domain. The peptide is an inducer

CC of formation of a channel for transport of cytochrome C out of

CC mitochondria. The peptide induces apoptosis in a cell. The peptide

CC changes the ion selectivity of an anti-apoptotic Bcl-2 family member

CC from potassium selective to chloride selective. The specification

CC also describes inhibitors of apoptosis in cells. The inhibitors and

CC inducers can be used to treat patients, preferably humans with a

CC condition mediated by excessive down-regulation of apoptosis,

CC especially conditions chosen from neoplasias, diseases caused by

CC Epstein Barr virus, African swine fever virus and adenovirus,

CC lymphoproliferative conditions, cancer, arthritis, Crohn's disease,

CC inflammation and autoimmune disease or a condition mediated by

CC excessive apoptosis, especially immunodeficiency diseases, senescence,

CC neurodegenerative disease, ischemic and reperfusion cell death,

CC infertility and wounds. The methods can also be used to identify

CC apoptosis-modulating compounds.

XX Sequence 192 AA;

SO

Query Match 100.0%; Score 135; DB 21; Length 192;

Best Local Similarity 100.0%; Pred. No. 7.9e-12;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 QDASTKRLSECLKRIgDELdSNMELQR 27

Db 52 qdastkrlseclkrigdeldsnmeiqr 78

RESULT 11

AA874121

ID AA874121 standard; protein; 192 AA.

XX AA874121;

AC 22-MAY-2001 (first entry)

XX Human bcl-2 associated x protein (Bax) #1.

DE Human; Bax; cytosolic; immunosuppressive; immunostimulant; infection;

XX apoptosis modulator; bcl-2 associated x protein; cancer therapy; AIDS;

KW autoimmunity; immunodeficiency; reperfusion injury; stroke; aging;

KW myocardial infarction; traumatic brain injury; ischemia;

KW neurodegenerative diseases; hepatitis; transplant rejection; toxemia;

KW lymphoproliferative disease.

XX Homo sapiens.

OS US6184202-B1.

XX 06-FEB-2001.

PD 11-SEP-1997; 97US-0927326.

XX 10-NOV-1994; 94US-0337646.

XX 26-AUG-1993; 93US-0112208.

XX 25-MAY-1994; 94US-0248819.

XX (UNIW) UNIV WASHINGTON.

XX Korsmeyer SJ;

XX WPI; 2001-256104/26.

XX N-PSDB; AAF77704.

XX Modulating apoptosis of a cell, useful in maintaining homeostasis in

PT adult tissues, or treating proliferative or autoimmune diseases,

PR comprises administering a bcl-2 polypeptide that interacts with a 21 kD

PT bcl-2 associated x protein -

XX Claim 3; Fig 3; 105pp; English.

XX The present invention relates to a method of modulating apoptosis of a

CC cell. The method comprises administering to the cell an agent,

CC comprising a BH1 domain or BH2 domain, capable of modulating formation of

CC at least one complex selected from bcl-2:bcl-2 complexes, bcl-XL:bcl-XL

CC complexes, bcl-2 associated x protein (Bax):Bax complexes, bcl-2:Bax

CC complexes or bcl-XL:Bax complexes. Modulating apoptosis is especially

CC useful in cancer therapy, and treating autoimmunity, immunodeficiency

CC diseases (e.g. AIDS), reperfusion injury, myocardial infarction, stroke,

CC traumatic brain injury, neurodegenerative diseases, aging, ischemia,

CC toxemia, infection, hepatitis, transplant rejection, and

CC lymphoproliferative diseases. The present sequence is human Bax, which

CC was used in the method of the present invention.

XX Sequence 192 AA;

SO

Query Match 100.0%; Score 135; DB 22; Length 192;

Best Local Similarity 100.0%; Pred. No. 7.9e-12;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 QDASTKRLSECLKRIgDELdSNMELQR 27

Db 52 qdastkrlseclkrigdeldsnmeiqr 78

RESULT 12

AA874126

```

ID AAB74126 standard; Protein: 192 AA.
XX
XX AAB74126;
AC
XX 22-MAY-2001 (first entry)
XX
DE Human bcl-2 associated X protein (Bax) #2.
XX
XX Human; Bax: cytosolic; immunosuppressive; immunostimulant; infection;
XX apoptosis modulator; bcl-2 associated X protein; cancer therapy; AIDS;
XX autoimmunity; immunodeficiency; reperfusion injury; stroke; aging;
XX myocardial infarction; traumatic brain injury; ischaemia;
XX neurodegenerative diseases; hepatitis; transplant rejection; toxemia;
XX lymphoproliferative disease.
XX
XX Homo sapiens.
XX
XX US6184202-B1.
XX
XX 06-FEB-2001.
XX
XX 11-SEP-1997; 97US-0927326.
XX
XX 10-NOV-1994; 94US-0337646-
XX 26-AUG-1993; 93US-0112208.
XX 25-MAY-1994; 94US-0246819.
XX
XX (UNITV ) UNIV WASHINGTON.
XX
XX Korsmeyer SJ;
XX
XX WPI; 2001-256104/26.
XX
XX Modulating apoptosis of a cell, useful in maintaining homeostasis in
XX adult tissues, or treating proliferative or autoimmune diseases,
XX comprises administering a bcl-2 polypeptide that interacts with a 21 kd
XX bcl-2 associated X protein -
XX
XX Example 7; Fig 7; 105pp; English.
XX
XX The present invention relates to a method of modulating apoptosis of a
XX cell. The method comprises administering to the cell an agent,
XX comprising a BHL domain or BH2 domain, capable of modulating formation of
XX at least one complex selected from bcl-2:bcl-2 complexes, bcl-XL:bcl-XL
XX complexes, bcl-2 associated X protein (Bax):Bax complexes, bcl-2:Bax
XX complexes or bcl-XL:Bax complexes. Modulating apoptosis is especially
XX useful in cancer therapy, and treating autoimmunity, immunodeficiency
XX diseases (e.g. AIDS), reperfusion injury, myocardial infarction, stroke,
XX traumatic brain injury, neurodegenerative diseases, aging, ischaemia,
XX toxemia, infection, hepatitis, transplant rejection, and
XX lymphoproliferative diseases. The present sequence is human Bax, which
XX was used in a sequence alignment in the present invention, with murine
XX Bax (AAB74125), human Bcl-2 (AAB74127) and murine Bcl-2 (AAB74128).
XX
XX Sequence 192 AA;
SQ

```

Query Match 100.0%; Score 135; DB 22; Length 192;
 Best Local Similarity 100.0%; Pred. No. 7.9e-12;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 QDASTKKLSKRLKRGDELDSNMEIQR 27
   |||||
DB 52 qdastkklskrlkrgdeldsnmeiqr 78

```

RESULT 13
 AAB48286
 ID AAB48286 standard; protein: 192 AA.
 XX
 XX AAB48286;
 AC
 XX 02-APR-2001 (first entry)
 DF

```

XX Human Bax protein.
DE
XX S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; 2F;
XX CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax;
XX Bad; Bcl-2; tumour; cytosolic.
XX
XX Homo sapiens.
XX
XX W0200075184-A1.
XX
XX 14-DEC-2000.
XX
XX 05-JUN-2000; 2000WO-US15449.
XX
XX 04-JUN-1999; 99US-0137494.
XX
XX (UYVA ) UNIV YALE.
XX
XX Zhang H, Tsvetkov LM, Kondo T;
XX
XX WPI; 2001-061703/07.
XX N-PSDB; AAC84598.
XX
XX Modulating polypeptide levels in a cell, diagnosing and treating tumor,
XX involves altering levels of proteins such as S-phase kinase associated
XX proteins 1, 2 and cullin/CDC53 proteins -
XX
XX Claim 5; Page 100-101; 162pp; English.
XX
XX The invention relates to methods of altering the polypeptide levels in a
XX cell, using proteins selected from S-phase kinase associated proteins 1
XX and 2 (SKP1, SKP2), SKP2-like proteins (ZF) and CUL-1 (a member of the
XX cullin/CDC53 family of proteins). The method is useful for altering the
XX level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2
XX polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for
XX detecting tumours, and in monitoring tumor treatment in a mammal. Agents
XX that modulate interactions between SKP and target proteins are useful for
XX treating tumours.
XX
XX Sequence 192 AA;
SQ

```

Query Match 100.0%; Score 135; DB 22; Length 192;
 Best Local Similarity 100.0%; Pred. No. 7.9e-12;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 QDASTKKLSKRLKRGDELDSNMEIQR 27
   |||||
DB 52 qdastkklskrlkrgdeldsnmeiqr 78

```

RESULT 14
 AAB35129
 ID AAB35129 standard; protein: 192 AA.
 XX
 XX AAB35129;
 AC
 XX 03-APR-2001 (first entry)
 DT
 XX Human Bax.
 DE
 XX Human; Bax; apoptosis modulator; BCL-2.
 XX
 XX Homo sapiens.
 XX
 XX US6165732-A.
 XX
 XX 26-DEC-2000.
 XX
 XX 31-JUL-1998; 98US-0127048.
 XX
 XX 14-OCT-1997; 97US-0061823.
 PR

XX (UNIW) UNIV WASHINGTON.
 PA
 XX Kormeyer SJ, Schlesinger PH;
 PI
 XX WPI: 2001-101692/11.
 DR
 XX Identifying apoptosis-modulating compounds by contacting the compound
 PT with lipid bilayer containing an ion channel formed by anti-apoptotic
 PT polypeptide of Bcl-2 family and determining ion selectivity of the
 PT channel
 PS
 XX Disclosure: Fig 11, 34pp; English.
 PS
 XX The present invention describes a method for identifying modulators of
 CC apoptosis which involves contacting a compound of interest with a lipid
 CC bilayer comprising a K⁺ or Cl⁻ selective channel. This channel is a
 CC member of the BCL-2 family. Apoptosis modulators are also provided,
 CC including Bcl-2deltaTM and baxdeltaTM.
 CC
 SQ Sequence 192 AA;

Query Match 100.0%; Score 135; DB 22; Length 192;
 Best Local Similarity 100.0%; Pred. No. 7.9e-12;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ODASTKKISECLKRIQDELDSNMEIQR 27
 |||
 DB 52 qdastkkiseclkrigdelidsnmeiqr 78

RESULT 15

AAB50539
 ID AAB50539 standard; Protein; 192 AA.

XX AAB50539;

XX 16-MAR-2001 (first entry)

XX Human Bax protein sequence SEQ ID NO:6.

XX Human; Bcl-2; Bcl-XL; Bax; VDAC; Apoptosis inhibitor; detection;

KW Apoptosis promoter; diagnosis.

XX Homo sapiens.

XX JP2000287689-A.

XX 17-OCT-2000.

XX 08-APR-1999; 99JP-0101888.

XX 08-APR-1999; 99JP-0101888.

XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

XX WPI: 2001-065575/08.

XX N-PSDB; AAC90811.

XX Screening of an apoptosis inhibitor or promoter which can be used as a
 PT drug and a diagnostic agent for various diseases caused by apoptosis
 PT inhibition or apoptosis promotion -

XX Claim 13; Page 17; 22pp; Japanese.

XX The present invention describes a method for screening for an apoptosis
 CC inhibitor or an apoptosis promoter in which VDAC-1liposome, an index
 CC substance which can pass VDAC and a sample are incubated, and the change
 CC in the concentration of the index substance during the incubation is
 CC detected to judge the presence of apoptosis inhibition or apoptosis
 CC promotion. The apoptosis inhibitor or the apoptosis promoter can be
 CC used as a drug and a diagnostic agent for various diseases caused by

CC apoptosis inhibition or apoptosis promotion. The present sequence
 CC represents the human Bax protein, which is an apoptosis inhibitor
 CC used in the exemplification of the present invention.

XX
 SQ Sequence 192 AA;

Query Match 100.0%; Score 135; DB 22; Length 192;
 Best Local Similarity 100.0%; Pred. No. 7.9e-12;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ODASTKKISECLKRIQDELDSNMEIQR 27
 |||
 DB 52 qdastkkiseclkrigdelidsnmeiqr 78

Search completed: September 20, 2002, 10:35:57
 Job time: 425 sec

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OM protein - protein search, using sw model

Run on: September 20, 2002, 10:37:19 ; Search time 75.64 Seconds
(without alignments)
8.719 Million cell updates/sec

Title: US-09-544-664-6

Perfect score: 135

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents, AA: *
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2: /cgn2-6/ptodata/2/1aa/5B_COMB.pep: *
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6: /cgn2-6/ptodata/2/1aa/Backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	135	100.0	34	1 US-08-440-391-13	Sequence 13, Appl
2	135	100.0	34	2 US-08-908-597A-13	Sequence 13, Appl
3	135	100.0	34	4 US-09-236-385A-13	Sequence 13, Appl
4	135	100.0	34	5 PCT-US96-06122-13	Sequence 13, Appl
5	135	100.0	192	1 US-08-112-208C-2	Sequence 2, Appl
6	135	100.0	192	1 US-08-112-208C-9	Sequence 9, Appl
7	135	100.0	192	1 US-08-248-819A-2	Sequence 2, Appl
8	135	100.0	192	1 US-08-248-819A-9	Sequence 9, Appl
9	135	100.0	192	1 US-08-607-269-25	Sequence 25, Appl
10	135	100.0	192	1 US-08-471-058-13	Sequence 13, Appl
11	135	100.0	192	2 US-08-337-646A-2	Sequence 2, Appl
12	135	100.0	192	2 US-08-337-646A-9	Sequence 9, Appl
13	135	100.0	192	2 US-08-856-531-2	Sequence 2, Appl
14	135	100.0	192	2 US-08-856-531-9	Sequence 9, Appl
15	135	100.0	192	2 US-08-856-034-2	Sequence 2, Appl
16	135	100.0	192	2 US-08-856-034-9	Sequence 9, Appl
17	135	100.0	192	3 US-08-471-057-13	Sequence 13, Appl
18	135	100.0	192	4 US-09-127-048-7	Sequence 7, Appl
19	135	100.0	192	4 US-08-927-326-2	Sequence 2, Appl
20	135	100.0	192	4 US-08-927-326-9	Sequence 9, Appl
21	135	100.0	192	5 PCT-US95-04600-25	Sequence 25, Appl
22	135	100.0	221	1 US-08-616-732A-9	Sequence 9, Appl
23	135	100.0	221	4 US-09-037-742B-9	Sequence 9, Appl
24	135	100.0	192	1 US-08-112-208C-3	Sequence 3, Appl
25	132	97.8	192	1 US-08-112-208C-8	Sequence 8, Appl
26	132	97.8	192	1 US-08-248-819A-3	Sequence 3, Appl
27	132	97.8	192	1 US-08-248-819A-8	Sequence 8, Appl

28	132	97.8	192	2 US-08-337-646A-3	Sequence 3, Appl
29	132	97.8	192	2 US-08-337-646A-8	Sequence 8, Appl
30	132	97.8	192	2 US-08-856-531-3	Sequence 3, Appl
31	132	97.8	192	2 US-08-856-531-8	Sequence 8, Appl
32	132	97.8	192	2 US-08-856-034-3	Sequence 3, Appl
33	132	97.8	192	2 US-08-856-034-8	Sequence 8, Appl
34	132	97.8	192	4 US-09-127-048-6	Sequence 6, Appl
35	132	97.8	192	4 US-08-927-326-3	Sequence 3, Appl
36	132	97.8	192	4 US-08-927-326-8	Sequence 8, Appl
37	130	96.3	26	1 US-08-440-391-6	Sequence 6, Appl
38	130	96.3	26	1 US-08-440-391-24	Sequence 24, Appl
39	130	96.3	26	2 US-08-908-597A-6	Sequence 6, Appl
40	130	96.3	26	2 US-08-908-597A-24	Sequence 24, Appl
41	130	96.3	26	4 US-09-236-385A-6	Sequence 6, Appl
42	130	96.3	26	4 US-09-236-385A-24	Sequence 24, Appl
43	130	96.3	26	5 PCT-US96-06122-6	Sequence 6, Appl
44	130	96.3	26	5 PCT-US96-06122-24	Sequence 24, Appl
45	105	77.8	42	1 US-08-798-897-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-08-440-391-13
: Sequence 13, Application US/08440391
: Patent No 5656725
: GENERAL INFORMATION:
: APPLICANT: CHITTENDEN, Thomas D.; and
: APPLICANT: LUTZ, Robert J.
: TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
: NUMBER OF SEQUENCES: 34
: CORRESPONDENCE ADDRESS:
: ADDRESS: Hale and Dorr
: STREET: 1455 Pennsylvania Avenue, N.W.
: CITY: Washington
: STATE: D.C.
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/440,391
: FILING DATE: 12-MAY-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: WIXON, HENRY N.
: REGISTRATION NUMBER: 32,073
: REFERENCE/DOCKET NUMBER: 104322.147
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-942-8400
: TELEFAX: 202-942-8484
: INFORMATION FOR SEQ ID NO: 13:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 34 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
US-08-440-391-13

Query Match 100.0%; Score 135; DB 1; Length 34;

Best Local Similarity 100.0%; Pred. No. 1.5e-13;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QDASTKKLSECLKRIQDELDSNMELQR 27
|||||
Db 3 QDASTKKLSECLKRIQDELDSNMELQR 29

RESULT 2
US-08-908-597A-13
Sequence 13, Application US/08908597A
Patent No. 5863795
GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.; and
APPLICANT: LUTZ, Robert J.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/908,597A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/440,391
FILING DATE: 12-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.147
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-908-597A-13
Query Match 100.0%; Score 135; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.5e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 0DASTKKLSECLKRIGDELDSNMEQLR 27
Db 3 0DASTKKLSECLKRIGDELDSNMEQLR 29
RESULT 3
US-09-236-385A-13
Sequence 13, Application US/09236385A
Patent No. 6221615
GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.; and
APPLICANT: LUTZ, Robert J.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/236,385A
FILING DATE: 25-Jan-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
TELECOMMUNICATION INFORMATION:
APPLICATION NUMBER: (C) ATTORNEY DOCKET NO. 104322.147CIP
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-236-385A-13
Query Match 100.0%; Score 135; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.5e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 0DASTKKLSECLKRIGDELDSNMEQLR 27
Db 3 0DASTKKLSECLKRIGDELDSNMEQLR 29
RESULT 4
PCT-US96-06122-13
Sequence 13, Application PC/TUS9606122
GENERAL INFORMATION:
APPLICANT: IMMUNOGEN, INC.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS
WHICH MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/06122
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/440,391
FILING DATE: 12-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.147PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US96-06122-13

Query Match 100.0%; Score 135; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.5e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 QDASTKKLSECKRIKIGDELDSNMELOR 27
Db 3 QDASTKKLSECKRIKIGDELDSNMELOR 29

RESULT 5
US-08-112-208C-2

; Sequence 2, Application US/08112208C
; Patent No. 5691179
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/112,208C
; FILING DATE: 26-Aug-1993
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-112-208C-2

Query Match 100.0%; Score 135; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 QDASTKKLSECKRIKIGDELDSNMELOR 27
Db 52 QDASTKKLSECKRIKIGDELDSNMELOR 78

RESULT 6
US-08-112-208C-9

; Sequence 9, Application US/08112208C
; Patent No. 5691179
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US

ZIP: 94301

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/112,208C
; FILING DATE: 26-Aug-1993
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-112-208C-9

Query Match 100.0%; Score 135; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 QDASTKKLSECKRIKIGDELDSNMELOR 27
Db 52 QDASTKKLSECKRIKIGDELDSNMELOR 78

RESULT 7
US-08-248-819A-2

; Sequence 2, Application US/08248819A
; Patent No. 5706538
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/248,819A
; FILING DATE: 25-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/112,208
; FILING DATE: 26-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-248-819A-2

Query Match 100.0%; Score 135; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDASTKRLSECLKRIQDELDSNMELOR 27
DB 52 QDASTKRLSECLKRIQDELDSNMELOR 78

RESULT 8
US-08-248-819A-9
Sequence 9, Application US/08248819A
Patent No. 5700638
GENERAL INFORMATION:

APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: CELL DEATH REGULATORS
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend Hourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/248, 819A
FILING DATE: 25-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/112,208
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-248-819A-9

Query Match 100.0%; Score 135; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDASTKRLSECLKRIQDELDSNMELOR 27
DB 52 QDASTKRLSECLKRIQDELDSNMELOR 78

RESULT 9
US-08-607-269-25
Sequence 25, Application US/08607269
Patent No. 5702897
GENERAL INFORMATION:

APPLICANT: Reed, John C.
APPLICANT: Sato, Takaki
TITLE OF INVENTION: Interaction of Proteins Involved in a
TITLE OF INVENTION: Cell Death Pathway
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESS: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/607,269
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/226,876
FILING DATE: 13-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 9882
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-607-269-25

Query Match 100.0%; Score 135; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDASTKRLSECLKRIQDELDSNMELOR 27
DB 52 QDASTKRLSECLKRIQDELDSNMELOR 78

RESULT 10
US-08-471-058-13
Sequence 13, Application US/08471058
Patent No. 5770443
GENERAL INFORMATION:
APPLICANT: Kiefer, Michael C.
TITLE OF INVENTION: NOVEL APOPTOSIS MODULATING
TITLE OF INVENTION: PROTEINS, DNA ENCODING THE PROTEINS AND METHODS OF USE
THEREOF
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESS: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,058

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; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/320,157
; FILING DATE: 07-OCT-1994
; APPLICATION NUMBER: 08/160,067
; FILING DATE: 30-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnardt, Susan K
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.12
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
;
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-471-058-13

Query Match          100.0%; Score 135; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDASTKKLSECLKRIGDELDSDNMEIQR 27
    |||
DB 52 QDASTKKLSECLKRIGDELDSDNMEIQR 78

RESULT 11
US-08-337-646A-2
; Sequence 2, Application US/08337646A
; Patent No. 5856171
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/337,646A
; FILING DATE: 10-NOV-1994
; CLASSIFICATION: 435
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-337-646A-9

Query Match          100.0%; Score 135; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDASTKKLSECLKRIGDELDSDNMEIQR 27
    |||
DB 52 QDASTKKLSECLKRIGDELDSDNMEIQR 78

RESULT 12
US-08-337-646A-9
; Sequence 9, Application US/08337646A
; Patent No. 5856171
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/337,646A
; FILING DATE: 10-NOV-1994
; CLASSIFICATION: 435
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-337-646A-9

Query Match          100.0%; Score 135; DB 2; Length 192;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDASTKKLSECLKRIGDELDSDNMEIQR 27
    |||
DB 52 QDASTKKLSECLKRIGDELDSDNMEIQR 78

RESULT 13
US-08-856-531-2
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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US-08-337-646A-2
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Query Match          100.0%; Score 135; DB 2; Length 192;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDASTKKLSECLKRIGDELDSDNMEIQR 27
    |||
DB 52 QDASTKKLSECLKRIGDELDSDNMEIQR 78
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```

RESULT 12
US-08-337-646A-9
; Sequence 9, Application US/08337646A
; Patent No. 5856171
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/337,646A
; FILING DATE: 10-NOV-1994
; CLASSIFICATION: 435
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-337-646A-9

Query Match          100.0%; Score 135; DB 2; Length 192;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDASTKKLSECLKRIGDELDSDNMEIQR 27
    |||
DB 52 QDASTKKLSECLKRIGDELDSDNMEIQR 78

RESULT 13
US-08-856-531-2
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; Sequence 2, Application US/08856531
; Patent No. 5942490
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howell & Haferkamp, L.C.
; STREET: 7733 Forsyth Blvd., Suite 1400
; CITY: St. Louis
; STATE: MO
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,531
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, Donald R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 976176
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-727-5188
; TELEFAX: 314-727-6092
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..192
; OTHER INFORMATION: /note="Human BAX polypeptide"
US-08-856-531-2

Query Match          100.0%; Score 135; DB 2; Length 192;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QDASTKRLSECLKRIGDELDSELMELOR 27
Db 52 QDASTKRLSECLKRIGDELDSELMELOR 78

RESULT 14
US-08-856-531-9
; Sequence 9, Application US/08856531
; Patent No. 5942490
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howell & Haferkamp, L.C.
; STREET: 7733 Forsyth Blvd., Suite 1400
; CITY: St. Louis
; STATE: MO
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/856,531
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, Donald R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 976176
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-727-5188
; TELEFAX: 314-727-6092
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..192
; OTHER INFORMATION: /note="Human BAX polypeptide"
US-08-856-531-9

Query Match          100.0%; Score 135; DB 2; Length 192;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QDASTKRLSECLKRIGDELDSELMELOR 27
Db 52 QDASTKRLSECLKRIGDELDSELMELOR 78

RESULT 15
US-08-856-034-2
; Sequence 2, Application US/08856034
; Patent No. 5955595
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howell & Haferkamp, L.C.
; STREET: 7733 Forsyth Blvd., Suite 1400
; CITY: St. Louis
; STATE: MO
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,034
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, Donald R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 976175
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-727-5188
; TELEFAX: 314-727-6092
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
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LOCATION: 1..192
OTHER INFORMATION: /note= "Human BAX polypeptide"
US-08-856-034-2

Query Match 100.08; Score 135; DB 2; Length 192;
Best Local Similarity 100.08; Pred. No. 1e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ODASTKKLSECLKRIQDELDLSNMEIQR 27
|||||
Db 52 ODASTKKLSECLKRIQDELDLSNMEIQR 78

Search completed: September 20, 2002, 10:37:19
Job time: 407 sec

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...

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 20, 2002, 10:39:02 ; Search time 95.59 Seconds
(without alignments)
27.141 Million cell updates/sec

Title: US-09-544-664-6
Perfect score: 135
Sequence: 1 QDASTKKLSECKIRIGDELDSNMELQR 27

Scoring table:
BIOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	135	100.0	179	2	JC7255
2	135	100.0	192	2	A47538
3	135	100.0	192	2	B47538
4	132	97.8	192	2	D47538
5	129	95.6	133	2	I53295
6	52	38.5	485	2	F64165
7	52	38.5	575	2	D96585
8	51.5	38.1	471	2	S64310
9	51	37.8	480	2	A37244
10	51	37.8	845	2	H71317
11	50	37.0	614	2	S43427
12	49	36.3	311	2	G86324
13	49	36.3	669	2	A90506
14	49	36.3	718	2	T51488
15	49	36.3	732	2	T19923
16	49	36.3	740	2	F82614
17	48	35.6	1957	2	A45627
18	48	35.6	1957	2	A45994
19	47.5	35.2	163	2	S43240
20	47.5	35.2	164	2	JM0060
21	47.5	35.2	164	2	JM0061
22	47	34.8	217	2	E71098
23	47	34.8	229	2	D72370
24	47	34.8	294	2	H84115
25	47	34.8	339	2	S08981
26	47	34.8	350	2	A47476
27	47	34.8	461	2	E96740
28	47	34.8	500	2	S64220
29	47	34.8	511	2	AC0941

30	47	34.8	591	2	S43428	omega-crystallin -
31	47	34.8	862	1	FAD0AA	alpha-actinin - s1
32	47	34.8	4151	2	T13734	groovin gene prote
33	46.5	34.4	163	2	F81374	hypothetical prote
34	46.5	34.4	1736	2	S49313	hypothetical prote
35	46	34.1	98	2	D87026	hypothetical prote
36	46	34.1	186	2	T21243	hypothetical prote
37	46	34.1	455	2	H68230	MDP-dependent gly
38	46	34.1	558	2	G90300	hypothetical prote
39	46	34.1	802	2	A87754	protein C43E11.11
40	46	34.1	1033	2	T38131	hypothetical prote
41	46	34.1	1094	2	S49313	protein kinase - s
42	46	34.1	1465	2	T23056	hypothetical prote
43	45.5	33.7	65	2	F97042	hypothetical prote
44	45.5	33.7	353	2	T00442	probable RNA (ade
45	45.5	33.7	3224	1	S58884	Ran-binding protei

ALIGNMENTS

RESULT 1
JC7255
Bax-delta protein - human
C:Species: Homo sapiens (man)
C>Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 17-Nov-2000
C:Accession: JC7255
R:Schmitt, E.; Paquet, C.; Beauchemin, M.; Deyer-Bertrand, J.; Bertrand, R.
Biochem. Biophys. Res. Commun. 270, 868-879, 2000
A:Title: Characterization of Bax-delta, a cell death-inducing isoform of Bax.
A:Reference number: JC7255
A:Accession: JC7255
A:Molecule type: mRNA
A:Residues: 1-179 <SOCH>
A:Cross-references: GB:AF247393
A:Experimental source: cancer promyelocytic cells
C:Comment: This protein, a member of the Bcl-2 family, has a proapoptotic effect. It
activation.
C:Superfamily: bcl transforming protein
C:Keywords: transmembrane protein

Query Match 100.0%; Score 135; DB 2; Length 179;
Best Local Similarity 100.0%; Pred. No. 2e-11;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QDASTKKLSECKIRIGDELDSNMELQR 27
|||||
Db 52 QDASTKKLSECKIRIGDELDSNMELQR 78
RESULT 2
A47538
bcl-2-associated protein x, alpha splice form - human
N:Alternate names: BAX; programmed cell death membrane protein x alpha
C:Species: Homo sapiens (man)
C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
R:Oltval, Z.N.; Millman, C.L.; Korsmeyer, S.J.
Cell 74, 609-619, 1993
A:Title: Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerate
A:Reference number: A47538; MUID:93364978
A:Accession: A47538
A:Molecule type: mRNA
A:Residues: 1-192 <OLT>
A:Cross-references: GB:L22473; NID:9388165; PIDN:AAA03619.1; PID:9388166
A>Note: the amino end of the mature protein is blocked
C:Genetics:
A:Gene: GDB:BAX
A:Cross-references: GDB:228082; OMIM:600040
A:Map position: 19q13.3-19q13.4
C:Superfamily: bcl transforming protein
C:Keywords: alternative splicing; blocked amino end; heterodimer; homodimer; transmem

F:172-191/Domain: transmembrane #status predicted <TM1>

Query Match 100.0%; Score 135; DB 2; Length 192;
Best Local Similarity 100.0%; Pred. No. 2.2e-11;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QDASTKKLSECLKRIQDELDNSMELOR 27
DB 52 QDASTKKLSECLKRIQDELDNSMELOR 78

RESULT 3

bcl-2-associated protein x, beta splice form - human
N:Alternate names: BAX; programmed cell death membrane protein x beta
C:Species: Homo sapiens (man)
C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
C:Accession: B47538
R:Olival, Z.N.; Millman, C.L.; Korsmeyer, S.J.
Cell 74, 609-619, 1993
A:Title: Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerates
A:Reference number: A47538; MUID:93364978
A:Accession: B47538
A:Molecule type: mRNA
A:Residues: 1-218
A:Cross-references: GB:L22474; NID:9388167; PIDN:AAA03620.1; PID:9388168
A:Note: the amino end of the mature protein is blocked
C:Genetics:
A:Gene: GDB:BAX
A:Cross-references: GDB:228082; OMIM:600040
A:Map position: 19q13.3-19q13.4
C:Superfamily: bcl transforming protein
C:Keywords: alternative splicing; blocked amino end; cytosol; heterodimer; homodimer

Query Match 100.0%; Score 135; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 2.5e-11;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QDASTKKLSECLKRIQDELDNSMELOR 27
DB 52 QDASTKKLSECLKRIQDELDNSMELOR 78

RESULT 4

bcl-2-associated protein x - mouse
N:Alternate names: BAX; programmed cell death membrane protein x
C:Species: Mus musculus (house mouse)
C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
C:Accession: D47538
R:Olival, Z.N.; Millman, C.L.; Korsmeyer, S.J.
Cell 74, 609-619, 1993
A:Title: Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerates
A:Reference number: A47538; MUID:93364978
A:Accession: D47538
A:Molecule type: mRNA
A:Residues: 1-192
A:Cross-references: GB:L22472
C:Genetics:
A:Gene: bax
C:Superfamily: bcl transforming protein

Query Match 97.8%; Score 133; DB 2; Length 192;
Best Local Similarity 96.3%; Pred. No. 5.7e-11;
Matches 26; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 QDASTKKLSECLKRIQDELDNSMELOR 27
DB 52 QDASTKKLSECLKRIQDELDNSMELOR 78

RESULT 5

bcl-2-associated protein x - rat (fragment)
N:Alternate names: BAX; programmed cell death membrane protein x
C:Species: Rattus norvegicus (Norway rat)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 03-Nov-2000
C:Accession: I53295
R:Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
Endocrinology 136, 232-241, 1995
A:Title: Expression of members of the bcl-2 gene family in the immature rat ovary: eg
constitutive bcl-2 and bcl-x long messenger ribonucleic acid levels.
A:Reference number: I53295; MUID:95129487
A:Accession: I53295
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-133 <RES>
A:Cross-references: EMBL:U32098; NID:975869; PIDN:AA75200.1; PID:975870
C:Genetics:
A:Gene: bax
C:Superfamily: bcl transforming protein

Query Match 95.6%; Score 129; DB 2; Length 133;
Best Local Similarity 92.6%; Pred. No. 1e-10;
Matches 25; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 QDASTKKLSECLKRIQDELDNSMELOR 27
DB 16 QDASTKKLSECLKRIQDELDNSMELOR 42

RESULT 6

hypothetical protein H11064 - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999
C:Accession: F64165
R:Flieschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhmann, J.L.; Geoghegan, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:93550630
A:Accession: F64165
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-485 <TIGR>
A:Cross-references: GB:U32786; GB:I42023; NID:91574605; PIDN:AAC22718.1; PID:91574615
A:Note: best homolog was a hypothetical protein from Escherichia coli
C:Genetics:
A:Start codon: GTG

Query Match 38.5%; Score 52; DB 2; Length 485;
Best Local Similarity 45.5%; Pred. No. 19;
Matches 10; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

OY 3 ASTKKLSECLKRIQDELDNSME 24
DB 402 SSIKKDFELKRYVDLEENVK 423

RESULT 7

hypothetical protein F2021.19 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: D96585
R:Rheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,

Best Local Similarity 38.1%; Pred. No. 46;
Matches 8; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

OY 5 TKRLSECLKRIQDELSDNMEL 25
DB 288 TNELANCKREIRDEYDNLNL 308

RESULT 12
G86324

hypothetical protein T29M8.1 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001

C:Accession: G86324

R:Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719

A:Accession: G86324

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-311 <STO>

A:Cross-References: GB:AE005172; NID:g8954052; PIDN:AAF82225.1; GSPDB:GN00141

C:Genetics:

A:Map position: 1

Query Match 36.3%; Score 49; DB 2; Length 311;
Best Local Similarity 42.1%; Pred. No. 32;
Matches 8; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

OY 8 LSECLKRIQDELSDNMELQ 26
DB 142 MDECLQLMDRIDSGDLQ 160

RESULT 13
A90506

ser/thr protein kinase, probable [Imported] - Sulfolobus solfataricus

C:Species: Sulfolobus solfataricus

C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001

C:Accession: A90506

R:She, O.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awaizer, M.J.; Chan,

Jung, I.; Jeffries, A.C.; Kozera, C.U.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R.

submitted to GenBank, April 2001

A:Description: Sulfolobus solfataricus complete genome.

A:Reference number: A99139

A:Accession: A90506

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-669 <KUR>

A:Cross-References: GB:AE006641; NID:g13816645; PIDN:AAK43304.1; GSPDB:GN00155

C:Genetics:

A:Gene: SSO3207

Query Match 36.3%; Score 49; DB 2; Length 669;
Best Local Similarity 50.0%; Pred. No. 69;
Matches 7; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

OY 8 LSECLKRIQDELSD 21
DB 175 VAOQMERIDLEA 188

RESULT 14
T51488

hypothetical protein T21H19.100 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000

C:Accession: T51488

R:Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.;

submitted to the Protein Sequence Database, August 2000

A:Reference number: Z25394

A:Accession: T51488

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-718 <SAT>

A:Cross-References: EMBL:AL391148

A:Experimental source: cultivar Columbia; BAC clone T21H19

C:Genetics:

A:Map position: 5

A:Insertions: 271/3; 381/1; 424/3; 539/3; 592/1; 690/3

A>Note: T21H19.100

Query Match 36.3%; Score 49; DB 2; Length 718;
Best Local Similarity 43.5%; Pred. No. 74;
Matches 10; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

OY 5 TKRLSECLKRIQDELSDNMELQ 27
DB 571 TNERECLKRIQKMSLVGR 593

RESULT 15
T19923

hypothetical protein C44C10.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C:Accession: T19923

R:Cottage, A.

submitted to the EMBL Data Library, February 1996

A:Reference number: Z19197

A:Accession: T19923

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-732 <WIL>

A:Cross-References: EMBL:Z69787; PIDN:CA93636.1; GSPDB:GN00028; CESP:C44C10.2

A:Experimental source: clone C44C10

C:Genetics:

A:Gene: CESP:C44C10.2

A:Map position: X

A:Insertions: 54/3; 102/3; 119/3; 388/1; 427/3; 490/3; 550/3; 619/1; 714/3

Query Match 36.3%; Score 49; DB 2; Length 732;
Best Local Similarity 42.3%; Pred. No. 76;
Matches 11; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

OY 2 DASTKRLSECLKRIQDELSDNMELQ 27
DB 154 DATKRLSEKRLQETPRKQTSQR 179

Search completed: September 20, 2002, 10:39:04
Job time: 476 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 20, 2002, 11:04:28 ; Search time 44.99 Seconds
(without alignments)
23.237 Million cell updates/sec

Title: US-09-544-664-6

Sequence: 1 QDASTKRLSECLKRGDELDSNMLQR 27

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	ID	Description
1	135	100.0	192	1	BAXA_BOVIN
2	135	100.0	192	1	BAXA_HUMAN
3	135	100.0	218	1	BAXB_HUMAN
4	132	97.8	192	1	BAXA_MOUSE
5	132	97.8	192	1	BAXA_RAT
6	52	38.5	485	1	YA64_HAEN
7	51.5	38.1	471	1	GATA_YEAST
8	51	37.8	879	1	SP10_HUMAN
9	47.5	35.2	163	1	TPC_BRALA
10	47	34.8	294	1	RBSK_BACHD
11	47	34.8	339	1	MDH_METFE
12	47	34.8	350	1	MCL1_HUMAN
13	47	34.8	500	1	AR08_HUMAN
14	47	34.8	862	1	AACT_DICDI
15	46	34.1	1033	1	YDK9_SCHPO
16	45.5	33.7	281	1	APF_BRARE
17	45.5	33.7	3224	1	RBP2_HUMAN
18	45	33.3	317	1	RPOA_AOUAE
19	45	33.3	482	1	T2EA_YEAST
20	45	33.3	496	1	MSSI_SCHPO
21	45	33.3	522	1	CPV1_ORENI
22	45	33.3	656	1	DNK1_ALCEU
23	45	33.3	657	1	BFS1_CHICK
24	45	33.3	850	1	LEM3_HUMAN
25	45	33.3	1704	1	ABC3_HUMAN
26	44.5	33.0	1325	1	G160_MOUSE
27	44	32.6	222	1	YA1V_ECOLI
28	44	32.6	281	1	KHSE_THEMA
29	44	32.6	506	1	DHA2_ALCEU
30	44	32.6	564	1	PROD_CAEEL
31	44	32.6	726	1	CO3_RABIT
32	44	32.6	899	1	VP3_EHDAV
33	43.5	32.2	236	1	STX8_HUMAN

34	43.5	32.2	236	1	STX8_RAT	Q92297	rattus norv
35	43	31.9	148	1	CATR_TETST	P43646	tetrastelmis
36	43	31.9	168	1	CATR_SCHDU	Q06847	scheriffella
37	43	31.9	184	1	RBF_BORBU	O51147	borreliella bu
38	43	31.9	195	1	BID_MOUSE	P70444	mus musculu
39	43	31.9	197	1	GRPE_SYNP7	Q59984	synochococc
40	43	31.9	197	1	MOBA_METHH	Q26246	methanobact
41	43	31.9	246	1	KAD_ARATH	O82514	arabidopsis
42	43	31.9	334	1	YH05_YEAST	P38803	saccharomyc
43	43	31.9	379	1	YAD2_YEAST	P28004	saccharomyc
44	43	31.9	385	1	LEF3_NPVAC	P41453	autographa
45	43	31.9	507	1	MCM6_RAT	Q62724	rattus norv

ALIGNMENTS

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RESULT 1
BAXA_BOVIN
ID BAXA_BOVIN STANDARD: PRT: 192 AA.
AC 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DI Apoptosis regulator BAX, membrane isoform alpha.
GN BAX.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N. A.
RC STRAIN=HOJSTEIN; TISSUE=Thymus;
RX MEDLINE=98162580; PubMed=9501056;
RA Reyes R.A., Cockrell G.L.;
RT "Increased ratio of bcl-2/bax expression is associated with bovine
RT leukemia virus-induced leukemogenesis in cattle.";
RL Virology 242:184-192(1998).
CC -!- FUNCTION: ACCELERATES PROGRAMED CELL DEATH BY BINDING TO, AND
CC ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS
CC HOMOLOG E1B 19K PROTEIN. INDUCES THE RELEASE OF CYTOCHROME C,
CC ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS. BAX DEFICIENCY
CC LEADS TO LYMPHOID HYPERPLASIA AND MALE STERILITY, BECAUSE OF THE
CC CESSATION OF SPERM PRODUCTION (BY SIMILARITY).
CC -!- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,
CC E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1 (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Membrane-bound (By similarity).
CC -!- ALTERNATIVE PRODUCTS: A 21 kDa MEMBRANE PROTEIN ALPHA AND THE TWO
CC CYTOPLASMIC PROTEINS BETA AND GAMMA ARE GENERATED BY ALTERNATIVE
CC SPLICING.
CC -!- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIR, BID, BAK, BAD AND
CC BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC APOPTOTIC MEMBERS OF THE BCL-2 FAMILY (BY SIMILARITY).
CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 1 (BH1).
CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 2 (BH2).
CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC -----
EMBL: U92569; AAC48806.1; -
HSSP: Q07817; IMAZ.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; BCL2.
DR Pfam: PF00452; BCL-2; 1.

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DR SMART; SM00337; BCL; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR APOPTOSIS; Transmembrane; Alternative splicing.
FT DOMAIN 59 73 BH3.
FT DOMAIN 98 118 BH1.
FT DOMAIN 150 165 BH2.
FT TRANSMEM 172 192 POTENTIAL.
SQ SEQUENCE 192 AA; 21259 MW; 6BAD5BAFID5F87E CRC64;

Query Match 100.0%; Score 135; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.8e-11;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QDASTKKLSCLKRIGDELDSELMELOR 27
DB 52 QDASTKKLSCLKRIGDELDSELMELOR 78

RESULT 2
ID BAXA_HUMAN STANDARD; PRT; 192 AA.
AC 007812;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Apoptosis regulator BAX, membrane isoform alpha.
GN BAX.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RX MEDLINE=93364978; PubMed=8358790;
RA Olvay Z.N., Millman C.L., Korsmeyer S.J.;
RT Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that
RT accelerates programmed cell death.";
RL Cell 74:609-619(1993).
RN [2]
RP MOTAGENESIS AND FUNCTION OF BH3 DOMAIN.
RX MEDLINE=96091131; PubMed=8521816;
RA Chittenden T., Flemington C., Houghton A.B., Ebb R.G., Gallo G.J.,
RA Elangovan B., Chinnadurai G., Lutz R.J.;
RT "A conserved domain in Bax, distinct from Bhl and Bh2, mediates cell
RT death and protein binding functions.";
RL EMBO J. 14:5589-5596(1995).
RN [3]
RP VARIANT T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA ARG-67.
RX MEDLINE=98200607; PubMed=9531611;
RA Mellerink J.P.P., Mensink E.J.B.M., Wang K., Sedlak T.W.,
RA Sloerjes A.W., de Witte T., Waksman G., Korsmeyer S.J.;
RT "Hematopoietic malignancies demonstrate loss-of-function mutations of
RT BAX";
RL Blood 91:2991-2997(1998).
RN [1]
RP FUNCTION: ACCELERATES PROGRAMED CELL DEATH BY BINDING TO, AND
RN ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS
RN HOMOLOG E1B 19K PROTEIN. INDUCES THE RELEASE OF CYTOCHROME C,
RN ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS.
RN [1]
RP SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,
RN E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1.
RN [1]
RP SUBCELLULAR LOCATION: Membrane-bound.
RN [1]
RP ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE
RN CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY
RN ALTERNATIVE SPLICING.
RN [1]
RP TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
RN [1]
RP DOMAIN: INACT BH3 DOMAIN IS REQUIRED FOR BIK, BID, BAK, BAD AND
RN BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
RN WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.

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CC APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC -1- DISEASE: DEFECTS IN BAX ARE FOUND IN SOME PATIENTS WITH T-CELL
CC ACUTE LYMPHOBLASTIC LEUKEMIA.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 1 (BH1).
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 2 (BH2).
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 3 (BH3).
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; L22473; AAA03619.1; .
DR PIR; A47538; A47538.
DR HSSP; 007817; 1MAZ.
DR MIM; 600040; .
DR InterPro; IPR002475; BCL2_family.
DR InterPro; IPR000712; BCL_2.
DR Pfam; PF00452; Bcl-2; 1.
DR SMART; SM00337; BCL; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR APOPTOSIS; Transmembrane; Alternative splicing; Disease mutation.
FT DOMAIN 59 73 BH3.
FT DOMAIN 98 118 BH1.
FT DOMAIN 150 165 BH2.
FT TRANSMEM 172 192 POTENTIAL.
FT VARIANT 67 67 G -> R (IN T-CELL ACUTE LYMPHOBLASTIC
FT LEUKEMIA).
FT /FTID=VAR_007809.
SQ SEQUENCE 192 AA; 21184 MW; 6C0CDB0A7DBE94994 CRC64;

Query Match 100.0%; Score 135; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.8e-11;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QDASTKKLSCLKRIGDELDSELMELOR 27
DB 52 QDASTKKLSCLKRIGDELDSELMELOR 78

RESULT 3
ID BAXB_HUMAN STANDARD; PRT; 218 AA.
AC 007814;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Apoptosis regulator BAX, cytoplasmic isoform beta.
GN BAX.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RX MEDLINE=93364978; PubMed=8358790;
RA Olvay Z.N., Millman C.L., Korsmeyer S.J.;
RT Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that
RT accelerates programmed cell death.";
RL Cell 74:609-619(1993).
RN [1]
RP FUNCTION: ACCELERATES PROGRAMED CELL DEATH BY BINDING TO, AND
RN ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS
RN HOMOLOG E1B 19K PROTEIN.
RN [1]
RP SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,

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CC      E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1.
CC      -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC      -1- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE
CC      CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY
CC      ALTERNATIVE SPLICING.
CC      -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
CC      -1- DOMAIN: INTRACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND
CC      BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
CC      WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC      -1- APOTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC      -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC      -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC      -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC      -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC      -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: L22474; AAA03620.1; -.
CC      DR      PIR: B47538; B47538.
CC      DR      HSSP: 007817; LMAZ.
CC      DR      MIM: 600040; -.
CC      DR      InterPro: IPR002475; BCL2_family.
CC      DR      InterPro: IPR00712; BCL_2.
CC      DR      Pfam: PF00452; BCL-2; 1.
CC      DR      SMART: SM00337; BCL; 1.
CC      DR      PROSITE: PS01080; BH1; 1.
CC      DR      PROSITE: PS01258; BH2; 1.
CC      DR      PROSITE: PS01259; BH3; 1.
CC      DR      PROSITE: PS00062; BCL2_FAMILY; 1.
CC      KW      Apoptosis; Alternative splicing.
CC      FT      DOMAIN 59 73 BH3.
CC      FT      DOMAIN 98 118 BH1.
CC      FT      DOMAIN 150 165 BH2.
CC      SQ      SEQUENCE 218 AA; 24220 MW; F69DCD70F960192F CRC64;

Query Match 100.0%; Score 135; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 2e-11;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QDASTKKLSECLKRIGDELSNMEIQR 27
DB      52 QDASTKKLSECLKRIGDELSNMEIQR 78

RESULT 4
BAXA_MOUSE
ID      BAXA_MOUSE STANDARD: PRT; 192 AA.
AC      007813;
DT      01-FEB-1995 (Rel. 31, Created)
DT      01-FEB-1995 (Rel. 31, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Apoptosis regulator BAX, membrane isoform alpha.
GN      BAX.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6 X DBA/2;
RX      MEDLINE=93364978; PubMed=8358790;
RT      Oliva J.N., Millman C.L., Korsmeyer S.J.;
RT      "Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that
RT      accelerates programmed cell death.";
RL      Cell 74:609-619(1993).
-1- FUNCTION: ACCELERATES PROGRAMED CELL DEATH BY BINDING TO, AND

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CC      HOMOLOG E1B 19K PROTEIN, INDUCES THE RELEASE OF CYTOCHROME C,
CC      ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS. BAX DEFICIENCY
CC      LEADS TO LYMPHOID HYPERPLASIA AND MALE STERILITY, BECAUSE OF THE
CC      CESSATION OF SPERM PRODUCTION.
CC      -1- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,
CC      E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1.
CC      -1- SUBCELLULAR LOCATION: Membrane-bound.
CC      -1- ALTERNATIVE PRODUCTS: A 21 kDa MEMBRANE PROTEIN ALPHA AND THE TWO
CC      CYTOPLASMIC PROTEINS BETA AND GAMMA ARE GENERATED BY ALTERNATIVE
CC      SPLICING.
CC      -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
CC      -1- DOMAIN: INTRACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND
CC      BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
CC      WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC      -1- APOTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC      -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC      -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC      -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC      -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC      -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: L22472; AAA03622.1; -.
CC      DR      HSSP: 007817; LMAZ.
CC      DR      MGD: 99702; BAX.
CC      DR      InterPro: IPR002475; BCL2_family.
CC      DR      InterPro: IPR00712; BCL_2.
CC      DR      Pfam: PF00452; BCL-2; 1.
CC      DR      SMART: SM00337; BCL; 1.
CC      DR      PROSITE: PS01080; BH1; 1.
CC      DR      PROSITE: PS01258; BH2; 1.
CC      DR      PROSITE: PS01259; BH3; 1.
CC      DR      PROSITE: PS00062; BCL2_FAMILY; 1.
CC      KW      Apoptosis; Transmembrane; Alternative splicing.
CC      FT      DOMAIN 59 73 BH3.
CC      FT      DOMAIN 98 118 BH1.
CC      FT      DOMAIN 150 165 BH2.
CC      FT      TRANSMEM 172 192 POTENTIAL.
CC      SQ      SEQUENCE 192 AA; 21394 MW; D2E0B356579FAFF CRC64;

Query Match 97.8%; Score 132; DB 1; Length 192;
Best Local Similarity 96.3%; Pred. No. 4.5e-11;
Matches 26; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 QDASTKKLSECLKRIGDELSNMEIQR 27
DB      52 QDASTKKLSECLKRIGDELSNMEIQR 78

RESULT 5
BAXA_RAT
ID      BAXA_RAT STANDARD: PRT; 192 AA.
AC      063690; 062995; 064383;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Apoptosis regulator BAX, membrane isoform alpha.
GN      Rattus norvegicus (Rat).
OS      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=96178771; PubMed=8600029;

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RA Han J., Sabbatini P., Perez D., Rao L., Modha D., White E.
 RT "The E1B 19K protein blocks apoptosis by interacting with and
 RT inhibiting the p53-inducible and death-promoting Bax protein."
 RL Genes Dev. 10:461-477(1996).
 RN [12]
 RP SEQUENCE OF 75-192 FROM N.A.
 RC TISSUE=Brain;
 RA MEDLINE=97147318; PubMed=8994223;
 RT Madison D.L., Pfeiffer S.E.;
 RT "Cloning of the 3' end of rat bax-alpha and corresponding
 RT developmental down-regulation in differentiating primary, cultured
 RT oligodendrocytes."
 RL Neurosci. Lett. 220:183-186(1996).
 RN [13]
 RP SEQUENCE OF 37-169 FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Ovary;
 RA MEDLINE=95129487; PubMed=7828536;
 RT Tilly J.L., Tilly K.L., Kenton M.L., Johnson A.L.;
 RT "Expression of members of the bcl-2 gene family in the immature rat
 RT ovary: equine chorionic gonadotropin-mediated inhibition of granulosa
 RT cell apoptosis is associated with decreased bax and constitutive
 RT bcl-2 and bcl-x-long messenger ribonucleic acid levels."
 RL Endocrinology 136:232-241(1995).
 CC -1- FUNCTION: ACCELERATES PROGRAMED CELL DEATH BY BINDING TO, AND
 CC ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOYRUS
 CC HOMOLOG E1B 19K PROTEIN. INDUCES THE RELEASE OF CYTOCHROME C,
 CC ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS.
 CC -1- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,
 CC E1B 19K PROTEIN, BCL-X(L), MCL-1 AND AL.
 CC -1- SUBCELLULAR LOCATION: Membrane-bound.
 CC -1- ALTERNATIVE PRODUCTS: A 21 KDA MEMBRANE PROTEIN ALPHA AND THE TWO
 CC CYTOPLASMIC PROTEINS BETA AND GAMMA ARE GENERATED BY ALTERNATIVE
 CC SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES, WITH
 CC HIGHEST LEVELS IN THE TESTIS AND OVARY.
 CC -1- DOMAIN: INTRACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND
 CC BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
 CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
 CC APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 1 (BH1).
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 2 (BH2).
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 3 (BH3).
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
 CC -----
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 CC -----
 CC EMBL: U49729; AAC26327.1; -
 CC EMBL: U59184; AAC52988.1; -
 CC EMBL: U32098; AAA75200.1; -
 CC EMBL: S76511; AAC60700.2; -
 CC HSSP: Q07817; 1MA2.
 CC InterPro: IPR002475; BCL2_family.
 CC InterPro: IPR000712; Bcl_2.
 CC Pfam: PF00452; Bcl-2; 1.
 CC SMART: SM00337; BCL.1.
 CC PROSITE: PS01080; BH1; 1.
 CC PROSITE: PS01258; BH2; 1.
 CC PROSITE: PS01259; BH3; 1.
 CC PROSITE: PS0062; BCL2_FAMILY; 1.
 DR Apoptosis; Transmembrane; Alternative splicing.
 KW DOMAIN
 FT 59 73 BH3.
 FT DOMAIN 98 118 BH1.
 FT 150 165 BH2.
 FT TRANSMEM 172 192 POTENTIAL.
 FT TRANSMEM 72 76 S -> N (IN REF. 3).
 FT TRANSMEM 76 76 L -> M (IN REF. 2).
 FT CONFLICT 126 126 C -> Y (IN REF. 2).
 FT CONFLICT 126 126

FT CONFLICT 149 149 L -> F (IN REF. 3).
 FT CONFLICT 159 159 D -> E (IN REF. 1).
 SQ SEQUENCE 192 AA; 21350 MW; 783CD198D56DF589 CRC64;
 Query Match 97.8%; Score 132; DB 1; Length 192;
 Best Local Similarity 96.3%; Pred. No. 4.5e-11;
 Matches 26; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 ODASTKLSCLKRTGDELDNSMELOR 27
 Db 52 ODASTKLSCLKRTGDELDNSMELOR 78
 RESULT 6
 YA64_HAEIN STANDARD; PRT; 485 AA.
 ID YA64_HAEIN
 AC P71367.
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein H11064.
 GN H11064
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Haemophilus.
 OX NCBI_TaxID=727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RD / ATCC 51907;
 RX MEDLINE=95350630; PubMed=7542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Gocayne J.D.,
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.M.,
 RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 RA Fine L.D., Fritchman J.L., Fuhrman J.L., Geoghagen N.S.M.,
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus
 RT influenzae Rd."
 RT Science 269:496-512(1995).
 RL -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- SIMILARITY: BELONGS TO THE UPF0141 FAMILY.
 CC -----
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 CC -----
 CC EMBL: U32786; AAC22718.1; -
 CC TIGR: H11064;
 DR InterPro: IPR003371; DUF146.
 DR Pfam: PF02418; DUF146; 1.
 KW Hypothetical protein; Transmembrane; Complete proteome.
 FT TRANSMEM 33 53 POTENTIAL.
 FT TRANSMEM 55 75 POTENTIAL.
 FT TRANSMEM 81 101 POTENTIAL.
 FT TRANSMEM 125 145 POTENTIAL.
 SQ SEQUENCE 485 AA; 55401 MW; 3C0D8285C64D5F55 CRC64;
 Query Match 38.5%; Score 52; DB 1; Length 485;
 Best Local Similarity 45.5%; Pred. No. 8.1;
 Matches 10; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
 Oy 3 ASTKKLSCLKRICDELDSNME 24
 Db 402 SSIKTKDELKRVYDLEENVK 423

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RESULT 7
GATA_YEAST
ID GATA_YEAST STANDARD; PRT; 471 AA.
AC P17649;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-OCT-1996 (Rel. 34, last sequence update)
DT 30-MAY-2000 (Rel. 39, last annotation update)
DE 4-aminobutyrate aminotransferase (EC 2.6.1.19) (gamma-amino-N-butyrate
transaminase) (GABA transaminase) (GABA aminotransferase) (GABA-AT).
GN UGAL OR YGR019W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-1278B;
RX MEDLINE-90272415; PubMed-2190186;
RA Andre B., Jauniaux J.-C.;
RT "Nucleotide sequence of the yeast UGAL gene encoding GABA
transaminase."
RL Nucleic Acids Res. 18:3049-3049(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C;
RX MEDLINE-97435481; PubMed-9290212;
RA Rieger M., Brueckner M., Schaefer M., Mueller-Auer S.;
RT "Sequence analysis of 203 kilobases from Saccharomyces cerevisiae
chromosome VII."
RL Yeast 13:1077-1090(1997).
CC -1- CATALYTIC ACTIVITY: 4-aminobutanoate + 2-oxoglutarate = succinate
+ semialdehyde + L-glutamate.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- SUBUNIT: HOMODIMER (POSSIBLE).
CC -1- SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT
AMINOTRANSFERASES.
CC -----
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CC -----
DR EMBL: X52600; CAA36833.1; -
DR EMBL: Z72804; CAA87002.1; -
DR PIR: S26708; S26708.
DR HSSP: P80147; 1GTX.
DR SGD: S0003251; UGAL.
DR InterPro: IPR000954; Aminotran_3.
DR Pfam: PF00202; aminotran_3.1.
DR PROSITE: PS00600; AA_TRANSFR_CLASS_3; 1.
KW Transferrase; Aminotransferase; Pyridoxal phosphate.
FT BINDING 326 326 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
FT CONFLICT 240 240 H -> R (IN REF. 1).
SO SEQUENCE 471 AA; 52946 MW; 33D446778A891F63 CRC64;

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Query Match 38.1%; Score 51.5; DB 1; Length 471;
Best local Similarity 46.4%; Pred. No. 9.2;
Matches 13; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

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OY 1 QDASTKKLSKRLKRGIDELDSNME-LQR 27
Db 367 QETSDKKLTQCGSRVDYLFKKLEGLOK 394

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RESULT 8
SP10_HUMAN STANDARD; PRT; 879 AA.
ID SP10_HUMAN

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AC P23497; Q13343; O75450; Q9UE32;
DT 01-NOV-1991 (Rel. 20, Created)
DT 16-OCT-2001 (Rel. 40, last sequence update)
DT 01-MAR-2002 (Rel. 41, last annotation update)
DE Nuclear autoantigen Sp100 (Speckled 100 kDa) (Nuclear dot-associated
Sp100 protein) (Iyvsp100b).
GN Sp100.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM SP100-HMG).
RC TISSUE-Breast cancer;
RX MEDLINE-98301571; PubMed-9636146;
RA Seeler J.-S., Marchio A., Sitterlin D., Transy C., Dejean A.;
RT "Interaction of SP100 with Hp1 proteins: a link between the
promyelocytic leukemia-associated nuclear bodies and the chromatin
compartment."
RL Proc. Natl. Acad. Sci. U.S.A. 95:7316-7321(1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM SP100-A).
RC TISSUE-Liver, and Placenta;
RX MEDLINE-91079525; PubMed-2258622;
RA Szostecki C., Guider H.H., Netter H.J., Will H.;
RT "Isolation and characterization of cDNA encoding a human nuclear
antigen predominantly recognized by autoantibodies from patients with
primary biliary cirrhosis."
RL J. Immunol. 145:4338-4347(1990).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM SP100-B).
RX MEDLINE-96329578; PubMed-8695863;
RA Dent A.L., Yewdell J., Puvion-Dutilleul F., Koken M.H.M., de The H.,
Staudt L.M.;
RT "LSP100-associated nuclear domains (LANDs): description of a new
class of subnuclear structures and their relationship to PML nuclear
bodies."
RL Blood 88:1423-1426(1996).
RN [4]
RP SEQUENCE OF 1-10 FROM N.A.
RC TISSUE-Lymphoma;
RX MEDLINE-96411734; PubMed-8810287;
RA Grotzinger T., Jensen K., Will H.;
RT "The interferon (IFN)-stimulated gene Sp100 promoter contains an IFN-
gamma activation site and an imperfect IFN-stimulated response element
which mediate type I IFN inducibility."
RL J. Biol. Chem. 271:25253-25260(1996).
RN [5]
RP ALTERNATIVE SPLICING (ISOFORMS SP100-B; SPALT-C AND SP100-HMG).
RC TISSUE-Cervical adenocarcinoma;
RX MEDLINE-99141186; PubMed-9973607;
RA Guider H.H., Szostecki C., Schroeder P., Matschl U., Jensen K.,
Lueders C., Will H., Sternsdorf T.;
RT "Splice variants of the nuclear dot-associated Sp100 protein contain
homologies to HMG-1 and a human nuclear phosphoprotein-box motif."
RL J. Cell Sci. 112:733-747(1999).
RN [6]
RP CHARACTERIZATION AND COVALENT BINDING TO SUMO-1.
RX MEDLINE-99230277; PubMed-10212234;
RA Sternsdorf T., Jensen K., Reich B., Will H.;
RT "The nuclear dot protein sp100, characterization of domains necessary
for dimerization, subcellular localization, and modification by small
ubiquitin-like modifiers."
RL J. Biol. Chem. 274:12555-12566(1999).
CC -1- FUNCTION: MAY PLAY A ROLE IN THE CONTROL OF GENE EXPRESSION.
CC -1- SUBUNIT: HOMODIMER. SPLICED VARIANTS HETERODIMERIZE. INTERACTS WITH
CC MEMBERS OF THE HPI FAMILY OF NONHISTONE CHROMOSOMAL PROTEIN, SUCH
CC AS HETEROCHROMATIN PROTEIN 1-ALPHA (HPI-ALPHA) AND HETEROCHROMATIN
CC PROTEIN 1-GAMMA (HPI-GAMMA).
CC -1- SUBCELLULAR LOCATION: NUCLEAR. FOUND IN THE NUCLEAR BODY, ALSO
CC KNOWN AS NUCLEAR DOMAIN 10 (ND10), PML ONCOGENIC DOMAIN (POD),
CC NUCLEAR DOTS (ND) AND KR BODY. THE NUCLEAR BODY IS A NUCLEOPOLASMIC
CC STRUCTURE OF PUNCTATE SHAPE, WHICH VARIES IN SIZE AND NUMBER.

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DT 01-MAR-2002 (Rel. 41, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
DR Ribokinase (EC 2.7.1.15).
GN RBSK OR BH3728.
OS Bacillus halodurans.
OC Bacteria: Firmicutes: Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=86665.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis."
RT Nucleic Acids Res. 28:4317-4331(2000).
CC -1- CATALYTIC ACTIVITY: ATP + D-ribose -> ADP + D-ribose 5-phosphate.
CC -1- PATHWAY: FIRST STEP IN RIBOSE METABOLISM.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE PKB FAMILY OF CARBOHYDRATE KINASES.
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CC -----
DR EMBL: AP001519; BAB07447.1;
DR HSSP: P05054; 1RKD.
DR InterPro: IPR002173; PKB.
DR InterPro: IPR002139; Ribokinase.
DR Pfam: PF00294; pfkb.1
DR PRINTS: PR00990; RIBOKINASE.
DR PROSITE: PS00583; PKB_KINASES_1; 1.
DR PROSITE: PS00584; PKB_KINASES_2; 1.
DR Transferrase: Kinase; Complete proteome.
KW SEQUENCE 294 AA; 31089 MW; 8C13E0FCF5E89FDE CRC64;

Query Match 34.8%; Score 47; DB 1; Length 294;
Best Local Similarity 53.3%; Pred. No. 23;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 9 SECLARKIGDELDSNM 23
DB 187 NECLQFGEDEPDANL 201
:||||:||||:|
:||||:||||:|

RESULT 11
MDL_METFE STANDARD: PRT; 339 AA.
AC F16142;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Malate/L-sulfolactate dehydrogenase (EC 1.1.1.37) (EC 1.1.1.82).
GN MDH.
OS Methanothermus fervidus.
OC Archaea: Euryarchaeota; Methanobacteriales; Methanothermaceae;
OC Methanothermus.
OX NCBI_TaxID=2180;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-24.
RC STRAIN=Y245 / DSM 2088;
RX MEDLINE=90235834; PubMed=2110059;
RA Honkx E., Fabry S., Niemann T., Palm P., Hensel R.;
RT "Properties and primary structure of the L-malate dehydrogenase from
RT the extremely thermophilic archaeobacterium Methanothermus fervidus";
RT Eur. J. Biochem. 188:623-632(1990).

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RN [2]
RP FUNCTION.
RX MEDLINE=20309698; PubMed=10850983;
RA Graupner M., Xu H., White R.H.;
RT "Identification of an archaeal 2-hydroxy acid dehydrogenase catalyzing
RT reactions involved in coenzyme biosynthesis in methanarchaea.";
RT J. Bacteriol. 182:3688-3692(2000).
RL 3. Bacteriol. 182:3688-3692(2000).
CC -1- FUNCTION: Acts on oxaloacetate, sulfolpyruvate but not on pyruvate.
CC -1- FUNCTION: Selective for the coenzyme NADH than for NADPH.
CC -1- CATALYTIC ACTIVITY: (S)-malate + NAD(P)(+) -> oxaloacetate +
CC NAD(P)H.
CC -1- CATALYTIC ACTIVITY: (R)-sulfolactate + NAD(P)(+) -> sulfolpyruvate +
CC NAD(P)H.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE LDH2/MDH2 OXIDOREDUCTASE FAMILY.
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CC -----
DR EMBL: X51714; CA36010.1;
DR EMBL: X51940; CA36133.1;
DR PIR: S08689; S08689.
DR PIR: S08981; S08981.
DR InterPro: IPR003767; ldh_2.
DR Pfam: PF02615; ldh_2; 1.
DR Oxidoreductase: Tricarboxylic acid cycle; NAD; NADP.
KW SEQUENCE 339 AA; 36762 MW; 2319D822D8275835 CRC64;

Query Match 34.8%; Score 47; DB 1; Length 339;
Best Local Similarity 65.0%; Pred. No. 27;
Matches 13; Conservative 1; Mismatches 4; Indels 2; Gaps 1;

OY 6 KRLSECLARKIGDELDSNMEL 25
DB 320 KRLVEXKREIADDEL--NIEL 337
|||||
|||||

RESULT 12
MCL1_HUMAN STANDARD: PRT; 350 AA.
AC Q07820; Q9NRQ3; Q9NRQ4;
DT 01-FEB-1995 (Rel. 31, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Induced myeloid leukemia cell differentiation protein Mcl-1.
GN MCL1.
OS Homo sapiens (Human).
OC Eukaryota: Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX TISSUE=Myeloid leukemia cells;
RX MEDLINE=9334528; PubMed=7682708;
RA Kozopas K.M., Yang T., Buchan H.L., Zhou P., Craig R.W.;
RT "MCL1, a gene expressed in programmed myeloid cell differentiation,
RT has sequence similarity to BCL2";
RT Proc. Natl. Acad. Sci. U.S.A. 90:3516-3520(1993).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX MEDLINE=20357335; PubMed=10766760;
RA Binque C.D., Craig R.W., Swales B.M., Singleton V., Zhou P.,
RA Whyte M.K.B.;
RT "Exon skipping in Mcl-1 results in a Bcl-2 homology domain 3 only gene
RT product that promotes cell death";
RT J. Biol. Chem. 275:22136-22146(2000).

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DR EMBL; Y00689; CAA68685.1; -;
 DR EMBL; X04324; CAA27855.1; -;
 DR PIR; S00103; FADDA.
 DR HSSP; Q01082; 1BKR.
 DR DICTYDB; DP01003; abpa.
 DR Interpro; IPR001589; Actinin_act_bind.
 DR Interpro; IPR001715; Calponin_hom.
 DR Interpro; IPR002048; EF-hand.
 DR Interpro; IPR002017; Spectrin.
 DR Pfam; PF00307; CH; 2.
 DR Pfam; PF00036; ehfand; 2.
 DR Pfam; PF00435; spectrin; 4.
 DR SMART; SM00033; CH; 2.
 DR SMART; SM00054; Eph; 2.
 DR SMART; SM00150; SPEC; 3.
 DR PROSITE; PS00019; ACTININ_1; 1.
 DR PROSITE; PS00020; ACTININ_2; 1.
 DR PROSITE; PS00021; CH; 2.
 DR PROSITE; PS00018; EF_HAND; 2.
 KW Actin-binding; Calcium-binding; Repeat.
 FT DOMAIN 1 240 ACTIN-BINDING.
 FT DOMAIN 22 128 CH 1.
 FT DOMAIN 137 240 CH 2.
 FT REPEAT 241 366 SPECTRIN 1.
 FT REPEAT 367 481 SPECTRIN 2.
 FT REPEAT 482 602 SPECTRIN 3.
 FT REPEAT 603 715 SPECTRIN 4.
 FT CA_BIND 743 754 EF_HAND 1 (BY SIMILARITY).
 FT CA_BIND 779 790 EF_HAND 2 (BY SIMILARITY).
 FT CONFLICT 360 360 T -> P (IN REF. 2).
 FT CONFLICT 501 501 I -> T (IN REF. 2).
 SQ SEQUENCE 862 AA; 97598 MW; 15608ADB71213226 CRC64;

Query Match 34.8%; Score 47; DB 1; Length 862;
 Best Local Similarity 69.2%; Pred. NO. 68;
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 KLSCECLKRIGDEL 19
 : | | | | | | | | | |
 Db 754 EFSSCLKSIGDEL 766

RESULT 15
 YDK9_SCHPO STANDARD: PRT; 1033 AA.
 AC P87115;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Hypothetical 116.5 kDa protein C20G8.09C in chromosome I.
 GN SPAC20G8.09C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 ON NCBI_TaxId=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RA Badcock K., Churcher C.M., Wood V., Barrell B.G., Rajandream M.A.;
 RL Submitted (May-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO YEAST YNL132W AND AN A.AMBISEXUALIS HYPOTHETICAL
 CC PROTEIN (AC P54008).
 CC -----

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DR EMBL; Z95334; CAB08603.1; -;
 DR KW Hypothetical protein; ATP-binding.
 FT NP_BIND 282 289 ATP (POTENTIAL).
 SQ SEQUENCE 1033 AA; 116463 MW; 8432B313DB18E135 CRC64;

Query Match 34.1%; Score 46; DB 1; Length 1033;
 Best Local Similarity 52.4%; Pred. NO. 1,1e+02;
 Matches 11; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 6 KKLSECLKRIGDELDSNMEIQ 26
 : | | | | | | | | | |
 Db 661 KAVKHSIKRIGDEFIENTALQ 681

Search completed: September 20, 2002, 11:04:30
 Job time: 1627 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 20, 2002, 11:03:36 : Search time 172.19 Seconds
(without alignments)
27.126 Million cell updates/sec

Title: US-09-544-664-6
Perfect score: 135
Sequence: 1 QDASTKRLSECLKRIQDELDSNMLQR 27

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SPREMBL_19:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mhcc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protist:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	135	100.0	149	6	Q9GMG7	Q9GMG7 ovis aries
2	135	100.0	164	4	Q9UD06	Q9UD06 homo sapien
3	135	100.0	179	4	Q9NT67	Q9NT67 homo sapien
4	129	95.6	173	11	Q9UKL3	Q9UKL3 ratius norv
5	107	79.3	221	13	Q98U13	Q98U13 xenopus lae
6	83	61.5	192	13	Q919N4	Q919N4 brachydanio
7	66	48.9	15	4	Q9UCZ7	Q9UCZ7 homo sapien
8	54	40.0	1124	12	Q9DWM1	Q9DWM1 pluteella xy
9	53	39.3	913	5	Q94883	Q94883 drosophila
10	53	39.3	1861	5	Q9VF02	Q9VF02 drosophila
11	52	38.5	575	10	Q9SLJ7	Q9SLJ7 arabidopsis
12	51	37.8	427	2	Q30773	Q30773 treponema p
13	51	37.8	480	4	Q96F70	Q96F70 homo sapien
14	51	37.8	845	16	Q83501	Q83501 treponema p
15	51	37.8	885	4	Q96T95	Q96T95 homo sapien
16	51	37.8	1252	5	Q9VTY9	Q9VTY9 drosophila

17	50	37.0	614	5	Q06270	Q06270 omastrephe
18	50	37.0	948	5	Q9VDQ7	Q9VDQ7 drosophila
19	50	37.0	1184	10	Q9LU70	Q9LU70 arabidopsis
20	50	37.0	1219	10	Q9LU84	Q9LU84 arabidopsis
21	49.5	36.7	675	5	Q9YS46	Q9YS46 drosophila
22	49.5	36.7	724	5	Q961W7	Q961W7 drosophila
23	49	36.3	196	10	Q94BU3	Q94BU3 arabidopsis
24	49	36.3	286	5	Q27341	Q27341 trichomegal
25	49	36.3	311	10	Q9LMB2	Q9LMB2 arabidopsis
26	49	36.3	342	10	Q9LMB3	Q9LMB3 arabidopsis
27	49	36.3	527	12	Q9JCP5	Q9JCP5 epizootic h
28	49	36.3	665	4	Q9H9N3	Q9H9N3 homo sapien
29	49	36.3	669	17	Q97U08	Q97U08 sulfolobus
30	49	36.3	718	10	Q9LFI0	Q9LFI0 arabidopsis
31	49	36.3	732	5	Q27480	Q27480 caenorhabdi
32	49	36.3	740	16	Q9PC07	Q9PC07 xylella fas
33	48.5	35.9	213	12	Q91MS6	Q91MS6 lumpy skin
34	48	35.6	126	5	Q95230	Q95230 plasmidium
35	48	35.6	1098	5	Q9VB48	Q9VB48 drosophila
36	48	35.6	1814	5	Q9B1M9	Q9B1M9 toxocara ca
37	48	35.6	1957	5	Q04009	Q04009 brugia mala
38	48	35.6	1957	5	Q04010	Q04010 onchocerca
39	47.5	35.2	164	5	P92198	P92198 branchiosto
40	47.5	35.2	164	5	P90687	P90687 branchiosto
41	47	34.8	72	15	Q9YR06	Q9YR06 human immun
42	47	34.8	92	4	Q9UHR9	Q9UHR9 homo sapien
43	47	34.8	94	4	Q9UHR7	Q9UHR7 homo sapien
44	47	34.8	108	4	Q9UHR8	Q9UHR8 homo sapien
45	47	34.8	217	17	Q58748	Q58748 pyrococcus

ALIGNMENTS

RESULT 1
ID Q9GMG7 PRELIMINARY: PRT: 149 AA.
AC Q9GMG7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE BCL2-ASSOCIATED PROTEIN BAX (FRAGMENT).
GN BAX.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Ovary;
RA Murray J.F., Dong Y.B., Leigh A.J., Scaramuzzi R.J., Carter N.D.;
RT "Bax in the sheep ovary";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF163774; AAP98242.1; -.
DR HSSP: Q07817; IMAZ.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR00712; Bcl_2.
DR Pfam: PF00452; Bcl_2; 1.
DR SMART: SM00337; BCL_1.
DR PROSITE: PSS0062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BHL; 1.
FT NON_TER 1 149
FT NON_TER 149 149
SQ SEQUENCE 149 AA: 16917 MW: ABC10CB5C64FA2D CRC64;

Query Match 100.0%; Score 135; DB 6; Length 149;
Best Local Similarity 100.0%; Pred. No. 2.1e-11;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QDASTKRLSECLKRIQDELDSNMLQR 27
|||||

Db 24 QDASTKLSKRLKRGIDELSDNMELOR 50

RESULT 2

Q9U0D6 PRELIMINARY; PRT; 164 AA.

AC Q9U0D6; 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

DE Bax EPSILON.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.

RC TISSUE=BRIN;

RX MEDLINE=99120940; PubMed=9920818; Shi B., Trlebe D., Kajiji S., Iwata K.K., Bruskin A., Mahajna J.; "Identification and characterization of baxepsilon, a novel bax variant missing the BH2 and the transmembrane domains."

RT Biochem. Biophys. Res. Commun. 254:779-785(1999).

RL EMBL; AF007826; AAD22706.1; -.

DR InterPro: IPR002475; BCL2_family.

DR Pfam: PF00452; BCL-2; 1.

DR SMART: SM00337; BCL; 1.

DR PROSITE: PS50062; BCL2_FAMILY; 1.

DR PROSITE: PS01080; BH1; 1.

DR PROSITE: PS01259; BH3; 1.

SQ SEQUENCE 164 AA; 18129 MW; 12CCDB8073EFA4C9E CRC64;

Query Match Best Local Similarity 100.0%; Score 135; DB 4; Length 164; Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QDASTKLSKRLKRGIDELSDNMELOR 27

Db 52 QDASTKLSKRLKRGIDELSDNMELOR 78

RESULT 3

Q9NYG7 PRELIMINARY; PRT; 179 AA.

AC Q9NYG7; 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE BAX-SIGMA.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.

RX MEDLINE=20237095; PubMed=10772918; Schmitt E., Paquet C., Beauchemin M., Dever-Bertrand J., Bertrand R.; "Characterization of bax-sigma, a cell death-inducing isoform of Bax."

RT Biochem. Biophys. Res. Commun. 270:868-879(2000).

RL EMBL; AF247393; AAF71267.1; -.

DR HSSP: Q07817; IMA2.

DR InterPro: IPR002475; BCL2_family.

DR Pfam: PF00452; BCL-2; 1.

DR SMART: SM00337; BCL; 1.

DR PROSITE: PS50062; BCL2_FAMILY; 1.

DR PROSITE: PS01080; BH1; 1.

DR PROSITE: PS01259; BH3; 1.

SQ SEQUENCE 179 AA; 19718 MW; 5802B0AC73B2E4CE CRC64;

Query Match Best Local Similarity 100.0%; Score 135; DB 4; Length 179; Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QDASTKLSKRLKRGIDELSDNMELOR 27

Db 52 QDASTKLSKRLKRGIDELSDNMELOR 78

RESULT 4

Q9JRL3 PRELIMINARY; PRT; 173 AA.

AC Q9JRL3; 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE BAX PROTEIN SPLICE VARIANT K.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RP SEQUENCE FROM N.A.

RC TISSUE=BRIN;

RX Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

RL EMBL; AF235993; AAF36411.1; -.

DR HSSP: Q07817; IMA2.

DR InterPro: IPR002475; BCL2_family.

DR Pfam: PF00452; BCL-2; 1.

DR SMART: SM00337; BCL; 1.

DR PROSITE: PS50062; BCL2_FAMILY; 1.

DR PROSITE: PS01080; BH1; 1.

DR PROSITE: PS01259; BH2; 1.

SQ SEQUENCE 173 AA; 19661 MW; F19A45BCF642C34F CRC64;

Query Match Best Local Similarity 95.6%; Score 129; DB 11; Length 173; Matches 25; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QDASTKLSKRLKRGIDELSDNMELOR 27

Db 33 QDASTKLSKRLKRGIDELSDNMELOR 59

RESULT 5

Q98U13 PRELIMINARY; PRT; 221 AA.

AC Q98U13; 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE BAX.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodidae; Xenopus.

OX NCBI_TaxID=8355;

RP SEQUENCE FROM N.A.

RX MEDLINE=21107661; PubMed=1158585; Finkelnstein C.V., Lewellyn A.L., Maller J.L.; "The midblastula transition in Xenopus embryos activates multiple pathways to prevent apoptosis in response to DNA damage."

RT Proc. Natl. Acad. Sci. U.S.A. 98:1006-1011(2001).

RL EMBL; AF288809; AAK06406.1; -.

DR HSSP: P53563; IAF3.

DR InterPro: IPR002475; BCL2_family.

DR Pfam: PF00452; BCL-2; 1.

RESULT	7	
ID	Q9UC27	
AC	Q9UC27	PRELIMINARY;
DT	01-MAY-2000 (Tremblrel. 13, Created)	PRT; 15 AA.
DT	01-MAY-2000 (Tremblrel. 13, Last sequence update)	
DT	01-JUN-2000 (Tremblrel. 14, Last annotation update)	
DE	BC12-INTERACTIVE CELL DEATH SUSCEPTIBILITY REGULATOR (FRAGMENT).	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
CC	NCBI_TaxId=9606;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=6071131; PubMed=7475270;	
RA	Meijerink J.P., Smetsers T.F., Sloeljes A.W., Linders E.H.,	
RA	Mensink E.J.;	
RT	*Bax mutations in cell lines derived from hematological	
RT	malignancies.*;	

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RESULT      9
094893
ID 094893      PRELIMINARY;      PRT: 913 AA.
AC 094893:
DT 01-FEB-1997 (TREMBLrel. 02. Created)
DT 01-NOV-1999 (TREMBLrel. 12. Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19. Last annotation update)
DE 89B HELICASE (FRAGMENT).
GN HEL89B OR CG4261.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=96371055; PubMed=8774890;
RA Goldman-Levi R., Miller C., Bogoch J., Zak N.B.;
RT "Expanding the Molt subfamily: 89B helicase encodes a new Drosophila
RT melanogaster SNF-related protein which binds to multiple sites on
RT polytene chromosomes.";
RN Nucleic Acids Res. 24:3121-3128(1996).
RL [2]
SEQUENCE FROM N.A.
RP Goldman-Levi R., Miller C., Bogoch J., Zak N.B.;
RL Submitted (Apr-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL, U45025; AM95091.2; -.
DR FlyBase; FBgn0022787; Hel89B.
DR

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DR InterPro: IPR001410; DEAD.
 DR InterPro: IPR001650; Helicase_C.
 DR InterPro: IPR000330; SNF2_N.
 DR Pfam: PF00271; helicase_C; 1.
 DR Pfam: PF00176; SNF2_N; 1.
 DR SMART: SM00487; DEXDC; 1.
 DR SMART: SM00490; HELIC_C; 1.
 KW ATP-binding; Helicase.
 FT NON_TER
 SQ SEQUENCE 913 AA: 102160 MW: 21E7E51E5559F691 CRC64;

Query Match 39.3%; Score 53; DB 5; Length 913;
 Best Local Similarity 39.1%; Pred. No. 46;
 Matches 9; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 1 QDASTKSLSECLKRIQDELDSNM 23
 Db 602 EDFSNNKHLKDCLOKLGSSSSASM 624

RESULT 10

Q9VFE02 PRELIMINARY; PRT; 1861 AA.

AC Q9VFE02; 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE HEL89B PROTEIN.
 GN HEL89B OR C04261.
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-BERKELEY;

RA MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.C., Mortan J.R., Yandell M.D., Zhang C., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champ M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-D., Andrews-Planckoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

RA Foslter C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodde A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris W.,

RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ileguam C.,

RA Jalali M., Kalish F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Matzel B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusker D.R., Pagle J.M.,

RA Palzerolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Ismos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weisenbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 DR EMBL: AEO03711; AAF55260.1; -
 DR FlyBase: FBgn0022787; Hel89B.
 DR InterPro: IPR001410; DEAD.
 DR InterPro: IPR001650; Helicase_C.
 DR InterPro: IPR000330; SNF2_N.
 DR Pfam: PF00271; helicase_C; 1.
 DR Pfam: PF00176; SNF2_N; 1.
 DR SMART: SM00487; DEXDC; 1.
 DR SMART: SM00490; HELIC_C; 1.
 KW ATP-binding; Helicase.
 SQ SEQUENCE 1861 AA: 206155 MW: B1B3B62188783B6 CRC64;

Query Match 39.3%; Score 53; DB 5; Length 1861;
 Best Local Similarity 39.1%; Pred. No. 98;
 Matches 9; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 1 QDASTKSLSECLKRIQDELDSNM 23
 Db 1550 EDFSNNKHLKDCLOKLGSSSSASM 1572

RESULT 11

Q9SLJ7 PRELIMINARY; PRT; 575 AA.

AC Q9SLJ7; 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE P20D21.19 PROTEIN.
 GN P20D21.19
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-CV. COLUMBIA;

RA Federspiel N.A., Falm C.J., Conway A.B., Conn L., Hansen N.F.,

RA Altati H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P.,

RA Gonzalez A., Kremetska I., Kim C., Lenz C., Li J., Liu S.,

RA Luros S., Schwartz J., Shin P., Toriumi M., Vysotskaia V.S.,

RA Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;

RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AC005287; AAD25617.1; -

DR InterPro: IPR000676; NaH_Exchange.

DR Pfam: PF00959; Na_H_Exchange; 1.

SQ SEQUENCE 575 AA: 64043 MW: 49B2E078070EE3D1 CRC64;

Query Match 38.5%; Score 52; DB 10; Length 575;
 Best Local Similarity 50.0%; Pred. No. 39;
 Matches 10; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 4 STKSLSECLKRIQDELDSNM 23
 Db 508 STCKMLEALVGVDDDDDDSM 527

RESULT 12

Q30773 PRELIMINARY; PRT; 427 AA.

AC Q30773; 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE MCP-2.
 GN MCP-2.

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